

(19) World Intellectual Property Organization
International Bureau(43) International Publication Date
20 September 2001 (20.09.2001)

PCT

(10) International Publication Number
WO 01/68848 A2

- (51) International Patent Classification⁷: C12N 15/12, 15/62, C07K 14/47, 14/705, 16/18, G01N 33/53, C12Q 1/68
- (21) International Application Number: PCT/US01/06520
- (22) International Filing Date: 28 February 2001 (28.02.2001)
- (25) Filing Language: English
- (26) Publication Language: English
- (30) Priority Data:
- | | | |
|----------------|-----------------------------|----|
| PCT/US00/05601 | 1 March 2000 (01.03.2000) | US |
| PCT/US00/05841 | 2 March 2000 (02.03.2000) | US |
| 60/187,202 | 3 March 2000 (03.03.2000) | US |
| 60/186,968 | 6 March 2000 (06.03.2000) | US |
| 60/189,328 | 14 March 2000 (14.03.2000) | US |
| 60/189,320 | 14 March 2000 (14.03.2000) | US |
| PCT/US00/06884 | 15 March 2000 (15.03.2000) | US |
| 60/191,048 | 21 March 2000 (21.03.2000) | US |
| 60/190,828 | 21 March 2000 (21.03.2000) | US |
| 60/191,314 | 21 March 2000 (21.03.2000) | US |
| 60/191,007 | 21 March 2000 (21.03.2000) | US |
| 60/192,655 | 28 March 2000 (28.03.2000) | US |
| 60/193,032 | 29 March 2000 (29.03.2000) | US |
| 60/193,053 | 29 March 2000 (29.03.2000) | US |
| PCT/US00/08439 | 30 March 2000 (30.03.2000) | US |
| 60/194,647 | 4 April 2000 (04.04.2000) | US |
| 60/194,449 | 4 April 2000 (04.04.2000) | US |
| 60/196,820 | 11 April 2000 (11.04.2000) | US |
| 60/195,975 | 11 April 2000 (11.04.2000) | US |
| 60/196,000 | 11 April 2000 (11.04.2000) | US |
| 60/196,187 | 11 April 2000 (11.04.2000) | US |
| 60/196,690 | 11 April 2000 (11.04.2000) | US |
| 60/198,121 | 18 April 2000 (18.04.2000) | US |
| 60/198,585 | 18 April 2000 (18.04.2000) | US |
| 60/199,654 | 25 April 2000 (25.04.2000) | US |
| 60/199,397 | 25 April 2000 (25.04.2000) | US |
| 60/199,550 | 25 April 2000 (25.04.2000) | US |
| 60/201,516 | 3 May 2000 (03.05.2000) | US |
| PCT/US00/13705 | 17 May 2000 (17.05.2000) | US |
| PCT/US00/14042 | 22 May 2000 (22.05.2000) | US |
| PCT/US00/14941 | 30 May 2000 (30.05.2000) | US |
| PCT/US00/15264 | 2 June 2000 (02.06.2000) | US |
| 60/209,832 | 5 June 2000 (05.06.2000) | US |
| PCT/US00/20710 | 28 July 2000 (28.07.2000) | US |
| 09/644,848 | 22 August 2000 (22.08.2000) | US |
| PCT/US00/23328 | 24 August 2000 (24.08.2000) | US |
- (71) Applicant (for all designated States except US): GENENTECH, INC. [US/US]; 1 DNA Way, South San Francisco, CA 94080-4990 (US).
- (72) Inventors; and
- (75) Inventors/Applicants (for US only): BAKER, Kevin, P. [GB/US]; 14006 Indian Run Drive, Darnestown, MD 20878 (US). CHEN, Jian [CN/US]; 121 York Drive, Princeton, NJ 08540 (US). DESNOYERS, Luc [CA/US]; 2050 Stockton Street, San Francisco, CA 94133 (US). GODDARD, Audrey [CA/US]; 110 Congo Street, San Francisco, CA 94131 (US). GODOWSKI, Paul, J. [US/US]; 2627 Easton Drive, Burlingame, CA 94010 (US). GURNEY, Austin, L. [US/US]; 1 Debbie Lane, Belmont, CA 94002 (US). PAN, James [CA/US]; 2705 Coronet Boulevard, Belmont, CA 94002 (US). SMITH, Victoria [AU/US]; 19 Dwight Road, Burlingame, CA 94010 (US). WATANABE, Colin, K. [US/US]; 128 Corliss Drive, Moraga, CA 94556 (US). WOOD, William, I. [US/US]; 35 Southdown Court, Hillsborough, CA 94010 (US). ZHANG, Zemin [CN/US]; 876 Taurus Drive, Foster City, CA 94404 (US).
- (74) Agents: BARNES, Elizabeth, M. et al.; c/o Genentech, Inc., MS49, 1 DNA Way, South San Francisco, CA 94080-4990 (US).
- (81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.
- (84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

[Continued on next page]

(54) Title: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

(57) Abstract: The present invention is directed to novel polypeptides and to nucleic acid molecules encoding those polypeptides. Also provided herein are vectors and host cells comprising those nucleic acid sequences, chimeric polypeptide molecules comprising the polypeptides of the present invention fused to heterologous polypeptide sequences, antibodies which bind to the polypeptides of the present invention and to methods for producing the polypeptides of the present invention.

WO 01/68848 A2

WO 01/68848 A2



Published:

— without international search report and to be republished
upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

FIELD OF THE INVENTION

5 The present invention relates generally to the identification and isolation of novel DNA and to the recombinant production of novel polypeptides.

BACKGROUND OF THE INVENTION

10 Extracellular proteins play important roles in, among other things, the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells, e.g., proliferation, migration, differentiation, or interaction with other cells, is typically governed by information received from other cells and/or the immediate environment. This information is often transmitted by secreted polypeptides (for instance, mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides, and hormones) which are, in turn, received and interpreted by diverse cell receptors or membrane-bound proteins. These secreted polypeptides or signaling molecules normally pass through the cellular secretory pathway to reach their site of
15 action in the extracellular environment.

Secreted proteins have various industrial applications, including as pharmaceuticals, diagnostics, biosensors and bioreactors. Most protein drugs available at present, such as thrombolytic agents, interferons, interleukins, erythropoietins, colony stimulating factors, and various other cytokines, are secretory proteins. Their receptors, which are membrane proteins, also have potential as therapeutic or diagnostic agents. Efforts
20 are being undertaken by both industry and academia to identify new, native secreted proteins. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel secreted proteins. Examples of screening methods and techniques are described in the literature [see, for example, Klein et al., *Proc. Natl. Acad. Sci.* 93:7108-7113 (1996); U.S. Patent No. 5,536,637].

Membrane-bound proteins and receptors can play important roles in, among other things, the formation,
25 differentiation and maintenance of multicellular organisms. The fate of many individual cells, e.g., proliferation, migration, differentiation, or interaction with other cells, is typically governed by information received from other cells and/or the immediate environment. This information is often transmitted by secreted polypeptides (for instance, mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides, and hormones) which are, in turn, received and interpreted by diverse cell receptors or membrane-bound proteins.
30 Such membrane-bound proteins and cell receptors include, but are not limited to, cytokine receptors, receptor kinases, receptor phosphatases, receptors involved in cell-cell interactions, and cellular adhesion molecules like selectins and integrins. For instance, transduction of signals that regulate cell growth and differentiation is regulated in part by phosphorylation of various cellular proteins. Protein tyrosine kinases, enzymes that catalyze that process, can also act as growth factor receptors. Examples include fibroblast growth factor receptor and

nerve growth factor receptor.

Membrane-bound proteins and receptor molecules have various industrial applications, including as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be employed as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction.

5 Efforts are being undertaken by both industry and academia to identify new, native receptor or membrane-bound proteins. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel receptor or membrane-bound proteins.

SUMMARY OF THE INVENTION

10 In one embodiment, the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence that encodes a PRO polypeptide.

15 In one aspect, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule encoding a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

25 In other aspects, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94%

nucleic acid sequence identity, alternatively at least about 95 % nucleic acid sequence identity, alternatively at least about 96 % nucleic acid sequence identity, alternatively at least about 97 % nucleic acid sequence identity, alternatively at least about 98 % nucleic acid sequence identity and alternatively at least about 99 % nucleic acid sequence identity to (a) a DNA molecule comprising the coding sequence of a full-length PRO polypeptide cDNA as disclosed herein, the coding sequence of a PRO polypeptide lacking the signal peptide as disclosed herein, the coding sequence of an extracellular domain of a transmembrane PRO polypeptide, with or without the signal peptide, as disclosed herein or the coding sequence of any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

In a further aspect, the invention concerns an isolated nucleic acid molecule comprising a nucleotide sequence having at least about 80 % nucleic acid sequence identity, alternatively at least about 81 % nucleic acid sequence identity, alternatively at least about 82 % nucleic acid sequence identity, alternatively at least about 83 % nucleic acid sequence identity, alternatively at least about 84 % nucleic acid sequence identity, alternatively at least about 85 % nucleic acid sequence identity, alternatively at least about 86 % nucleic acid sequence identity, alternatively at least about 87 % nucleic acid sequence identity, alternatively at least about 88 % nucleic acid sequence identity, alternatively at least about 89 % nucleic acid sequence identity, alternatively at least about 90 % nucleic acid sequence identity, alternatively at least about 91 % nucleic acid sequence identity, alternatively at least about 92 % nucleic acid sequence identity, alternatively at least about 93 % nucleic acid sequence identity, alternatively at least about 94 % nucleic acid sequence identity, alternatively at least about 95 % nucleic acid sequence identity, alternatively at least about 96 % nucleic acid sequence identity, alternatively at least about 97 % nucleic acid sequence identity, alternatively at least about 98 % nucleic acid sequence identity and alternatively at least about 99 % nucleic acid sequence identity to (a) a DNA molecule that encodes the same mature polypeptide encoded by any of the human protein cDNAs deposited with the ATCC as disclosed herein, or (b) the complement of the DNA molecule of (a).

Another aspect the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence encoding a PRO polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated, or is complementary to such encoding nucleotide sequence, wherein the transmembrane domain(s) of such polypeptide are disclosed herein. Therefore, soluble extracellular domains of the herein described PRO polypeptides are contemplated.

Another embodiment is directed to fragments of a PRO polypeptide coding sequence, or the complement thereof, that may find use as, for example, hybridization probes, for encoding fragments of a PRO polypeptide that may optionally encode a polypeptide comprising a binding site for an anti-PRO antibody or as antisense oligonucleotide probes. Such nucleic acid fragments are usually at least about 10 nucleotides in length, alternatively at least about 15 nucleotides in length, alternatively at least about 20 nucleotides in length, alternatively at least about 30 nucleotides in length, alternatively at least about 40 nucleotides in length, alternatively at least about 50 nucleotides in length, alternatively at least about 60 nucleotides in length, alternatively at least about 70 nucleotides in length, alternatively at least about 80 nucleotides in length, alternatively at least about 90 nucleotides in length, alternatively at least about 100 nucleotides in length, alternatively at least about 110 nucleotides in length, alternatively at least about 120 nucleotides in length,

alternatively at least about 130 nucleotides in length, alternatively at least about 140 nucleotides in length, alternatively at least about 150 nucleotides in length, alternatively at least about 160 nucleotides in length, alternatively at least about 170 nucleotides in length, alternatively at least about 180 nucleotides in length, alternatively at least about 190 nucleotides in length, alternatively at least about 200 nucleotides in length, alternatively at least about 250 nucleotides in length, alternatively at least about 300 nucleotides in length, alternatively at least about 350 nucleotides in length, alternatively at least about 400 nucleotides in length, alternatively at least about 450 nucleotides in length, alternatively at least about 500 nucleotides in length, alternatively at least about 600 nucleotides in length, alternatively at least about 700 nucleotides in length, alternatively at least about 800 nucleotides in length, alternatively at least about 900 nucleotides in length and alternatively at least about 1000 nucleotides in length, wherein in this context the term "about" means the referenced nucleotide sequence length plus or minus 10% of that referenced length. It is noted that novel fragments of a PRO polypeptide-encoding nucleotide sequence may be determined in a routine manner by aligning the PRO polypeptide-encoding nucleotide sequence with other known nucleotide sequences using any of a number of well known sequence alignment programs and determining which PRO polypeptide-encoding nucleotide sequence fragment(s) are novel. All of such PRO polypeptide-encoding nucleotide sequences are contemplated herein. Also contemplated are the PRO polypeptide fragments encoded by these nucleotide molecule fragments, preferably those PRO polypeptide fragments that comprise a binding site for an anti-PRO antibody.

In another embodiment, the invention provides isolated PRO polypeptide encoded by any of the isolated nucleic acid sequences hereinabove identified.

In a certain aspect, the invention concerns an isolated PRO polypeptide, comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein.

In a further aspect, the invention concerns an isolated PRO polypeptide comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83%

amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to an amino acid sequence encoded by any of the human protein cDNAs deposited with the ATCC as disclosed herein.

In a specific aspect, the invention provides an isolated PRO polypeptide without the N-terminal signal sequence and/or the initiating methionine and is encoded by a nucleotide sequence that encodes such an amino acid sequence as hereinbefore described. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture.

Another aspect the invention provides an isolated PRO polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture.

In yet another embodiment, the invention concerns agonists and antagonists of a native PRO polypeptide as defined herein. In a particular embodiment, the agonist or antagonist is an anti-PRO antibody or a small molecule.

In a further embodiment, the invention concerns a method of identifying agonists or antagonists to a PRO polypeptide which comprise contacting the PRO polypeptide with a candidate molecule and monitoring a biological activity mediated by said PRO polypeptide. Preferably, the PRO polypeptide is a native PRO polypeptide.

In a still further embodiment, the invention concerns a composition of matter comprising a PRO polypeptide, or an agonist or antagonist of a PRO polypeptide as herein described, or an anti-PRO antibody, in combination with a carrier. Optionally, the carrier is a pharmaceutically acceptable carrier.

Another embodiment of the present invention is directed to the use of a PRO polypeptide, or an agonist or antagonist thereof as hereinbefore described, or an anti-PRO antibody, for the preparation of a medicament useful in the treatment of a condition which is responsive to the PRO polypeptide, an agonist or antagonist thereof or an anti-PRO antibody.

In other embodiments of the present invention, the invention provides vectors comprising DNA encoding any of the herein described polypeptides. Host cell comprising any such vector are also provided. By way of example, the host cells may be CHO cells, *E. coli*, or yeast. A process for producing any of the herein described

polypeptides is further provided and comprises culturing host cells under conditions suitable for expression of the desired polypeptide and recovering the desired polypeptide from the cell culture.

In other embodiments, the invention provides chimeric molecules comprising any of the herein described polypeptides fused to a heterologous polypeptide or amino acid sequence. Example of such chimeric molecules comprise any of the herein described polypeptides fused to an epitope tag sequence or a Fc region of an immunoglobulin.

In another embodiment, the invention provides an antibody which binds, preferably specifically, to any of the above or below described polypeptides. Optionally, the antibody is a monoclonal antibody, humanized antibody, antibody fragment or single-chain antibody.

In yet other embodiments, the invention provides oligonucleotide probes which may be useful for isolating genomic and cDNA nucleotide sequences, measuring or detecting expression of an associated gene or as antisense probes, wherein those probes may be derived from any of the above or below described nucleotide sequences. Preferred probe lengths are described above.

In yet other embodiments, the present invention is directed to methods of using the PRO polypeptides of the present invention for a variety of uses based upon the functional biological assay data presented in the Examples below.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows a nucleotide sequence (SEQ ID NO:1) of a native sequence PRO276 cDNA, wherein SEQ ID NO:1 is a clone designated herein as "DNA16435-1208".

Figure 2 shows the amino acid sequence (SEQ ID NO:2) derived from the coding sequence of SEQ ID NO:1 shown in Figure 1.

Figure 3 shows a nucleotide sequence (SEQ ID NO:3) of a native sequence PRO284 cDNA, wherein SEQ ID NO:3 is a clone designated herein as "DNA23318-1211".

Figure 4 shows the amino acid sequence (SEQ ID NO:4) derived from the coding sequence of SEQ ID NO:3 shown in Figure 3.

Figure 5 shows a nucleotide sequence (SEQ ID NO:5) of a native sequence PRO193 cDNA, wherein SEQ ID NO:5 is a clone designated herein as "DNA23322-1393".

Figure 6 shows the amino acid sequence (SEQ ID NO:6) derived from the coding sequence of SEQ ID NO:5 shown in Figure 5.

Figure 7 shows a nucleotide sequence (SEQ ID NO:7) of a native sequence PRO190 cDNA, wherein SEQ ID NO:7 is a clone designated herein as "DNA23334-1392".

Figure 8 shows the amino acid sequence (SEQ ID NO:8) derived from the coding sequence of SEQ ID NO:7 shown in Figure 7.

Figure 9 shows a nucleotide sequence (SEQ ID NO:9) of a native sequence PRO180 cDNA, wherein SEQ ID NO:9 is a clone designated herein as "DNA26843-1389".

Figure 10 shows the amino acid sequence (SEQ ID NO:10) derived from the coding sequence of SEQ ID NO:9 shown in Figure 9.

Figure 11 shows a nucleotide sequence (SEQ ID NO:11) of a native sequence PRO194 cDNA, wherein SEQ ID NO:11 is a clone designated herein as "DNA26844-1394".

Figure 12 shows the amino acid sequence (SEQ ID NO:12) derived from the coding sequence of SEQ ID NO:11 shown in Figure 11.

5 Figure 13 shows a nucleotide sequence (SEQ ID NO:13) of a native sequence PRO218 cDNA, wherein SEQ ID NO:13 is a clone designated herein as "DNA30867-1335".

Figure 14 shows the amino acid sequence (SEQ ID NO:14) derived from the coding sequence of SEQ ID NO:13 shown in Figure 13.

Figure 15 shows a nucleotide sequence (SEQ ID NO:15) of a native sequence PRO260 cDNA, wherein SEQ ID NO:15 is a clone designated herein as "DNA33470-1175".

10 Figure 16 shows the amino acid sequence (SEQ ID NO:16) derived from the coding sequence of SEQ ID NO:15 shown in Figure 15.

Figure 17 shows a nucleotide sequence (SEQ ID NO:17) of a native sequence PRO233 cDNA, wherein SEQ ID NO:17 is a clone designated herein as "DNA34436-1238".

15 Figure 18 shows the amino acid sequence (SEQ ID NO:18) derived from the coding sequence of SEQ ID NO:17 shown in Figure 17.

Figure 19 shows a nucleotide sequence (SEQ ID NO:19) of a native sequence PRO234 cDNA, wherein SEQ ID NO:19 is a clone designated herein as "DNA35557-1137".

Figure 20 shows the amino acid sequence (SEQ ID NO:20) derived from the coding sequence of SEQ ID NO:19 shown in Figure 19.

20 Figure 21 shows a nucleotide sequence (SEQ ID NO:21) of a native sequence PRO236 cDNA, wherein SEQ ID NO:21 is a clone designated herein as "DNA35599-1168".

Figure 22 shows the amino acid sequence (SEQ ID NO:22) derived from the coding sequence of SEQ ID NO:21 shown in Figure 21.

25 Figure 23 shows a nucleotide sequence (SEQ ID NO:23) of a native sequence PRO244 cDNA, wherein SEQ ID NO:23 is a clone designated herein as "DNA35668-1171".

Figure 24 shows the amino acid sequence (SEQ ID NO:24) derived from the coding sequence of SEQ ID NO:23 shown in Figure 23.

Figure 25 shows a nucleotide sequence (SEQ ID NO:25) of a native sequence PRO262 cDNA, wherein SEQ ID NO:25 is a clone designated herein as "DNA36992-1168".

30 Figure 26 shows the amino acid sequence (SEQ ID NO:26) derived from the coding sequence of SEQ ID NO:25 shown in Figure 25.

Figure 27 shows a nucleotide sequence (SEQ ID NO:27) of a native sequence PRO271 cDNA, wherein SEQ ID NO:27 is a clone designated herein as "DNA39423-1182".

35 Figure 28 shows the amino acid sequence (SEQ ID NO:28) derived from the coding sequence of SEQ ID NO:27 shown in Figure 27.

Figure 29 shows a nucleotide sequence (SEQ ID NO:29) of a native sequence PRO268 cDNA, wherein SEQ ID NO:29 is a clone designated herein as "DNA39427-1179".

Figure 30 shows the amino acid sequence (SEQ ID NO:30) derived from the coding sequence of SEQ ID NO:29 shown in Figure 29.

Figure 31 shows a nucleotide sequence (SEQ ID NO:31) of a native sequence PRO270 cDNA, wherein SEQ ID NO:31 is a clone designated herein as "DNA39510-1181".

5 Figure 32 shows the amino acid sequence (SEQ ID NO:32) derived from the coding sequence of SEQ ID NO:31 shown in Figure 31.

Figure 33 shows a nucleotide sequence (SEQ ID NO:33) of a native sequence PRO355 cDNA, wherein SEQ ID NO:33 is a clone designated herein as "DNA39518-1247".

Figure 34 shows the amino acid sequence (SEQ ID NO:34) derived from the coding sequence of SEQ ID NO:33 shown in Figure 33.

10 Figure 35 shows a nucleotide sequence (SEQ ID NO:35) of a native sequence PRO298 cDNA, wherein SEQ ID NO:35 is a clone designated herein as "DNA39975-1210".

Figure 36 shows the amino acid sequence (SEQ ID NO:36) derived from the coding sequence of SEQ ID NO:35 shown in Figure 35.

15 Figure 37 shows a nucleotide sequence (SEQ ID NO:37) of a native sequence PRO299 cDNA, wherein SEQ ID NO:37 is a clone designated herein as "DNA39976-1215".

Figure 38 shows the amino acid sequence (SEQ ID NO:38) derived from the coding sequence of SEQ ID NO:37 shown in Figure 37.

Figure 39 shows a nucleotide sequence (SEQ ID NO:39) of a native sequence PRO296 cDNA, wherein SEQ ID NO:39 is a clone designated herein as "DNA39979-1213".

20 Figure 40 shows the amino acid sequence (SEQ ID NO:40) derived from the coding sequence of SEQ ID NO:39 shown in Figure 39.

Figure 41 shows a nucleotide sequence (SEQ ID NO:41) of a native sequence PRO329 cDNA, wherein SEQ ID NO:41 is a clone designated herein as "DNA40594-1233".

25 Figure 42 shows the amino acid sequence (SEQ ID NO:42) derived from the coding sequence of SEQ ID NO:41 shown in Figure 41.

Figure 43 shows a nucleotide sequence (SEQ ID NO:43) of a native sequence PRO330 cDNA, wherein SEQ ID NO:43 is a clone designated herein as "DNA40603-1232".

Figure 44 shows the amino acid sequence (SEQ ID NO:44) derived from the coding sequence of SEQ ID NO:43 shown in Figure 43.

30 Figure 45 shows a nucleotide sequence (SEQ ID NO:45) of a native sequence PRO294 cDNA, wherein SEQ ID NO:45 is a clone designated herein as "DNA40604-1187".

Figure 46 shows the amino acid sequence (SEQ ID NO:46) derived from the coding sequence of SEQ ID NO:45 shown in Figure 45.

35 Figure 47 shows a nucleotide sequence (SEQ ID NO:47) of a native sequence PRO300 cDNA, wherein SEQ ID NO:47 is a clone designated herein as "DNA40625-1189".

Figure 48 shows the amino acid sequence (SEQ ID NO:48) derived from the coding sequence of SEQ ID NO:47 shown in Figure 47.

Figure 49 shows a nucleotide sequence (SEQ ID NO:49) of a native sequence PRO307 cDNA, wherein SEQ ID NO:49 is a clone designated herein as "DNA41225-1217".

Figure 50 shows the amino acid sequence (SEQ ID NO:50) derived from the coding sequence of SEQ ID NO:49 shown in Figure 49.

5 Figure 51 shows a nucleotide sequence (SEQ ID NO:51) of a native sequence PRO334 cDNA, wherein SEQ ID NO:51 is a clone designated herein as "DNA41379-1236".

Figure 52 shows the amino acid sequence (SEQ ID NO:52) derived from the coding sequence of SEQ ID NO:51 shown in Figure 51.

Figure 53 shows a nucleotide sequence (SEQ ID NO:53) of a native sequence PRO352 cDNA, wherein SEQ ID NO:53 is a clone designated herein as "DNA41386-1316".

10 Figure 54 shows the amino acid sequence (SEQ ID NO:54) derived from the coding sequence of SEQ ID NO:53 shown in Figure 53.

Figure 55 shows a nucleotide sequence (SEQ ID NO:55) of a native sequence PRO710 cDNA, wherein SEQ ID NO:55 is a clone designated herein as "DNA44161-1434".

15 Figure 56 shows the amino acid sequence (SEQ ID NO:56) derived from the coding sequence of SEQ ID NO:55 shown in Figure 55.

Figure 57 shows a nucleotide sequence (SEQ ID NO:57) of a native sequence PRO873 cDNA, wherein SEQ ID NO:57 is a clone designated herein as "DNA44179-1362".

Figure 58 shows the amino acid sequence (SEQ ID NO:58) derived from the coding sequence of SEQ ID NO:57 shown in Figure 57.

20 Figure 59 shows a nucleotide sequence (SEQ ID NO:59) of a native sequence PRO354 cDNA, wherein SEQ ID NO:59 is a clone designated herein as "DNA44192-1246".

Figure 60 shows the amino acid sequence (SEQ ID NO:60) derived from the coding sequence of SEQ ID NO:59 shown in Figure 59.

25 Figure 61 shows a nucleotide sequence (SEQ ID NO:61) of a native sequence PRO1151 cDNA, wherein SEQ ID NO:61 is a clone designated herein as "DNA44694-1500".

Figure 62 shows the amino acid sequence (SEQ ID NO:62) derived from the coding sequence of SEQ ID NO:61 shown in Figure 61.

Figure 63 shows a nucleotide sequence (SEQ ID NO:63) of a native sequence PRO382 cDNA, wherein SEQ ID NO:63 is a clone designated herein as "DNA45234-1277".

30 Figure 64 shows the amino acid sequence (SEQ ID NO:64) derived from the coding sequence of SEQ ID NO:63 shown in Figure 63.

Figure 65 shows a nucleotide sequence (SEQ ID NO:65) of a native sequence PRO1864 cDNA, wherein SEQ ID NO:65 is a clone designated herein as "DNA45409-2511".

35 Figure 66 shows the amino acid sequence (SEQ ID NO:66) derived from the coding sequence of SEQ ID NO:65 shown in Figure 65.

Figure 67 shows a nucleotide sequence (SEQ ID NO:67) of a native sequence PRO386 cDNA, wherein SEQ ID NO:67 is a clone designated herein as "DNA45415-1318".

Figure 68 shows the amino acid sequence (SEQ ID NO:68) derived from the coding sequence of SEQ ID NO:67 shown in Figure 67.

Figure 69 shows a nucleotide sequence (SEQ ID NO:69) of a native sequence PRO541 cDNA, wherein SEQ ID NO:69 is a clone designated herein as "DNA45417-1432".

5 Figure 70 shows the amino acid sequence (SEQ ID NO:70) derived from the coding sequence of SEQ ID NO:69 shown in Figure 69.

Figure 71 shows a nucleotide sequence (SEQ ID NO:71) of a native sequence PRO852 cDNA, wherein SEQ ID NO:71 is a clone designated herein as "DNA45493-1349".

Figure 72 shows the amino acid sequence (SEQ ID NO:72) derived from the coding sequence of SEQ ID NO:71 shown in Figure 71.

10 Figure 73 shows a nucleotide sequence (SEQ ID NO:73) of a native sequence PRO700 cDNA, wherein SEQ ID NO:73 is a clone designated herein as "DNA46776-1284".

Figure 74 shows the amino acid sequence (SEQ ID NO:74) derived from the coding sequence of SEQ ID NO:73 shown in Figure 73.

15 Figures 75A-75B show a nucleotide sequence (SEQ ID NO:75) of a native sequence PRO708 cDNA, wherein SEQ ID NO:75 is a clone designated herein as "DNA48296-1292".

Figure 76 shows the amino acid sequence (SEQ ID NO:76) derived from the coding sequence of SEQ ID NO:75 shown in Figures 75A-75B.

Figure 77 shows a nucleotide sequence (SEQ ID NO:77) of a native sequence PRO707 cDNA, wherein SEQ ID NO:77 is a clone designated herein as "DNA48306-1291".

20 Figure 78 shows the amino acid sequence (SEQ ID NO:78) derived from the coding sequence of SEQ ID NO:77 shown in Figure 77.

Figure 79 shows a nucleotide sequence (SEQ ID NO:79) of a native sequence PRO864 cDNA, wherein SEQ ID NO:79 is a clone designated herein as "DNA48328-1355".

25 Figure 80 shows the amino acid sequence (SEQ ID NO:80) derived from the coding sequence of SEQ ID NO:79 shown in Figure 79.

Figure 81 shows a nucleotide sequence (SEQ ID NO:81) of a native sequence PRO706 cDNA, wherein SEQ ID NO:81 is a clone designated herein as "DNA48329-1290".

Figure 82 shows the amino acid sequence (SEQ ID NO:82) derived from the coding sequence of SEQ ID NO:81 shown in Figure 81.

30 Figure 83 shows a nucleotide sequence (SEQ ID NO:83) of a native sequence PRO732 cDNA, wherein SEQ ID NO:83 is a clone designated herein as "DNA48334-1435".

Figure 84 shows the amino acid sequence (SEQ ID NO:84) derived from the coding sequence of SEQ ID NO:83 shown in Figure 83.

35 Figure 85 shows a nucleotide sequence (SEQ ID NO:85) of a native sequence PRO537 cDNA, wherein SEQ ID NO:85 is a clone designated herein as "DNA49141-1431".

Figure 86 shows the amino acid sequence (SEQ ID NO:86) derived from the coding sequence of SEQ ID NO:85 shown in Figure 85.

Figure 87 shows a nucleotide sequence (SEQ ID NO:87) of a native sequence PRO545 cDNA, wherein SEQ ID NO:87 is a clone designated herein as "DNA49624-1279".

Figure 88 shows the amino acid sequence (SEQ ID NO:88) derived from the coding sequence of SEQ ID NO:87 shown in Figure 87.

5 Figure 89 shows a nucleotide sequence (SEQ ID NO:89) of a native sequence PRO718 cDNA, wherein SEQ ID NO:89 is a clone designated herein as "DNA49647-1398".

Figure 90 shows the amino acid sequence (SEQ ID NO:90) derived from the coding sequence of SEQ ID NO:89 shown in Figure 89.

Figure 91 shows a nucleotide sequence (SEQ ID NO:91) of a native sequence PRO872 cDNA, wherein SEQ ID NO:91 is a clone designated herein as "DNA49819-1439".

10 Figure 92 shows the amino acid sequence (SEQ ID NO:92) derived from the coding sequence of SEQ ID NO:91 shown in Figure 91.

Figure 93 shows a nucleotide sequence (SEQ ID NO:93) of a native sequence PRO704 cDNA, wherein SEQ ID NO:93 is a clone designated herein as "DNA50911-1288".

15 Figure 94 shows the amino acid sequence (SEQ ID NO:94) derived from the coding sequence of SEQ ID NO:93 shown in Figure 93.

Figure 95 shows a nucleotide sequence (SEQ ID NO:95) of a native sequence PRO705 cDNA, wherein SEQ ID NO:95 is a clone designated herein as "DNA50914-1289".

Figure 96 shows the amino acid sequence (SEQ ID NO:96) derived from the coding sequence of SEQ ID NO:95 shown in Figure 95.

20 Figure 97 shows a nucleotide sequence (SEQ ID NO:97) of a native sequence PRO871 cDNA, wherein SEQ ID NO:97 is a clone designated herein as "DNA50919-1361".

Figure 98 shows the amino acid sequence (SEQ ID NO:98) derived from the coding sequence of SEQ ID NO:97 shown in Figure 97.

25 Figure 99 shows a nucleotide sequence (SEQ ID NO:99) of a native sequence PRO702 cDNA, wherein SEQ ID NO:99 is a clone designated herein as "DNA50980-1286".

Figure 100 shows the amino acid sequence (SEQ ID NO:100) derived from the coding sequence of SEQ ID NO:99 shown in Figure 99.

Figure 101 shows a nucleotide sequence (SEQ ID NO:101) of a native sequence PRO944 cDNA, wherein SEQ ID NO:101 is a clone designated herein as "DNA52185-1370".

30 Figure 102 shows the amino acid sequence (SEQ ID NO:102) derived from the coding sequence of SEQ ID NO:101 shown in Figure 101.

Figure 103 shows a nucleotide sequence (SEQ ID NO:103) of a native sequence PRO739 cDNA, wherein SEQ ID NO:103 is a clone designated herein as "DNA52756".

35 Figure 104 shows the amino acid sequence (SEQ ID NO:104) derived from the coding sequence of SEQ ID NO:103 shown in Figure 103.

Figure 105 shows a nucleotide sequence (SEQ ID NO:105) of a native sequence PRO941 cDNA, wherein SEQ ID NO:105 is a clone designated herein as "DNA53906-1368".

Figure 106 shows the amino acid sequence (SEQ ID NO:106) derived from the coding sequence of SEQ ID NO:105 shown in Figure 105.

Figure 107 shows a nucleotide sequence (SEQ ID NO:107) of a native sequence PRO1082 cDNA, wherein SEQ ID NO:107 is a clone designated herein as "DNA53912-1457".

5 Figure 108 shows the amino acid sequence (SEQ ID NO:108) derived from the coding sequence of SEQ ID NO:107 shown in Figure 107.

Figure 109 shows a nucleotide sequence (SEQ ID NO:109) of a native sequence PRO1133 cDNA, wherein SEQ ID NO:109 is a clone designated herein as "DNA53913-1490".

Figure 110 shows the amino acid sequence (SEQ ID NO:110) derived from the coding sequence of SEQ ID NO:109 shown in Figure 109.

10 Figure 111 shows a nucleotide sequence (SEQ ID NO:111) of a native sequence PRO983 cDNA, wherein SEQ ID NO:111 is a clone designated herein as "DNA53977-1371".

Figure 112 shows the amino acid sequence (SEQ ID NO:112) derived from the coding sequence of SEQ ID NO:111 shown in Figure 111.

15 Figure 113 shows a nucleotide sequence (SEQ ID NO:113) of a native sequence PRO784 cDNA, wherein SEQ ID NO:113 is a clone designated herein as "DNA53978-1443".

Figure 114 shows the amino acid sequence (SEQ ID NO:114) derived from the coding sequence of SEQ ID NO:113 shown in Figure 113.

Figure 115 shows a nucleotide sequence (SEQ ID NO:115) of a native sequence PRO783 cDNA, wherein SEQ ID NO:115 is a clone designated herein as "DNA53996-1442".

20 Figure 116 shows the amino acid sequence (SEQ ID NO:116) derived from the coding sequence of SEQ ID NO:115 shown in Figure 115.

Figure 117 shows a nucleotide sequence (SEQ ID NO:117) of a native sequence PRO940 cDNA, wherein SEQ ID NO:117 is a clone designated herein as "DNA54002-1367".

25 Figure 118 shows the amino acid sequence (SEQ ID NO:118) derived from the coding sequence of SEQ ID NO:117 shown in Figure 117.

Figure 119 shows a nucleotide sequence (SEQ ID NO:119) of a native sequence PRO768 cDNA, wherein SEQ ID NO:119 is a clone designated herein as "DNA55737-1345".

Figure 120 shows the amino acid sequence (SEQ ID NO:120) derived from the coding sequence of SEQ ID NO:119 shown in Figure 119.

30 Figure 121 shows a nucleotide sequence (SEQ ID NO:121) of a native sequence PRO1079 cDNA, wherein SEQ ID NO:121 is a clone designated herein as "DNA56050-1455".

Figure 122 shows the amino acid sequence (SEQ ID NO:122) derived from the coding sequence of SEQ ID NO:121 shown in Figure 121.

35 Figure 123 shows a nucleotide sequence (SEQ ID NO:123) of a native sequence PRO1078 cDNA, wherein SEQ ID NO:123 is a clone designated herein as "DNA56052-1454".

Figure 124 shows the amino acid sequence (SEQ ID NO:124) derived from the coding sequence of SEQ ID NO:123 shown in Figure 123.

Figure 125 shows a nucleotide sequence (SEQ ID NO:125) of a native sequence PRO1018 cDNA, wherein SEQ ID NO:125 is a clone designated herein as "DNA56107-1415".

Figure 126 shows the amino acid sequence (SEQ ID NO:126) derived from the coding sequence of SEQ ID NO:125 shown in Figure 125.

5 Figure 127 shows a nucleotide sequence (SEQ ID NO:127) of a native sequence PRO793 cDNA, wherein SEQ ID NO:127 is a clone designated herein as "DNA56110-1437".

Figure 128 shows the amino acid sequence (SEQ ID NO:128) derived from the coding sequence of SEQ ID NO:127 shown in Figure 127.

Figure 129 shows a nucleotide sequence (SEQ ID NO:129) of a native sequence PRO1773 cDNA, wherein SEQ ID NO:129 is a clone designated herein as "DNA56406-1704".

10 Figure 130 shows the amino acid sequence (SEQ ID NO:130) derived from the coding sequence of SEQ ID NO:129 shown in Figure 129.

Figure 131 shows a nucleotide sequence (SEQ ID NO:131) of a native sequence PRO1014 cDNA, wherein SEQ ID NO:131 is a clone designated herein as "DNA56409-1377".

15 Figure 132 shows the amino acid sequence (SEQ ID NO:132) derived from the coding sequence of SEQ ID NO:131 shown in Figure 131.

Figure 133 shows a nucleotide sequence (SEQ ID NO:133) of a native sequence PRO1013 cDNA, wherein SEQ ID NO:133 is a clone designated herein as "DNA56410-1414".

Figure 134 shows the amino acid sequence (SEQ ID NO:134) derived from the coding sequence of SEQ ID NO:133 shown in Figure 133.

20 Figure 135 shows a nucleotide sequence (SEQ ID NO:135) of a native sequence PRO937 cDNA, wherein SEQ ID NO:135 is a clone designated herein as "DNA56436-1448".

Figure 136 shows the amino acid sequence (SEQ ID NO:136) derived from the coding sequence of SEQ ID NO:135 shown in Figure 135.

25 Figure 137 shows a nucleotide sequence (SEQ ID NO:137) of a native sequence PRO1477 cDNA, wherein SEQ ID NO:137 is a clone designated herein as "DNA56529-1647".

Figure 138 shows the amino acid sequence (SEQ ID NO:138) derived from the coding sequence of SEQ ID NO:137 shown in Figure 137.

Figure 139 shows a nucleotide sequence (SEQ ID NO:139) of a native sequence PRO842 cDNA, wherein SEQ ID NO:139 is a clone designated herein as "DNA56855-1447".

30 Figure 140 shows the amino acid sequence (SEQ ID NO:140) derived from the coding sequence of SEQ ID NO:139 shown in Figure 139.

Figure 141 shows a nucleotide sequence (SEQ ID NO:141) of a native sequence PRO839 cDNA, wherein SEQ ID NO:141 is a clone designated herein as "DNA56859-1445".

35 Figure 142 shows the amino acid sequence (SEQ ID NO:142) derived from the coding sequence of SEQ ID NO:141 shown in Figure 141.

Figure 143 shows a nucleotide sequence (SEQ ID NO:143) of a native sequence PRO1180 cDNA, wherein SEQ ID NO:143 is a clone designated herein as "DNA56860-1510".

Figure 144 shows the amino acid sequence (SEQ ID NO:144) derived from the coding sequence of SEQ ID NO:143 shown in Figure 143.

Figure 145 shows a nucleotide sequence (SEQ ID NO:145) of a native sequence PRO1134 cDNA, wherein SEQ ID NO:145 is a clone designated herein as "DNA56865-1491".

5 Figure 146 shows the amino acid sequence (SEQ ID NO:146) derived from the coding sequence of SEQ ID NO:145 shown in Figure 145.

Figure 147 shows a nucleotide sequence (SEQ ID NO:147) of a native sequence PRO1115 cDNA, wherein SEQ ID NO:147 is a clone designated herein as "DNA56868-1478".

Figure 148 shows the amino acid sequence (SEQ ID NO:148) derived from the coding sequence of SEQ ID NO:147 shown in Figure 147.

10 Figure 149 shows a nucleotide sequence (SEQ ID NO:149) of a native sequence PRO1277 cDNA, wherein SEQ ID NO:149 is a clone designated herein as "DNA56869-1545".

Figure 150 shows the amino acid sequence (SEQ ID NO:150) derived from the coding sequence of SEQ ID NO:149 shown in Figure 149.

15 Figure 151 shows a nucleotide sequence (SEQ ID NO:151) of a native sequence PRO1135 cDNA, wherein SEQ ID NO:151 is a clone designated herein as "DNA56870-1492".

Figure 152 shows the amino acid sequence (SEQ ID NO:152) derived from the coding sequence of SEQ ID NO:151 shown in Figure 151.

Figure 153 shows a nucleotide sequence (SEQ ID NO:153) of a native sequence PRO827 cDNA, wherein SEQ ID NO:153 is a clone designated herein as "DNA57039-1402".

20 Figure 154 shows the amino acid sequence (SEQ ID NO:154) derived from the coding sequence of SEQ ID NO:153 shown in Figure 153.

Figure 155 shows a nucleotide sequence (SEQ ID NO:155) of a native sequence PRO1057 cDNA, wherein SEQ ID NO:155 is a clone designated herein as "DNA57253-1382".

25 Figure 156 shows the amino acid sequence (SEQ ID NO:156) derived from the coding sequence of SEQ ID NO:155 shown in Figure 155.

Figure 157 shows a nucleotide sequence (SEQ ID NO:157) of a native sequence PRO1113 cDNA, wherein SEQ ID NO:157 is a clone designated herein as "DNA57254-1477".

Figure 158 shows the amino acid sequence (SEQ ID NO:158) derived from the coding sequence of SEQ ID NO:157 shown in Figure 157.

30 Figure 159 shows a nucleotide sequence (SEQ ID NO:159) of a native sequence PRO1006 cDNA, wherein SEQ ID NO:159 is a clone designated herein as "DNA57699-1412".

Figure 160 shows the amino acid sequence (SEQ ID NO:160) derived from the coding sequence of SEQ ID NO:159 shown in Figure 159.

35 Figure 161 shows a nucleotide sequence (SEQ ID NO:161) of a native sequence PRO1074 cDNA, wherein SEQ ID NO:161 is a clone designated herein as "DNA57704-1452".

Figure 162 shows the amino acid sequence (SEQ ID NO:162) derived from the coding sequence of SEQ ID NO:161 shown in Figure 161.

Figure 163 shows a nucleotide sequence (SEQ ID NO:163) of a native sequence PRO1073 cDNA, wherein SEQ ID NO:163 is a clone designated herein as "DNA57710-1451".

Figure 164 shows the amino acid sequence (SEQ ID NO:164) derived from the coding sequence of SEQ ID NO:163 shown in Figure 163.

5 Figure 165 shows a nucleotide sequence (SEQ ID NO:165) of a native sequence PRO1136 cDNA, wherein SEQ ID NO:165 is a clone designated herein as "DNA57827-1493".

Figure 166 shows the amino acid sequence (SEQ ID NO:166) derived from the coding sequence of SEQ ID NO:165 shown in Figure 165.

Figure 167 shows a nucleotide sequence (SEQ ID NO:167) of a native sequence PRO1004 cDNA, wherein SEQ ID NO:167 is a clone designated herein as "DNA57844-1410".

10 Figure 168 shows the amino acid sequence (SEQ ID NO:168) derived from the coding sequence of SEQ ID NO:167 shown in Figure 167.

Figure 169 shows a nucleotide sequence (SEQ ID NO:169) of a native sequence PRO1344 cDNA, wherein SEQ ID NO:169 is a clone designated herein as "DNA58723-1588".

15 Figure 170 shows the amino acid sequence (SEQ ID NO:170) derived from the coding sequence of SEQ ID NO:169 shown in Figure 169.

Figure 171 shows a nucleotide sequence (SEQ ID NO:171) of a native sequence PRO1110 cDNA, wherein SEQ ID NO:171 is a clone designated herein as "DNA58727-1474".

Figure 172 shows the amino acid sequence (SEQ ID NO:172) derived from the coding sequence of SEQ ID NO:171 shown in Figure 171.

20 Figure 173 shows a nucleotide sequence (SEQ ID NO:173) of a native sequence PRO1378 cDNA, wherein SEQ ID NO:173 is a clone designated herein as "DNA58730-1607".

Figure 174 shows the amino acid sequence (SEQ ID NO:174) derived from the coding sequence of SEQ ID NO:173 shown in Figure 173.

25 Figure 175 shows a nucleotide sequence (SEQ ID NO:175) of a native sequence PRO1481 cDNA, wherein SEQ ID NO:175 is a clone designated herein as "DNA58732-1650".

Figure 176 shows the amino acid sequence (SEQ ID NO:176) derived from the coding sequence of SEQ ID NO:175 shown in Figure 175.

Figure 177 shows a nucleotide sequence (SEQ ID NO:177) of a native sequence PRO1109 cDNA, wherein SEQ ID NO:177 is a clone designated herein as "DNA58737-1473".

30 Figure 178 shows the amino acid sequence (SEQ ID NO:178) derived from the coding sequence of SEQ ID NO:177 shown in Figure 177.

Figure 179 shows a nucleotide sequence (SEQ ID NO:179) of a native sequence PRO1383 cDNA, wherein SEQ ID NO:179 is a clone designated herein as "DNA58743-1609".

35 Figure 180 shows the amino acid sequence (SEQ ID NO:180) derived from the coding sequence of SEQ ID NO:179 shown in Figure 179.

Figure 181 shows a nucleotide sequence (SEQ ID NO:181) of a native sequence PRO1072 cDNA, wherein SEQ ID NO:181 is a clone designated herein as "DNA58747-1384".

Figure 182 shows the amino acid sequence (SEQ ID NO:182) derived from the coding sequence of SEQ ID NO:181 shown in Figure 181.

Figure 183 shows a nucleotide sequence (SEQ ID NO:183) of a native sequence PRO1189 cDNA, wherein SEQ ID NO:183 is a clone designated herein as "DNA58828-1519".

5 Figure 184 shows the amino acid sequence (SEQ ID NO:184) derived from the coding sequence of SEQ ID NO:183 shown in Figure 183.

Figure 185 shows a nucleotide sequence (SEQ ID NO:185) of a native sequence PRO1003 cDNA, wherein SEQ ID NO:185 is a clone designated herein as "DNA58846-1409".

Figure 186 shows the amino acid sequence (SEQ ID NO:186) derived from the coding sequence of SEQ ID NO:185 shown in Figure 185.

10 Figure 187 shows a nucleotide sequence (SEQ ID NO:187) of a native sequence PRO1108 cDNA, wherein SEQ ID NO:187 is a clone designated herein as "DNA58848-1472".

Figure 188 shows the amino acid sequence (SEQ ID NO:188) derived from the coding sequence of SEQ ID NO:187 shown in Figure 187.

15 Figure 189 shows a nucleotide sequence (SEQ ID NO:189) of a native sequence PRO1137 cDNA, wherein SEQ ID NO:189 is a clone designated herein as "DNA58849-1494".

Figure 190 shows the amino acid sequence (SEQ ID NO:190) derived from the coding sequence of SEQ ID NO:189 shown in Figure 189.

Figure 191 shows a nucleotide sequence (SEQ ID NO:191) of a native sequence PRO1138 cDNA, wherein SEQ ID NO:191 is a clone designated herein as "DNA58850-1495".

20 Figure 192 shows the amino acid sequence (SEQ ID NO:192) derived from the coding sequence of SEQ ID NO:191 shown in Figure 191.

Figure 193 shows a nucleotide sequence (SEQ ID NO:193) of a native sequence PRO1415 cDNA, wherein SEQ ID NO:193 is a clone designated herein as "DNA58852-1637".

25 Figure 194 shows the amino acid sequence (SEQ ID NO:194) derived from the coding sequence of SEQ ID NO:193 shown in Figure 193.

Figure 195 shows a nucleotide sequence (SEQ ID NO:195) of a native sequence PRO1054 cDNA, wherein SEQ ID NO:195 is a clone designated herein as "DNA58853-1423".

Figure 196 shows the amino acid sequence (SEQ ID NO:196) derived from the coding sequence of SEQ ID NO:195 shown in Figure 195.

30 Figure 197 shows a nucleotide sequence (SEQ ID NO:197) of a native sequence PRO994 cDNA, wherein SEQ ID NO:197 is a clone designated herein as "DNA58855-1422".

Figure 198 shows the amino acid sequence (SEQ ID NO:198) derived from the coding sequence of SEQ ID NO:197 shown in Figure 197.

35 Figure 199 shows a nucleotide sequence (SEQ ID NO:199) of a native sequence PRO1069 cDNA, wherein SEQ ID NO:199 is a clone designated herein as "DNA59211-1450".

Figure 200 shows the amino acid sequence (SEQ ID NO:200) derived from the coding sequence of SEQ ID NO:199 shown in Figure 199.

Figure 201 shows a nucleotide sequence (SEQ ID NO:201) of a native sequence PRO1411 cDNA, wherein SEQ ID NO:201 is a clone designated herein as "DNA59212-1627".

Figure 202 shows the amino acid sequence (SEQ ID NO:202) derived from the coding sequence of SEQ ID NO:201 shown in Figure 201.

5 Figure 203 shows a nucleotide sequence (SEQ ID NO:203) of a native sequence PRO1129 cDNA, wherein SEQ ID NO:203 is a clone designated herein as "DNA59213-1487".

Figure 204 shows the amino acid sequence (SEQ ID NO:204) derived from the coding sequence of SEQ ID NO:203 shown in Figure 203.

Figure 205 shows a nucleotide sequence (SEQ ID NO:205) of a native sequence PRO1359 cDNA, wherein SEQ ID NO:205 is a clone designated herein as "DNA59219-1613".

10 Figure 206 shows the amino acid sequence (SEQ ID NO:206) derived from the coding sequence of SEQ ID NO:205 shown in Figure 205.

Figure 207 shows a nucleotide sequence (SEQ ID NO:207) of a native sequence PRO1139 cDNA, wherein SEQ ID NO:207 is a clone designated herein as "DNA59497-1496".

15 Figure 208 shows the amino acid sequence (SEQ ID NO:208) derived from the coding sequence of SEQ ID NO:207 shown in Figure 207.

Figure 209 shows a nucleotide sequence (SEQ ID NO:209) of a native sequence PRO1065 cDNA, wherein SEQ ID NO:209 is a clone designated herein as "DNA59602-1436".

Figure 210 shows the amino acid sequence (SEQ ID NO:210) derived from the coding sequence of SEQ ID NO:209 shown in Figure 209.

20 Figure 211 shows a nucleotide sequence (SEQ ID NO:211) of a native sequence PRO1028 cDNA, wherein SEQ ID NO:211 is a clone designated herein as "DNA59603-1419".

Figure 212 shows the amino acid sequence (SEQ ID NO:212) derived from the coding sequence of SEQ ID NO:211 shown in Figure 211.

25 Figure 213 shows a nucleotide sequence (SEQ ID NO:213) of a native sequence PRO1027 cDNA, wherein SEQ ID NO:213 is a clone designated herein as "DNA59605-1418".

Figure 214 shows the amino acid sequence (SEQ ID NO:214) derived from the coding sequence of SEQ ID NO:213 shown in Figure 213.

Figure 215 shows a nucleotide sequence (SEQ ID NO:215) of a native sequence PRO1140 cDNA, wherein SEQ ID NO:215 is a clone designated herein as "DNA59607-1497".

30 Figure 216 shows the amino acid sequence (SEQ ID NO:216) derived from the coding sequence of SEQ ID NO:215 shown in Figure 215.

Figure 217 shows a nucleotide sequence (SEQ ID NO:217) of a native sequence PRO1291 cDNA, wherein SEQ ID NO:217 is a clone designated herein as "DNA59610-1556".

35 Figure 218 shows the amino acid sequence (SEQ ID NO:218) derived from the coding sequence of SEQ ID NO:217 shown in Figure 217.

Figure 219 shows a nucleotide sequence (SEQ ID NO:219) of a native sequence PRO1105 cDNA, wherein SEQ ID NO:219 is a clone designated herein as "DNA59612-1466".

Figure 220 shows the amino acid sequence (SEQ ID NO:220) derived from the coding sequence of SEQ ID NO:219 shown in Figure 219.

Figure 221 shows a nucleotide sequence (SEQ ID NO:221) of a native sequence PRO1026 cDNA, wherein SEQ ID NO:221 is a clone designated herein as "DNA59613-1417".

5 Figure 222 shows the amino acid sequence (SEQ ID NO:222) derived from the coding sequence of SEQ ID NO:221 shown in Figure 221.

Figure 223 shows a nucleotide sequence (SEQ ID NO:223) of a native sequence PRO1104 cDNA, wherein SEQ ID NO:223 is a clone designated herein as "DNA59616-1465".

Figure 224 shows the amino acid sequence (SEQ ID NO:224) derived from the coding sequence of SEQ ID NO:223 shown in Figure 223.

10 Figure 225 shows a nucleotide sequence (SEQ ID NO:225) of a native sequence PRO1100 cDNA, wherein SEQ ID NO:225 is a clone designated herein as "DNA59619-1464".

Figure 226 shows the amino acid sequence (SEQ ID NO:226) derived from the coding sequence of SEQ ID NO:225 shown in Figure 225.

15 Figure 227 shows a nucleotide sequence (SEQ ID NO:227) of a native sequence PRO1141 cDNA, wherein SEQ ID NO:227 is a clone designated herein as "DNA59625-1498".

Figure 228 shows the amino acid sequence (SEQ ID NO:228) derived from the coding sequence of SEQ ID NO:227 shown in Figure 227.

Figure 229 shows a nucleotide sequence (SEQ ID NO:229) of a native sequence PRO1772 cDNA, wherein SEQ ID NO:229 is a clone designated herein as "DNA59817-1703".

20 Figure 230 shows the amino acid sequence (SEQ ID NO:230) derived from the coding sequence of SEQ ID NO:229 shown in Figure 229.

Figure 231 shows a nucleotide sequence (SEQ ID NO:231) of a native sequence PRO1064 cDNA, wherein SEQ ID NO:231 is a clone designated herein as "DNA59827-1426".

25 Figure 232 shows the amino acid sequence (SEQ ID NO:232) derived from the coding sequence of SEQ ID NO:231 shown in Figure 231.

Figure 233 shows a nucleotide sequence (SEQ ID NO:233) of a native sequence PRO1379 cDNA, wherein SEQ ID NO:233 is a clone designated herein as "DNA59828-1608".

Figure 234 shows the amino acid sequence (SEQ ID NO:234) derived from the coding sequence of SEQ ID NO:233 shown in Figure 233.

30 Figure 235 shows a nucleotide sequence (SEQ ID NO:235) of a native sequence PRO3573 cDNA, wherein SEQ ID NO:235 is a clone designated herein as "DNA59837-2545".

Figure 236 shows the amino acid sequence (SEQ ID NO:236) derived from the coding sequence of SEQ ID NO:235 shown in Figure 235.

35 Figure 237 shows a nucleotide sequence (SEQ ID NO:237) of a native sequence PRO3566 cDNA, wherein SEQ ID NO:237 is a clone designated herein as "DNA59844-2542".

Figure 238 shows the amino acid sequence (SEQ ID NO:238) derived from the coding sequence of SEQ ID NO:237 shown in Figure 237.

Figure 239 shows a nucleotide sequence (SEQ ID NO:239) of a native sequence PRO1156 cDNA, wherein SEQ ID NO:239 is a clone designated herein as "DNA59853-1505".

Figure 240 shows the amino acid sequence (SEQ ID NO:240) derived from the coding sequence of SEQ ID NO:239 shown in Figure 239.

5 Figure 241 shows a nucleotide sequence (SEQ ID NO:241) of a native sequence PRO1098 cDNA, wherein SEQ ID NO:241 is a clone designated herein as "DNA59854-1459".

Figure 242 shows the amino acid sequence (SEQ ID NO:242) derived from the coding sequence of SEQ ID NO:241 shown in Figure 241.

Figure 243 shows a nucleotide sequence (SEQ ID NO:243) of a native sequence PRO1128 cDNA, wherein SEQ ID NO:243 is a clone designated herein as "DNA59855-1485".

10 Figure 244 shows the amino acid sequence (SEQ ID NO:244) derived from the coding sequence of SEQ ID NO:243 shown in Figure 243.

Figure 245 shows a nucleotide sequence (SEQ ID NO:245) of a native sequence PRO1248 cDNA, wherein SEQ ID NO:245 is a clone designated herein as "DNA60278-1530".

15 Figure 246 shows the amino acid sequence (SEQ ID NO:246) derived from the coding sequence of SEQ ID NO:245 shown in Figure 245.

Figure 247 shows a nucleotide sequence (SEQ ID NO:247) of a native sequence PRO1127 cDNA, wherein SEQ ID NO:247 is a clone designated herein as "DNA60283-1484".

Figure 248 shows the amino acid sequence (SEQ ID NO:248) derived from the coding sequence of SEQ ID NO:247 shown in Figure 247.

20 Figure 249 shows a nucleotide sequence (SEQ ID NO:249) of a native sequence PRO1316 cDNA, wherein SEQ ID NO:249 is a clone designated herein as "DNA60608-1577".

Figure 250 shows the amino acid sequence (SEQ ID NO:250) derived from the coding sequence of SEQ ID NO:249 shown in Figure 249.

25 Figure 251 shows a nucleotide sequence (SEQ ID NO:251) of a native sequence PRO1197 cDNA, wherein SEQ ID NO:251 is a clone designated herein as "DNA60611-1524".

Figure 252 shows the amino acid sequence (SEQ ID NO:252) derived from the coding sequence of SEQ ID NO:251 shown in Figure 251.

Figure 253 shows a nucleotide sequence (SEQ ID NO:253) of a native sequence PRO1125 cDNA, wherein SEQ ID NO:253 is a clone designated herein as "DNA60619-1482".

30 Figure 254 shows the amino acid sequence (SEQ ID NO:254) derived from the coding sequence of SEQ ID NO:253 shown in Figure 253.

Figure 255 shows a nucleotide sequence (SEQ ID NO:255) of a native sequence PRO1158 cDNA, wherein SEQ ID NO:255 is a clone designated herein as "DNA60625-1507".

35 Figure 256 shows the amino acid sequence (SEQ ID NO:256) derived from the coding sequence of SEQ ID NO:255 shown in Figure 255.

Figure 257 shows a nucleotide sequence (SEQ ID NO:257) of a native sequence PRO1124 cDNA, wherein SEQ ID NO:257 is a clone designated herein as "DNA60629-1481".

Figure 258 shows the amino acid sequence (SEQ ID NO:258) derived from the coding sequence of SEQ ID NO:257 shown in Figure 257.

Figure 259 shows a nucleotide sequence (SEQ ID NO:259) of a native sequence PRO1380 cDNA, wherein SEQ ID NO:259 is a clone designated herein as "DNA60740-1615".

5 Figure 260 shows the amino acid sequence (SEQ ID NO:260) derived from the coding sequence of SEQ ID NO:259 shown in Figure 259.

Figure 261 shows a nucleotide sequence (SEQ ID NO:261) of a native sequence PRO1377 cDNA, wherein SEQ ID NO:261 is a clone designated herein as "DNA61608-1606".

Figure 262 shows the amino acid sequence (SEQ ID NO:262) derived from the coding sequence of SEQ ID NO:261 shown in Figure 261.

10 Figure 263 shows a nucleotide sequence (SEQ ID NO:263) of a native sequence PRO1287 cDNA, wherein SEQ ID NO:263 is a clone designated herein as "DNA61755-1554".

Figure 264 shows the amino acid sequence (SEQ ID NO:264) derived from the coding sequence of SEQ ID NO:263 shown in Figure 263.

15 Figure 265 shows a nucleotide sequence (SEQ ID NO:265) of a native sequence PRO1249 cDNA, wherein SEQ ID NO:265 is a clone designated herein as "DNA62809-1531".

Figure 266 shows the amino acid sequence (SEQ ID NO:266) derived from the coding sequence of SEQ ID NO:265 shown in Figure 265.

Figure 267 shows a nucleotide sequence (SEQ ID NO:267) of a native sequence PRO1335 cDNA, wherein SEQ ID NO:267 is a clone designated herein as "DNA62812-1594".

20 Figure 268 shows the amino acid sequence (SEQ ID NO:268) derived from the coding sequence of SEQ ID NO:267 shown in Figure 267.

Figure 269 shows a nucleotide sequence (SEQ ID NO:269) of a native sequence PRO3572 cDNA, wherein SEQ ID NO:269 is a clone designated herein as "DNA62813-2544".

25 Figure 270 shows the amino acid sequence (SEQ ID NO:270) derived from the coding sequence of SEQ ID NO:269 shown in Figure 269.

Figure 271 shows a nucleotide sequence (SEQ ID NO:271) of a native sequence PRO1599 cDNA, wherein SEQ ID NO:271 is a clone designated herein as "DNA62845-1684".

Figure 272 shows the amino acid sequence (SEQ ID NO:272) derived from the coding sequence of SEQ ID NO:271 shown in Figure 271.

30 Figure 273 shows a nucleotide sequence (SEQ ID NO:273) of a native sequence PRO1374 cDNA, wherein SEQ ID NO:273 is a clone designated herein as "DNA64849-1604".

Figure 274 shows the amino acid sequence (SEQ ID NO:274) derived from the coding sequence of SEQ ID NO:273 shown in Figure 273.

35 Figure 275 shows a nucleotide sequence (SEQ ID NO:275) of a native sequence PRO1345 cDNA, wherein SEQ ID NO:275 is a clone designated herein as "DNA64852-1589".

Figure 276 shows the amino acid sequence (SEQ ID NO:276) derived from the coding sequence of SEQ ID NO:275 shown in Figure 275.

Figure 277 shows a nucleotide sequence (SEQ ID NO:277) of a native sequence PRO1311 cDNA, wherein SEQ ID NO:277 is a clone designated herein as "DNA64863-1573".

Figure 278 shows the amino acid sequence (SEQ ID NO:278) derived from the coding sequence of SEQ ID NO:277 shown in Figure 277.

5 Figure 279 shows a nucleotide sequence (SEQ ID NO:279) of a native sequence PRO1357 cDNA, wherein SEQ ID NO:279 is a clone designated herein as "DNA64881-1602".

Figure 280 shows the amino acid sequence (SEQ ID NO:280) derived from the coding sequence of SEQ ID NO:279 shown in Figure 279.

Figure 281 shows a nucleotide sequence (SEQ ID NO:281) of a native sequence PRO1557 cDNA, wherein SEQ ID NO:281 is a clone designated herein as "DNA64902-1667".

10 Figure 282 shows the amino acid sequence (SEQ ID NO:282) derived from the coding sequence of SEQ ID NO:281 shown in Figure 281.

Figure 283 shows a nucleotide sequence (SEQ ID NO:283) of a native sequence PRO1305 cDNA, wherein SEQ ID NO:283 is a clone designated herein as "DNA64952-1568".

15 Figure 284 shows the amino acid sequence (SEQ ID NO:284) derived from the coding sequence of SEQ ID NO:283 shown in Figure 283.

Figure 285 shows a nucleotide sequence (SEQ ID NO:285) of a native sequence PRO1302 cDNA, wherein SEQ ID NO:285 is a clone designated herein as "DNA65403-1565".

Figure 286 shows the amino acid sequence (SEQ ID NO:286) derived from the coding sequence of SEQ ID NO:285 shown in Figure 285.

20 Figure 287 shows a nucleotide sequence (SEQ ID NO:287) of a native sequence PRO1266 cDNA, wherein SEQ ID NO:287 is a clone designated herein as "DNA65413-1534".

Figure 288 shows the amino acid sequence (SEQ ID NO:288) derived from the coding sequence of SEQ ID NO:287 shown in Figure 287.

25 Figures 289A-289B show a nucleotide sequence (SEQ ID NO:289) of a native sequence PRO1336 cDNA, wherein SEQ ID NO:289 is a clone designated herein as "DNA65423-1595".

Figure 290 shows the amino acid sequence (SEQ ID NO:290) derived from the coding sequence of SEQ ID NO:289 shown in Figures 289A-289B.

Figure 291 shows a nucleotide sequence (SEQ ID NO:291) of a native sequence PRO1278 cDNA, wherein SEQ ID NO:291 is a clone designated herein as "DNA66304-1546".

30 Figure 292 shows the amino acid sequence (SEQ ID NO:292) derived from the coding sequence of SEQ ID NO:291 shown in Figure 291.

Figure 293 shows a nucleotide sequence (SEQ ID NO:293) of a native sequence PRO1270 cDNA, wherein SEQ ID NO:293 is a clone designated herein as "DNA66308-1537".

35 Figure 294 shows the amino acid sequence (SEQ ID NO:294) derived from the coding sequence of SEQ ID NO:293 shown in Figure 293.

Figure 295 shows a nucleotide sequence (SEQ ID NO:295) of a native sequence PRO1298 cDNA, wherein SEQ ID NO:295 is a clone designated herein as "DNA66511-1563".

Figure 296 shows the amino acid sequence (SEQ ID NO:296) derived from the coding sequence of SEQ ID NO:295 shown in Figure 295.

Figure 297 shows a nucleotide sequence (SEQ ID NO:297) of a native sequence PRO1301 cDNA, wherein SEQ ID NO:297 is a clone designated herein as "DNA66512-1564".

5 Figure 298 shows the amino acid sequence (SEQ ID NO:298) derived from the coding sequence of SEQ ID NO:297 shown in Figure 297.

Figure 299 shows a nucleotide sequence (SEQ ID NO:299) of a native sequence PRO1268 cDNA, wherein SEQ ID NO:299 is a clone designated herein as "DNA66519-1535".

Figure 300 shows the amino acid sequence (SEQ ID NO:300) derived from the coding sequence of SEQ ID NO:299 shown in Figure 299.

10 Figure 301 shows a nucleotide sequence (SEQ ID NO:301) of a native sequence PRO1327 cDNA, wherein SEQ ID NO:301 is a clone designated herein as "DNA66521-1583".

Figure 302 shows the amino acid sequence (SEQ ID NO:302) derived from the coding sequence of SEQ ID NO:301 shown in Figure 301.

15 Figure 303 shows a nucleotide sequence (SEQ ID NO:303) of a native sequence PRO1328 cDNA, wherein SEQ ID NO:303 is a clone designated herein as "DNA66658-1584".

Figure 304 shows the amino acid sequence (SEQ ID NO:304) derived from the coding sequence of SEQ ID NO:303 shown in Figure 303.

Figure 305 shows a nucleotide sequence (SEQ ID NO:305) of a native sequence PRO1329 cDNA, wherein SEQ ID NO:305 is a clone designated herein as "DNA66660-1585".

20 Figure 306 shows the amino acid sequence (SEQ ID NO:306) derived from the coding sequence of SEQ ID NO:305 shown in Figure 305.

Figure 307 shows a nucleotide sequence (SEQ ID NO:307) of a native sequence PRO1339 cDNA, wherein SEQ ID NO:307 is a clone designated herein as "DNA66669-1597".

25 Figure 308 shows the amino acid sequence (SEQ ID NO:308) derived from the coding sequence of SEQ ID NO:307 shown in Figure 307.

Figure 309 shows a nucleotide sequence (SEQ ID NO:309) of a native sequence PRO1342 cDNA, wherein SEQ ID NO:309 is a clone designated herein as "DNA66674-1599".

Figure 310 shows the amino acid sequence (SEQ ID NO:310) derived from the coding sequence of SEQ ID NO:309 shown in Figure 309.

30 Figures 311A-311B show a nucleotide sequence (SEQ ID NO:311) of a native sequence PRO1487 cDNA, wherein SEQ ID NO:311 is a clone designated herein as "DNA68836-1656".

Figure 312 shows the amino acid sequence (SEQ ID NO:312) derived from the coding sequence of SEQ ID NO:311 shown in Figures 311A-311B.

35 Figure 313 shows a nucleotide sequence (SEQ ID NO:313) of a native sequence PRO3579 cDNA, wherein SEQ ID NO:313 is a clone designated herein as "DNA68862-2546".

Figure 314 shows the amino acid sequence (SEQ ID NO:314) derived from the coding sequence of SEQ ID NO:313 shown in Figure 313.

Figure 315 shows a nucleotide sequence (SEQ ID NO:315) of a native sequence PRO1472 cDNA, wherein SEQ ID NO:315 is a clone designated herein as "DNA68866-1644".

Figure 316 shows the amino acid sequence (SEQ ID NO:316) derived from the coding sequence of SEQ ID NO:315 shown in Figure 315.

5 Figure 317 shows a nucleotide sequence (SEQ ID NO:317) of a native sequence PRO1385 cDNA, wherein SEQ ID NO:317 is a clone designated herein as "DNA68869-1610".

Figure 318 shows the amino acid sequence (SEQ ID NO:318) derived from the coding sequence of SEQ ID NO:317 shown in Figure 317.

Figure 319 shows a nucleotide sequence (SEQ ID NO:319) of a native sequence PRO1461 cDNA, wherein SEQ ID NO:319 is a clone designated herein as "DNA68871-1638".

10 Figure 320 shows the amino acid sequence (SEQ ID NO:320) derived from the coding sequence of SEQ ID NO:319 shown in Figure 319.

Figure 321 shows a nucleotide sequence (SEQ ID NO:321) of a native sequence PRO1429 cDNA, wherein SEQ ID NO:321 is a clone designated herein as "DNA68879-1631".

15 Figure 322 shows the amino acid sequence (SEQ ID NO:322) derived from the coding sequence of SEQ ID NO:321 shown in Figure 321.

Figure 323 shows a nucleotide sequence (SEQ ID NO:323) of a native sequence PRO1568 cDNA, wherein SEQ ID NO:323 is a clone designated herein as "DNA68880-1676".

Figure 324 shows the amino acid sequence (SEQ ID NO:324) derived from the coding sequence of SEQ ID NO:323 shown in Figure 323.

20 Figure 325 shows a nucleotide sequence (SEQ ID NO:325) of a native sequence PRO1569 cDNA, wherein SEQ ID NO:325 is a clone designated herein as "DNA68882-1677".

Figure 326 shows the amino acid sequence (SEQ ID NO:326) derived from the coding sequence of SEQ ID NO:325 shown in Figure 325.

25 Figure 327 shows a nucleotide sequence (SEQ ID NO:327) of a native sequence PRO1753 cDNA, wherein SEQ ID NO:327 is a clone designated herein as "DNA68883-1691".

Figure 328 shows the amino acid sequence (SEQ ID NO:328) derived from the coding sequence of SEQ ID NO:327 shown in Figure 327.

Figure 329 shows a nucleotide sequence (SEQ ID NO:329) of a native sequence PRO1570 cDNA, wherein SEQ ID NO:329 is a clone designated herein as "DNA68885-1678".

30 Figure 330 shows the amino acid sequence (SEQ ID NO:330) derived from the coding sequence of SEQ ID NO:329 shown in Figure 329.

Figure 331 shows a nucleotide sequence (SEQ ID NO:331) of a native sequence PRO1559 cDNA, wherein SEQ ID NO:331 is a clone designated herein as "DNA68886".

35 Figure 332 shows the amino acid sequence (SEQ ID NO:332) derived from the coding sequence of SEQ ID NO:331 shown in Figure 331.

Figure 333 shows a nucleotide sequence (SEQ ID NO:333) of a native sequence PRO1486 cDNA, wherein SEQ ID NO:333 is a clone designated herein as "DNA71180-1655".

Figure 334 shows the amino acid sequence (SEQ ID NO:334) derived from the coding sequence of SEQ ID NO:333 shown in Figure 333.

Figure 335 shows a nucleotide sequence (SEQ ID NO:335) of a native sequence PRO1433 cDNA, wherein SEQ ID NO:335 is a clone designated herein as "DNA71184-1634".

5 Figure 336 shows the amino acid sequence (SEQ ID NO:336) derived from the coding sequence of SEQ ID NO:335 shown in Figure 335.

Figure 337 shows a nucleotide sequence (SEQ ID NO:337) of a native sequence PRO1490 cDNA, wherein SEQ ID NO:337 is a clone designated herein as "DNA71213-1659".

Figure 338 shows the amino acid sequence (SEQ ID NO:338) derived from the coding sequence of SEQ ID NO:337 shown in Figure 337.

10 Figure 339 shows a nucleotide sequence (SEQ ID NO:339) of a native sequence PRO1482 cDNA, wherein SEQ ID NO:339 is a clone designated herein as "DNA71234-1651".

Figure 340 shows the amino acid sequence (SEQ ID NO:340) derived from the coding sequence of SEQ ID NO:339 shown in Figure 339.

15 Figure 341 shows a nucleotide sequence (SEQ ID NO:341) of a native sequence PRO1409 cDNA, wherein SEQ ID NO:341 is a clone designated herein as "DNA71269-1621".

Figure 342 shows the amino acid sequence (SEQ ID NO:342) derived from the coding sequence of SEQ ID NO:341 shown in Figure 341.

Figure 343 shows a nucleotide sequence (SEQ ID NO:343) of a native sequence PRO1446 cDNA, wherein SEQ ID NO:343 is a clone designated herein as "DNA71277-1636".

20 Figure 344 shows the amino acid sequence (SEQ ID NO:344) derived from the coding sequence of SEQ ID NO:343 shown in Figure 343.

Figure 345 shows a nucleotide sequence (SEQ ID NO:345) of a native sequence PRO1604 cDNA, wherein SEQ ID NO:345 is a clone designated herein as "DNA71286-1687".

25 Figure 346 shows the amino acid sequence (SEQ ID NO:346) derived from the coding sequence of SEQ ID NO:345 shown in Figure 345.

Figure 347 shows a nucleotide sequence (SEQ ID NO:347) of a native sequence PRO1491 cDNA, wherein SEQ ID NO:347 is a clone designated herein as "DNA71883-1660".

Figure 348 shows the amino acid sequence (SEQ ID NO:348) derived from the coding sequence of SEQ ID NO:347 shown in Figure 347.

30 Figure 349 shows a nucleotide sequence (SEQ ID NO:349) of a native sequence PRO1431 cDNA, wherein SEQ ID NO:349 is a clone designated herein as "DNA73401-1633".

Figure 350 shows the amino acid sequence (SEQ ID NO:350) derived from the coding sequence of SEQ ID NO:349 shown in Figure 349.

35 Figures 351A-351B show a nucleotide sequence (SEQ ID NO:351) of a native sequence PRO1563 cDNA, wherein SEQ ID NO:351 is a clone designated herein as "DNA73492-1671".

Figure 352 shows the amino acid sequence (SEQ ID NO:352) derived from the coding sequence of SEQ ID NO:351 shown in Figures 351A-351B.

Figure 353 shows a nucleotide sequence (SEQ ID NO:353) of a native sequence PRO1571 cDNA, wherein SEQ ID NO:353 is a clone designated herein as "DNA73730-1679".

Figure 354 shows the amino acid sequence (SEQ ID NO:354) derived from the coding sequence of SEQ ID NO:353 shown in Figure 353.

5 Figure 355 shows a nucleotide sequence (SEQ ID NO:355) of a native sequence PRO1572 cDNA, wherein SEQ ID NO:355 is a clone designated herein as "DNA73734-1680".

Figure 356 shows the amino acid sequence (SEQ ID NO:356) derived from the coding sequence of SEQ ID NO:355 shown in Figure 355.

Figure 357 shows a nucleotide sequence (SEQ ID NO:357) of a native sequence PRO1573 cDNA, wherein SEQ ID NO:357 is a clone designated herein as "DNA73735-1681".

10 Figure 358 shows the amino acid sequence (SEQ ID NO:358) derived from the coding sequence of SEQ ID NO:357 shown in Figure 357.

Figure 359 shows a nucleotide sequence (SEQ ID NO:359) of a native sequence PRO1508 cDNA, wherein SEQ ID NO:359 is a clone designated herein as "DNA73742-1662".

15 Figure 360 shows the amino acid sequence (SEQ ID NO:360) derived from the coding sequence of SEQ ID NO:359 shown in Figure 359.

Figure 361 shows a nucleotide sequence (SEQ ID NO:361) of a native sequence PRO1485 cDNA, wherein SEQ ID NO:361 is a clone designated herein as "DNA73746-1654".

Figure 362 shows the amino acid sequence (SEQ ID NO:362) derived from the coding sequence of SEQ ID NO:361 shown in Figure 361.

20 Figure 363 shows a nucleotide sequence (SEQ ID NO:363) of a native sequence PRO1564 cDNA, wherein SEQ ID NO:363 is a clone designated herein as "DNA73760-1672".

Figure 364 shows the amino acid sequence (SEQ ID NO:364) derived from the coding sequence of SEQ ID NO:363 shown in Figure 363.

25 Figure 365 shows a nucleotide sequence (SEQ ID NO:365) of a native sequence PRO1550 cDNA, wherein SEQ ID NO:365 is a clone designated herein as "DNA76393-1664".

Figure 366 shows the amino acid sequence (SEQ ID NO:366) derived from the coding sequence of SEQ ID NO:365 shown in Figure 365.

Figure 367 shows a nucleotide sequence (SEQ ID NO:367) of a native sequence PRO1757 cDNA, wherein SEQ ID NO:367 is a clone designated herein as "DNA76398-1699".

30 Figure 368 shows the amino acid sequence (SEQ ID NO:368) derived from the coding sequence of SEQ ID NO:367 shown in Figure 367.

Figure 369 shows a nucleotide sequence (SEQ ID NO:369) of a native sequence PRO1758 cDNA, wherein SEQ ID NO:369 is a clone designated herein as "DNA76399-1700".

35 Figure 370 shows the amino acid sequence (SEQ ID NO:370) derived from the coding sequence of SEQ ID NO:369 shown in Figure 369.

Figure 371 shows a nucleotide sequence (SEQ ID NO:371) of a native sequence PRO1781 cDNA, wherein SEQ ID NO:371 is a clone designated herein as "DNA76522-2500".

Figure 372 shows the amino acid sequence (SEQ ID NO:372) derived from the coding sequence of SEQ ID NO:371 shown in Figure 371.

Figure 373 shows a nucleotide sequence (SEQ ID NO:373) of a native sequence PRO1606 cDNA, wherein SEQ ID NO:373 is a clone designated herein as "DNA76533-1689".

5 Figure 374 shows the amino acid sequence (SEQ ID NO:374) derived from the coding sequence of SEQ ID NO:373 shown in Figure 373.

Figure 375 shows a nucleotide sequence (SEQ ID NO:375) of a native sequence PRO1784 cDNA, wherein SEQ ID NO:375 is a clone designated herein as "DNA77303-2502".

Figure 376 shows the amino acid sequence (SEQ ID NO:376) derived from the coding sequence of SEQ ID NO:375 shown in Figure 375.

10 Figure 377 shows a nucleotide sequence (SEQ ID NO:377) of a native sequence PRO1774 cDNA, wherein SEQ ID NO:377 is a clone designated herein as "DNA77626-1705".

Figure 378 shows the amino acid sequence (SEQ ID NO:378) derived from the coding sequence of SEQ ID NO:377 shown in Figure 377.

15 Figure 379 shows a nucleotide sequence (SEQ ID NO:379) of a native sequence PRO1605 cDNA, wherein SEQ ID NO:379 is a clone designated herein as "DNA77648-1688".

Figure 380 shows the amino acid sequence (SEQ ID NO:380) derived from the coding sequence of SEQ ID NO:379 shown in Figure 379.

Figure 381 shows a nucleotide sequence (SEQ ID NO:381) of a native sequence PRO1928 cDNA, wherein SEQ ID NO:381 is a clone designated herein as "DNA81754-2532".

20 Figure 382 shows the amino acid sequence (SEQ ID NO:382) derived from the coding sequence of SEQ ID NO:381 shown in Figure 381.

Figure 383 shows a nucleotide sequence (SEQ ID NO:383) of a native sequence PRO1865 cDNA, wherein SEQ ID NO:383 is a clone designated herein as "DNA81757-2512".

25 Figure 384 shows the amino acid sequence (SEQ ID NO:384) derived from the coding sequence of SEQ ID NO:383 shown in Figure 383.

Figure 385 shows a nucleotide sequence (SEQ ID NO:385) of a native sequence PRO1925 cDNA, wherein SEQ ID NO:385 is a clone designated herein as "DNA82302-2529".

Figure 386 shows the amino acid sequence (SEQ ID NO:386) derived from the coding sequence of SEQ ID NO:385 shown in Figure 385.

30 Figure 387 shows a nucleotide sequence (SEQ ID NO:387) of a native sequence PRO1926 cDNA, wherein SEQ ID NO:387 is a clone designated herein as "DNA82340-2530".

Figure 388 shows the amino acid sequence (SEQ ID NO:388) derived from the coding sequence of SEQ ID NO:387 shown in Figure 387.

35 Figure 389 shows a nucleotide sequence (SEQ ID NO:389) of a native sequence PRO2630 cDNA, wherein SEQ ID NO:389 is a clone designated herein as "DNA83551".

Figure 390 shows the amino acid sequence (SEQ ID NO:390) derived from the coding sequence of SEQ ID NO:389 shown in Figure 389.

Figure 391 shows a nucleotide sequence (SEQ ID NO:391) of a native sequence PRO3443 cDNA, wherein SEQ ID NO:391 is a clone designated herein as "DNA87991-2540".

Figure 392 shows the amino acid sequence (SEQ ID NO:392) derived from the coding sequence of SEQ ID NO:391 shown in Figure 391.

5 Figure 393 shows a nucleotide sequence (SEQ ID NO:393) of a native sequence PRO3301 cDNA, wherein SEQ ID NO:393 is a clone designated herein as "DNA88002".

Figure 394 shows the amino acid sequence (SEQ ID NO:394) derived from the coding sequence of SEQ ID NO:393 shown in Figure 393.

Figure 395 shows a nucleotide sequence (SEQ ID NO:395) of a native sequence PRO3442 cDNA, wherein SEQ ID NO:395 is a clone designated herein as "DNA92238-2539".

10 Figure 396 shows the amino acid sequence (SEQ ID NO:396) derived from the coding sequence of SEQ ID NO:395 shown in Figure 395.

Figure 397 shows a nucleotide sequence (SEQ ID NO:397) of a native sequence PRO4978 cDNA, wherein SEQ ID NO:397 is a clone designated herein as "DNA95930".

15 Figure 398 shows the amino acid sequence (SEQ ID NO:398) derived from the coding sequence of SEQ ID NO:397 shown in Figure 397.

Figure 399 shows a nucleotide sequence (SEQ ID NO:399) of a native sequence PRO5801 cDNA, wherein SEQ ID NO:399 is a clone designated herein as "DNA115291-2681".

Figure 400 shows the amino acid sequence (SEQ ID NO:400) derived from the coding sequence of SEQ ID NO:399 shown in Figure 399.

20 Figure 401 shows a nucleotide sequence (SEQ ID NO:401) of a native sequence PRO19630 cDNA, wherein SEQ ID NO:401 is a clone designated herein as "DNA23336-2861".

Figure 402 shows the amino acid sequence (SEQ ID NO:402) derived from the coding sequence of SEQ ID NO:401 shown in Figure 401.

25 Figure 403 shows a nucleotide sequence (SEQ ID NO:403) of a native sequence PRO203 cDNA, wherein SEQ ID NO:403 is a clone designated herein as "DNA30862-1396".

Figure 404 shows the amino acid sequence (SEQ ID NO:404) derived from the coding sequence of SEQ ID NO:403 shown in Figure 403.

Figure 405 shows a nucleotide sequence (SEQ ID NO:405) of a native sequence PRO204 cDNA, wherein SEQ ID NO:405 is a clone designated herein as "DNA30871-1157".

30 Figure 406 shows the amino acid sequence (SEQ ID NO:406) derived from the coding sequence of SEQ ID NO:405 shown in Figure 405.

Figure 407 shows a nucleotide sequence (SEQ ID NO:407) of a native sequence PRO210 cDNA, wherein SEQ ID NO:407 is a clone designated herein as "DNA32279-1131".

35 Figure 408 shows the amino acid sequence (SEQ ID NO:408) derived from the coding sequence of SEQ ID NO:407 shown in Figure 407.

Figure 409 shows a nucleotide sequence (SEQ ID NO:409) of a native sequence PRO223 cDNA, wherein SEQ ID NO:409 is a clone designated herein as "DNA33206-1165".

Figure 410 shows the amino acid sequence (SEQ ID NO:410) derived from the coding sequence of SEQ ID NO:409 shown in Figure 409.

Figure 411 shows a nucleotide sequence (SEQ ID NO:411) of a native sequence PRO247 cDNA, wherein SEQ ID NO:411 is a clone designated herein as "DNA35673-1201".

5 Figure 412 shows the amino acid sequence (SEQ ID NO:412) derived from the coding sequence of SEQ ID NO:411 shown in Figure 411.

Figure 413 shows a nucleotide sequence (SEQ ID NO:413) of a native sequence PRO358 cDNA, wherein SEQ ID NO:413 is a clone designated herein as "DNA47361-1154-2".

Figure 414 shows the amino acid sequence (SEQ ID NO:414) derived from the coding sequence of SEQ ID NO:413 shown in Figure 413.

10 Figure 415 shows a nucleotide sequence (SEQ ID NO:415) of a native sequence PRO724 cDNA, wherein SEQ ID NO:415 is a clone designated herein as "DNA49631-1328".

Figure 416 shows the amino acid sequence (SEQ ID NO:416) derived from the coding sequence of SEQ ID NO:415 shown in Figure 415.

15 Figure 417 shows a nucleotide sequence (SEQ ID NO:417) of a native sequence PRO868 cDNA, wherein SEQ ID NO:417 is a clone designated herein as "DNA52594-1270".

Figure 418 shows the amino acid sequence (SEQ ID NO:418) derived from the coding sequence of SEQ ID NO:417 shown in Figure 417.

Figure 419 shows a nucleotide sequence (SEQ ID NO:419) of a native sequence PRO740 cDNA, wherein SEQ ID NO:419 is a clone designated herein as "DNA55800-1263".

20 Figure 420 shows the amino acid sequence (SEQ ID NO:420) derived from the coding sequence of SEQ ID NO:419 shown in Figure 419.

Figure 421 shows a nucleotide sequence (SEQ ID NO:421) of a native sequence PRO1478 cDNA, wherein SEQ ID NO:421 is a clone designated herein as "DNA56531-1648".

25 Figure 422 shows the amino acid sequence (SEQ ID NO:422) derived from the coding sequence of SEQ ID NO:421 shown in Figure 421.

Figure 423 shows a nucleotide sequence (SEQ ID NO:423) of a native sequence PRO162 cDNA, wherein SEQ ID NO:423 is a clone designated herein as "DNA56965-1356".

Figure 424 shows the amino acid sequence (SEQ ID NO:424) derived from the coding sequence of SEQ ID NO:423 shown in Figure 423.

30 Figure 425 shows a nucleotide sequence (SEQ ID NO:425) of a native sequence PRO828 cDNA, wherein SEQ ID NO:425 is a clone designated herein as "DNA57037-1444".

Figure 426 shows the amino acid sequence (SEQ ID NO:426) derived from the coding sequence of SEQ ID NO:425 shown in Figure 425.

35 Figure 427 shows a nucleotide sequence (SEQ ID NO:427) of a native sequence PRO819 cDNA, wherein SEQ ID NO:427 is a clone designated herein as "DNA57695-1340".

Figure 428 shows the amino acid sequence (SEQ ID NO:428) derived from the coding sequence of SEQ ID NO:427 shown in Figure 427.

Figure 429 shows a nucleotide sequence (SEQ ID NO:429) of a native sequence PRO813 cDNA, wherein SEQ ID NO:429 is a clone designated herein as "DNA57834-1339".

Figure 430 shows the amino acid sequence (SEQ ID NO:430) derived from the coding sequence of SEQ ID NO:429 shown in Figure 429.

5 Figure 431 shows a nucleotide sequence (SEQ ID NO:431) of a native sequence PRO1194 cDNA, wherein SEQ ID NO:431 is a clone designated herein as "DNA57841-1522".

Figure 432 shows the amino acid sequence (SEQ ID NO:432) derived from the coding sequence of SEQ ID NO:431 shown in Figure 431.

Figure 433 shows a nucleotide sequence (SEQ ID NO:433) of a native sequence PRO887 cDNA, wherein SEQ ID NO:433 is a clone designated herein as "DNA58130".

10 Figure 434 shows the amino acid sequence (SEQ ID NO:434) derived from the coding sequence of SEQ ID NO:433 shown in Figure 433.

Figure 435 shows a nucleotide sequence (SEQ ID NO:435) of a native sequence PRO1071 cDNA, wherein SEQ ID NO:435 is a clone designated herein as "DNA58847-1383".

15 Figure 436 shows the amino acid sequence (SEQ ID NO:436) derived from the coding sequence of SEQ ID NO:435 shown in Figure 435.

Figure 437 shows a nucleotide sequence (SEQ ID NO:437) of a native sequence PRO1029 cDNA, wherein SEQ ID NO:437 is a clone designated herein as "DNA59493-1420".

Figure 438 shows the amino acid sequence (SEQ ID NO:438) derived from the coding sequence of SEQ ID NO:437 shown in Figure 437.

20 Figure 439 shows a nucleotide sequence (SEQ ID NO:439) of a native sequence PRO1190 cDNA, wherein SEQ ID NO:439 is a clone designated herein as "DNA59586-1520".

Figure 440 shows the amino acid sequence (SEQ ID NO:440) derived from the coding sequence of SEQ ID NO:439 shown in Figure 439.

25 Figure 441 shows a nucleotide sequence (SEQ ID NO:441) of a native sequence PRO4334 cDNA, wherein SEQ ID NO:441 is a clone designated herein as "DNA59608-2577".

Figure 442 shows the amino acid sequence (SEQ ID NO:442) derived from the coding sequence of SEQ ID NO:441 shown in Figure 441.

Figure 443 shows a nucleotide sequence (SEQ ID NO:443) of a native sequence PRO1155 cDNA, wherein SEQ ID NO:443 is a clone designated herein as "DNA59849-1504".

30 Figure 444 shows the amino acid sequence (SEQ ID NO:444) derived from the coding sequence of SEQ ID NO:443 shown in Figure 443.

Figure 445 shows a nucleotide sequence (SEQ ID NO:445) of a native sequence PRO1157 cDNA, wherein SEQ ID NO:445 is a clone designated herein as "DNA60292-1506".

35 Figure 446 shows the amino acid sequence (SEQ ID NO:446) derived from the coding sequence of SEQ ID NO:445 shown in Figure 445.

Figure 447 shows a nucleotide sequence (SEQ ID NO:447) of a native sequence PRO1122 cDNA, wherein SEQ ID NO:447 is a clone designated herein as "DNA62377-1381-1".

Figure 448 shows the amino acid sequence (SEQ ID NO:448) derived from the coding sequence of SEQ ID NO:447 shown in Figure 447.

Figure 449 shows a nucleotide sequence (SEQ ID NO:449) of a native sequence PRO1183 cDNA, wherein SEQ ID NO:449 is a clone designated herein as "DNA62880-1513".

5 Figure 450 shows the amino acid sequence (SEQ ID NO:450) derived from the coding sequence of SEQ ID NO:449 shown in Figure 449.

Figure 451 shows a nucleotide sequence (SEQ ID NO:451) of a native sequence PRO1337 cDNA, wherein SEQ ID NO:451 is a clone designated herein as "DNA66672-1586".

Figure 452 shows the amino acid sequence (SEQ ID NO:452) derived from the coding sequence of SEQ ID NO:451 shown in Figure 451.

10 Figure 453 shows a nucleotide sequence (SEQ ID NO:453) of a native sequence PRO1480 cDNA, wherein SEQ ID NO:453 is a clone designated herein as "DNA67962-1649".

Figure 454 shows the amino acid sequence (SEQ ID NO:454) derived from the coding sequence of SEQ ID NO:453 shown in Figure 453.

15 Figure 455 shows a nucleotide sequence (SEQ ID NO:455) of a native sequence PRO19645 cDNA, wherein SEQ ID NO:455 is a clone designated herein as "DNA69555-2867".

Figure 456 shows the amino acid sequence (SEQ ID NO:456) derived from the coding sequence of SEQ ID NO:455 shown in Figure 455.

Figure 457 shows a nucleotide sequence (SEQ ID NO:457) of a native sequence PRO9782 cDNA, wherein SEQ ID NO:457 is a clone designated herein as "DNA71162-2764".

20 Figure 458 shows the amino acid sequence (SEQ ID NO:458) derived from the coding sequence of SEQ ID NO:457 shown in Figure 457.

Figure 459 shows a nucleotide sequence (SEQ ID NO:459) of a native sequence PRO1419 cDNA, wherein SEQ ID NO:459 is a clone designated herein as "DNA71290-1630".

25 Figure 460 shows the amino acid sequence (SEQ ID NO:460) derived from the coding sequence of SEQ ID NO:459 shown in Figure 459.

Figure 461 shows a nucleotide sequence (SEQ ID NO:461) of a native sequence PRO1575 cDNA, wherein SEQ ID NO:461 is a clone designated herein as "DNA76401-1683".

Figure 462 shows the amino acid sequence (SEQ ID NO:462) derived from the coding sequence of SEQ ID NO:461 shown in Figure 461.

30 Figure 463 shows a nucleotide sequence (SEQ ID NO:463) of a native sequence PRO1567 cDNA, wherein SEQ ID NO:463 is a clone designated herein as "DNA76541-1675".

Figure 464 shows the amino acid sequence (SEQ ID NO:464) derived from the coding sequence of SEQ ID NO:463 shown in Figure 463.

35 Figure 465 shows a nucleotide sequence (SEQ ID NO:465) of a native sequence PRO1891 cDNA, wherein SEQ ID NO:465 is a clone designated herein as "DNA76788-2526".

Figure 466 shows the amino acid sequence (SEQ ID NO:466) derived from the coding sequence of SEQ ID NO:465 shown in Figure 465.

Figure 467 shows a nucleotide sequence (SEQ ID NO:467) of a native sequence PRO1889 cDNA, wherein SEQ ID NO:467 is a clone designated herein as "DNA77623-2524".

Figure 468 shows the amino acid sequence (SEQ ID NO:468) derived from the coding sequence of SEQ ID NO:467 shown in Figure 467.

5 Figure 469 shows a nucleotide sequence (SEQ ID NO:469) of a native sequence PRO1785 cDNA, wherein SEQ ID NO:469 is a clone designated herein as "DNA80136-2503".

Figure 470 shows the amino acid sequence (SEQ ID NO:470) derived from the coding sequence of SEQ ID NO:469 shown in Figure 469.

Figure 471 shows a nucleotide sequence (SEQ ID NO:471) of a native sequence PRO6003 cDNA, wherein SEQ ID NO:471 is a clone designated herein as "DNA83568-2692".

10 Figure 472 shows the amino acid sequence (SEQ ID NO:472) derived from the coding sequence of SEQ ID NO:471 shown in Figure 471.

Figure 473 shows a nucleotide sequence (SEQ ID NO:473) of a native sequence PRO4333 cDNA, wherein SEQ ID NO:473 is a clone designated herein as "DNA84210-2576".

15 Figure 474 shows the amino acid sequence (SEQ ID NO:474) derived from the coding sequence of SEQ ID NO:473 shown in Figure 473.

Figure 475 shows a nucleotide sequence (SEQ ID NO:475) of a native sequence PRO4356 cDNA, wherein SEQ ID NO:475 is a clone designated herein as "DNA86576-2595".

Figure 476 shows the amino acid sequence (SEQ ID NO:476) derived from the coding sequence of SEQ ID NO:475 shown in Figure 475.

20 Figure 477 shows a nucleotide sequence (SEQ ID NO:477) of a native sequence PRO4352 cDNA, wherein SEQ ID NO:477 is a clone designated herein as "DNA87976-2593".

Figure 478 shows the amino acid sequence (SEQ ID NO:478) derived from the coding sequence of SEQ ID NO:477 shown in Figure 477.

25 Figure 479 shows a nucleotide sequence (SEQ ID NO:479) of a native sequence PRO4354 cDNA, wherein SEQ ID NO:479 is a clone designated herein as "DNA92256-2596".

Figure 480 shows the amino acid sequence (SEQ ID NO:480) derived from the coding sequence of SEQ ID NO:479 shown in Figure 479.

Figure 481 shows a nucleotide sequence (SEQ ID NO:481) of a native sequence PRO4369 cDNA, wherein SEQ ID NO:481 is a clone designated herein as "DNA92289-2598".

30 Figure 482 shows the amino acid sequence (SEQ ID NO:482) derived from the coding sequence of SEQ ID NO:481 shown in Figure 481.

Figure 483 shows a nucleotide sequence (SEQ ID NO:483) of a native sequence PRO6030 cDNA, wherein SEQ ID NO:483 is a clone designated herein as "DNA96850-2705".

35 Figure 484 shows the amino acid sequence (SEQ ID NO:484) derived from the coding sequence of SEQ ID NO:483 shown in Figure 483.

Figure 485 shows a nucleotide sequence (SEQ ID NO:485) of a native sequence PRO4433 cDNA, wherein SEQ ID NO:485 is a clone designated herein as "DNA96855-2629".

Figure 486 shows the amino acid sequence (SEQ ID NO:486) derived from the coding sequence of SEQ ID NO:485 shown in Figure 485.

Figure 487 shows a nucleotide sequence (SEQ ID NO:487) of a native sequence PRO4424 cDNA, wherein SEQ ID NO:487 is a clone designated herein as "DNA96857-2636".

5 Figure 488 shows the amino acid sequence (SEQ ID NO:488) derived from the coding sequence of SEQ ID NO:487 shown in Figure 487.

Figure 489 shows a nucleotide sequence (SEQ ID NO:489) of a native sequence PRO6017 cDNA, wherein SEQ ID NO:489 is a clone designated herein as "DNA96860-2700".

Figure 490 shows the amino acid sequence (SEQ ID NO:490) derived from the coding sequence of SEQ ID NO:489 shown in Figure 489.

10 Figure 491 shows a nucleotide sequence (SEQ ID NO:491) of a native sequence PRO19563 cDNA, wherein SEQ ID NO:491 is a clone designated herein as "DNA96861-2844".

Figure 492 shows the amino acid sequence (SEQ ID NO:492) derived from the coding sequence of SEQ ID NO:491 shown in Figure 491.

15 Figure 493 shows a nucleotide sequence (SEQ ID NO:493) of a native sequence PRO6015 cDNA, wherein SEQ ID NO:493 is a clone designated herein as "DNA96866-2698".

Figure 494 shows the amino acid sequence (SEQ ID NO:494) derived from the coding sequence of SEQ ID NO:493 shown in Figure 493.

Figure 495 shows a nucleotide sequence (SEQ ID NO:495) of a native sequence PRO5779 cDNA, wherein SEQ ID NO:495 is a clone designated herein as "DNA96870-2676".

20 Figure 496 shows the amino acid sequence (SEQ ID NO:496) derived from the coding sequence of SEQ ID NO:495 shown in Figure 495.

Figure 497 shows a nucleotide sequence (SEQ ID NO:497) of a native sequence PRO5776 cDNA, wherein SEQ ID NO:497 is a clone designated herein as "DNA96872-2674".

25 Figure 498 shows the amino acid sequence (SEQ ID NO:498) derived from the coding sequence of SEQ ID NO:497 shown in Figure 497.

Figure 499 shows a nucleotide sequence (SEQ ID NO:499) of a native sequence PRO4430 cDNA, wherein SEQ ID NO:499 is a clone designated herein as "DNA96878-2626".

Figure 500 shows the amino acid sequence (SEQ ID NO:500) derived from the coding sequence of SEQ ID NO:499 shown in Figure 499.

30 Figure 501 shows a nucleotide sequence (SEQ ID NO:501) of a native sequence PRO4421 cDNA, wherein SEQ ID NO:501 is a clone designated herein as "DNA96879-2619".

Figure 502 shows the amino acid sequence (SEQ ID NO:502) derived from the coding sequence of SEQ ID NO:501 shown in Figure 501.

35 Figure 503 shows a nucleotide sequence (SEQ ID NO:503) of a native sequence PRO4499 cDNA, wherein SEQ ID NO:503 is a clone designated herein as "DNA96889-2641".

Figure 504 shows the amino acid sequence (SEQ ID NO:504) derived from the coding sequence of SEQ ID NO:503 shown in Figure 503.

Figure 505 shows a nucleotide sequence (SEQ ID NO:505) of a native sequence PRO4423 cDNA, wherein SEQ ID NO:505 is a clone designated herein as "DNA96893-2621".

Figure 506 shows the amino acid sequence (SEQ ID NO:506) derived from the coding sequence of SEQ ID NO:505 shown in Figure 505.

5 Figure 507 shows a nucleotide sequence (SEQ ID NO:507) of a native sequence PRO5998 cDNA, wherein SEQ ID NO:507 is a clone designated herein as "DNA96897-2688".

Figure 508 shows the amino acid sequence (SEQ ID NO:508) derived from the coding sequence of SEQ ID NO:507 shown in Figure 507.

Figure 509 shows a nucleotide sequence (SEQ ID NO:509) of a native sequence PRO4501 cDNA, wherein SEQ ID NO:509 is a clone designated herein as "DNA98564-2643".

10 Figure 510 shows the amino acid sequence (SEQ ID NO:510) derived from the coding sequence of SEQ ID NO:509 shown in Figure 509.

Figure 511 shows a nucleotide sequence (SEQ ID NO:511) of a native sequence PRO6240 cDNA, wherein SEQ ID NO:511 is a clone designated herein as "DNA107443-2718".

15 Figure 512 shows the amino acid sequence (SEQ ID NO:512) derived from the coding sequence of SEQ ID NO:511 shown in Figure 511.

Figure 513 shows a nucleotide sequence (SEQ ID NO:513) of a native sequence PRO6245 cDNA, wherein SEQ ID NO:513 is a clone designated herein as "DNA107786-2723".

Figure 514 shows the amino acid sequence (SEQ ID NO:514) derived from the coding sequence of SEQ ID NO:513 shown in Figure 513.

20 Figure 515 shows a nucleotide sequence (SEQ ID NO:515) of a native sequence PRO6175 cDNA, wherein SEQ ID NO:515 is a clone designated herein as "DNA108682-2712".

Figure 516 shows the amino acid sequence (SEQ ID NO:516) derived from the coding sequence of SEQ ID NO:515 shown in Figure 515.

25 Figure 517 shows a nucleotide sequence (SEQ ID NO:517) of a native sequence PRO9742 cDNA, wherein SEQ ID NO:517 is a clone designated herein as "DNA108684-2761".

Figure 518 shows the amino acid sequence (SEQ ID NO:518) derived from the coding sequence of SEQ ID NO:517 shown in Figure 517.

Figure 519 shows a nucleotide sequence (SEQ ID NO:519) of a native sequence PRO7179 cDNA, wherein SEQ ID NO:519 is a clone designated herein as "DNA108701-2749".

30 Figure 520 shows the amino acid sequence (SEQ ID NO:520) derived from the coding sequence of SEQ ID NO:519 shown in Figure 519.

Figure 521 shows a nucleotide sequence (SEQ ID NO:521) of a native sequence PRO6239 cDNA, wherein SEQ ID NO:521 is a clone designated herein as "DNA108720-2717".

35 Figure 522 shows the amino acid sequence (SEQ ID NO:522) derived from the coding sequence of SEQ ID NO:521 shown in Figure 521.

Figure 523 shows a nucleotide sequence (SEQ ID NO:523) of a native sequence PRO6493 cDNA, wherein SEQ ID NO:523 is a clone designated herein as "DNA108726-2729".

Figure 524 shows the amino acid sequence (SEQ ID NO:524) derived from the coding sequence of SEQ ID NO:523 shown in Figure 523.

Figures 525A-525B show a nucleotide sequence (SEQ ID NO:525) of a native sequence PRO9741 cDNA, wherein SEQ ID NO:525 is a clone designated herein as "DNA108728-2760".

5 Figure 526 shows the amino acid sequence (SEQ ID NO:526) derived from the coding sequence of SEQ ID NO:525 shown in Figures 525A-525B.

Figure 527 shows a nucleotide sequence (SEQ ID NO:527) of a native sequence PRO9822 cDNA, wherein SEQ ID NO:527 is a clone designated herein as "DNA108738-2767".

Figure 528 shows the amino acid sequence (SEQ ID NO:528) derived from the coding sequence of SEQ ID NO:527 shown in Figure 527.

10 Figure 529 shows a nucleotide sequence (SEQ ID NO:529) of a native sequence PRO6244 cDNA, wherein SEQ ID NO:529 is a clone designated herein as "DNA108743-2722".

Figure 530 shows the amino acid sequence (SEQ ID NO:530) derived from the coding sequence of SEQ ID NO:529 shown in Figure 529.

15 Figure 531 shows a nucleotide sequence (SEQ ID NO:531) of a native sequence PRO9740 cDNA, wherein SEQ ID NO:531 is a clone designated herein as "DNA108758-2759".

Figure 532 shows the amino acid sequence (SEQ ID NO:532) derived from the coding sequence of SEQ ID NO:531 shown in Figure 531.

Figure 533 shows a nucleotide sequence (SEQ ID NO:533) of a native sequence PRO9739 cDNA, wherein SEQ ID NO:533 is a clone designated herein as "DNA108765-2758".

20 Figure 534 shows the amino acid sequence (SEQ ID NO:534) derived from the coding sequence of SEQ ID NO:533 shown in Figure 533.

Figure 535 shows a nucleotide sequence (SEQ ID NO:535) of a native sequence PRO7177 cDNA, wherein SEQ ID NO:535 is a clone designated herein as "DNA108783-2747".

25 Figure 536 shows the amino acid sequence (SEQ ID NO:536) derived from the coding sequence of SEQ ID NO:535 shown in Figure 535.

Figure 537 shows a nucleotide sequence (SEQ ID NO:537) of a native sequence PRO7178 cDNA, wherein SEQ ID NO:537 is a clone designated herein as "DNA108789-2748".

Figure 538 shows the amino acid sequence (SEQ ID NO:538) derived from the coding sequence of SEQ ID NO:537 shown in Figure 537.

30 Figure 539 shows a nucleotide sequence (SEQ ID NO:539) of a native sequence PRO6246 cDNA, wherein SEQ ID NO:539 is a clone designated herein as "DNA108806-2724".

Figure 540 shows the amino acid sequence (SEQ ID NO:540) derived from the coding sequence of SEQ ID NO:539 shown in Figure 539.

35 Figure 541 shows a nucleotide sequence (SEQ ID NO:541) of a native sequence PRO6241 cDNA, wherein SEQ ID NO:541 is a clone designated herein as "DNA108936-2719".

Figure 542 shows the amino acid sequence (SEQ ID NO:542) derived from the coding sequence of SEQ ID NO:541 shown in Figure 541.

Figure 543 shows a nucleotide sequence (SEQ ID NO:543) of a native sequence PRO9835 cDNA, wherein SEQ ID NO:543 is a clone designated herein as "DNA119510-2771".

Figure 544 shows the amino acid sequence (SEQ ID NO:544) derived from the coding sequence of SEQ ID NO:543 shown in Figure 543.

5 Figure 545 shows a nucleotide sequence (SEQ ID NO:545) of a native sequence PRO9857 cDNA, wherein SEQ ID NO:545 is a clone designated herein as "DNA119517-2778".

Figure 546 shows the amino acid sequence (SEQ ID NO:546) derived from the coding sequence of SEQ ID NO:545 shown in Figure 545.

Figure 547 shows a nucleotide sequence (SEQ ID NO:547) of a native sequence PRO7436 cDNA, wherein SEQ ID NO:547 is a clone designated herein as "DNA119535-2756".

10 Figure 548 shows the amino acid sequence (SEQ ID NO:548) derived from the coding sequence of SEQ ID NO:547 shown in Figure 547.

Figure 549 shows a nucleotide sequence (SEQ ID NO:549) of a native sequence PRO9856 cDNA, wherein SEQ ID NO:549 is a clone designated herein as "DNA119537-2777".

15 Figure 550 shows the amino acid sequence (SEQ ID NO:550) derived from the coding sequence of SEQ ID NO:549 shown in Figure 549.

Figure 551 shows a nucleotide sequence (SEQ ID NO:551) of a native sequence PRO19605 cDNA, wherein SEQ ID NO:551 is a clone designated herein as "DNA119714-2851".

Figure 552 shows the amino acid sequence (SEQ ID NO:552) derived from the coding sequence of SEQ ID NO:551 shown in Figure 551.

20 Figure 553 shows a nucleotide sequence (SEQ ID NO:553) of a native sequence PRO9859 cDNA, wherein SEQ ID NO:553 is a clone designated herein as "DNA125170-2780".

Figure 554 shows the amino acid sequence (SEQ ID NO:554) derived from the coding sequence of SEQ ID NO:553 shown in Figure 553.

25 Figure 555 shows a nucleotide sequence (SEQ ID NO:555) of a native sequence PRO12970 cDNA, wherein SEQ ID NO:555 is a clone designated herein as "DNA129594-2841".

Figure 556 shows the amino acid sequence (SEQ ID NO:556) derived from the coding sequence of SEQ ID NO:555 shown in Figure 555.

Figure 557 shows a nucleotide sequence (SEQ ID NO:557) of a native sequence PRO19626 cDNA, wherein SEQ ID NO:557 is a clone designated herein as "DNA129793-2857".

30 Figure 558 shows the amino acid sequence (SEQ ID NO:558) derived from the coding sequence of SEQ ID NO:557 shown in Figure 557.

Figure 559 shows a nucleotide sequence (SEQ ID NO:559) of a native sequence PRO9833 cDNA, wherein SEQ ID NO:559 is a clone designated herein as "DNA130809-2769".

35 Figure 560 shows the amino acid sequence (SEQ ID NO:560) derived from the coding sequence of SEQ ID NO:559 shown in Figure 559.

Figure 561 shows a nucleotide sequence (SEQ ID NO:561) of a native sequence PRO19670 cDNA, wherein SEQ ID NO:561 is a clone designated herein as "DNA131639-2874".

Figure 562 shows the amino acid sequence (SEQ ID NO:562) derived from the coding sequence of SEQ ID NO:561 shown in Figure 561.

Figure 563 shows a nucleotide sequence (SEQ ID NO:563) of a native sequence PRO19624 cDNA, wherein SEQ ID NO:563 is a clone designated herein as "DNA131649-2855".

5 Figure 564 shows the amino acid sequence (SEQ ID NO:564) derived from the coding sequence of SEQ ID NO:563 shown in Figure 563.

Figure 565 shows a nucleotide sequence (SEQ ID NO:565) of a native sequence PRO19680 cDNA, wherein SEQ ID NO:565 is a clone designated herein as "DNA131652-2876".

Figure 566 shows the amino acid sequence (SEQ ID NO:566) derived from the coding sequence of SEQ ID NO:565 shown in Figure 565.

10 Figure 567 shows a nucleotide sequence (SEQ ID NO:567) of a native sequence PRO19675 cDNA, wherein SEQ ID NO:567 is a clone designated herein as "DNA131658-2875".

Figure 568 shows the amino acid sequence (SEQ ID NO:568) derived from the coding sequence of SEQ ID NO:567 shown in Figure 567.

15 Figure 569 shows a nucleotide sequence (SEQ ID NO:569) of a native sequence PRO9834 cDNA, wherein SEQ ID NO:569 is a clone designated herein as "DNA132162-2770".

Figure 570 shows the amino acid sequence (SEQ ID NO:570) derived from the coding sequence of SEQ ID NO:569 shown in Figure 569.

Figure 571 shows a nucleotide sequence (SEQ ID NO:571) of a native sequence PRO9744 cDNA, wherein SEQ ID NO:571 is a clone designated herein as "DNA136110-2763".

20 Figure 572 shows the amino acid sequence (SEQ ID NO:572) derived from the coding sequence of SEQ ID NO:571 shown in Figure 571.

Figure 573 shows a nucleotide sequence (SEQ ID NO:573) of a native sequence PRO19644 cDNA, wherein SEQ ID NO:573 is a clone designated herein as "DNA139592-2866".

25 Figure 574 shows the amino acid sequence (SEQ ID NO:574) derived from the coding sequence of SEQ ID NO:573 shown in Figure 573.

Figure 575 shows a nucleotide sequence (SEQ ID NO:575) of a native sequence PRO19625 cDNA, wherein SEQ ID NO:575 is a clone designated herein as "DNA139608-2856".

Figure 576 shows the amino acid sequence (SEQ ID NO:576) derived from the coding sequence of SEQ ID NO:575 shown in Figure 575.

30 Figure 577 shows a nucleotide sequence (SEQ ID NO:577) of a native sequence PRO19597 cDNA, wherein SEQ ID NO:577 is a clone designated herein as "DNA143292-2848".

Figure 578 shows the amino acid sequence (SEQ ID NO:578) derived from the coding sequence of SEQ ID NO:577 shown in Figure 577.

35 Figure 579 shows a nucleotide sequence (SEQ ID NO:579) of a native sequence PRO16090 cDNA, wherein SEQ ID NO:579 is a clone designated herein as "DNA144844-2843".

Figure 580 shows the amino acid sequence (SEQ ID NO:580) derived from the coding sequence of SEQ ID NO:579 shown in Figure 579.

Figure 581 shows a nucleotide sequence (SEQ ID NO:581) of a native sequence PRO19576 cDNA, wherein SEQ ID NO:581 is a clone designated herein as "DNA144857-2845".

Figure 582 shows the amino acid sequence (SEQ ID NO:582) derived from the coding sequence of SEQ ID NO:581 shown in Figure 581.

Figure 583 shows a nucleotide sequence (SEQ ID NO:583) of a native sequence PRO19646 cDNA, wherein SEQ ID NO:583 is a clone designated herein as "DNA145841-2868".

Figure 584 shows the amino acid sequence (SEQ ID NO:584) derived from the coding sequence of SEQ ID NO:583 shown in Figure 583.

Figure 585 shows a nucleotide sequence (SEQ ID NO:585) of a native sequence PRO19814 cDNA, wherein SEQ ID NO:585 is a clone designated herein as "DNA148004-2882".

Figure 586 shows the amino acid sequence (SEQ ID NO:586) derived from the coding sequence of SEQ ID NO:585 shown in Figure 585.

Figure 587 shows a nucleotide sequence (SEQ ID NO:587) of a native sequence PRO19669 cDNA, wherein SEQ ID NO:587 is a clone designated herein as "DNA149893-2873".

Figure 588 shows the amino acid sequence (SEQ ID NO:588) derived from the coding sequence of SEQ ID NO:587 shown in Figure 587.

Figure 589 shows a nucleotide sequence (SEQ ID NO:589) of a native sequence PRO19818 cDNA, wherein SEQ ID NO:589 is a clone designated herein as "DNA149930-2884".

Figure 590 shows the amino acid sequence (SEQ ID NO:590) derived from the coding sequence of SEQ ID NO:589 shown in Figure 589.

Figure 591 shows a nucleotide sequence (SEQ ID NO:591) of a native sequence PRO20088 cDNA, wherein SEQ ID NO:591 is a clone designated herein as "DNA150157-2898".

Figure 592 shows the amino acid sequence (SEQ ID NO:592) derived from the coding sequence of SEQ ID NO:591 shown in Figure 591.

Figure 593 shows a nucleotide sequence (SEQ ID NO:593) of a native sequence PRO16089 cDNA, wherein SEQ ID NO:593 is a clone designated herein as "DNA150163-2842".

Figure 594 shows the amino acid sequence (SEQ ID NO:594) derived from the coding sequence of SEQ ID NO:593 shown in Figure 593.

Figure 595 shows a nucleotide sequence (SEQ ID NO:595) of a native sequence PRO20025 cDNA, wherein SEQ ID NO:595 is a clone designated herein as "DNA153579-2894".

Figure 596 shows the amino acid sequence (SEQ ID NO:596) derived from the coding sequence of SEQ ID NO:595 shown in Figure 595.

Figure 597 shows a nucleotide sequence (SEQ ID NO:597) of a native sequence PRO20040 cDNA, wherein SEQ ID NO:597 is a clone designated herein as "DNA164625-2890".

Figure 598 shows the amino acid sequence (SEQ ID NO:598) derived from the coding sequence of SEQ ID NO:597 shown in Figure 597.

Figure 599 shows a nucleotide sequence (SEQ ID NO:599) of a native sequence PRO791 cDNA, wherein SEQ ID NO:599 is a clone designated herein as "DNA57838-1337".

Figure 600 shows the amino acid sequence (SEQ ID NO:600) derived from the coding sequence of SEQ ID NO:599 shown in Figure 599.

Figure 601 shows a nucleotide sequence (SEQ ID NO:601) of a native sequence PRO1131 cDNA, wherein SEQ ID NO:601 is a clone designated herein as "DNA59777-1480".

5 Figure 602 shows the amino acid sequence (SEQ ID NO:602) derived from the coding sequence of SEQ ID NO:601 shown in Figure 601.

Figure 603 shows a nucleotide sequence (SEQ ID NO:603) of a native sequence PRO1343 cDNA, wherein SEQ ID NO:603 is a clone designated herein as "DNA66675-1587".

Figure 604 shows the amino acid sequence (SEQ ID NO:604) derived from the coding sequence of SEQ ID NO:603 shown in Figure 603.

10 Figure 605 shows a nucleotide sequence (SEQ ID NO:605) of a native sequence PRO1760 cDNA, wherein SEQ ID NO:605 is a clone designated herein as "DNA76532-1702".

Figure 606 shows the amino acid sequence (SEQ ID NO:606) derived from the coding sequence of SEQ ID NO:605 shown in Figure 605.

15 Figure 607 shows a nucleotide sequence (SEQ ID NO:607) of a native sequence PRO6029 cDNA, wherein SEQ ID NO:607 is a clone designated herein as "DNA105849-2704".

Figure 608 shows the amino acid sequence (SEQ ID NO:608) derived from the coding sequence of SEQ ID NO:607 shown in Figure 607.

Figure 609 shows a nucleotide sequence (SEQ ID NO:609) of a native sequence PRO1801 cDNA, wherein SEQ ID NO:609 is a clone designated herein as "DNA83500-2506".

20 Figure 610 shows the amino acid sequence (SEQ ID NO:610) derived from the coding sequence of SEQ ID NO:609 shown in Figure 609.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

I. Definitions

25 The terms "PRO polypeptide" and "PRO" as used herein and when immediately followed by a numerical designation refer to various polypeptides, wherein the complete designation (i.e., PRO/number) refers to specific polypeptide sequences as described herein. The terms "PRO/number polypeptide" and "PRO/number" wherein the term "number" is provided as an actual numerical designation as used herein encompass native sequence polypeptides and polypeptide variants (which are further defined herein). The PRO polypeptides described herein
30 may be isolated from a variety of sources, such as from human tissue types or from another source, or prepared by recombinant or synthetic methods. The term "PRO polypeptide" refers to each individual PRO/number polypeptide disclosed herein. All disclosures in this specification which refer to the "PRO polypeptide" refer to each of the polypeptides individually as well as jointly. For example, descriptions of the preparation of, purification of, derivation of, formation of antibodies to or against, administration of, compositions containing, treatment of a disease with, etc., pertain to each polypeptide of the invention individually. The term "PRO
35 polypeptide" also includes variants of the PRO/number polypeptides disclosed herein.

A "native sequence PRO polypeptide" comprises a polypeptide having the same amino acid sequence as

the corresponding PRO polypeptide derived from nature. Such native sequence PRO polypeptides can be isolated from nature or can be produced by recombinant or synthetic means. The term "native sequence PRO polypeptide" specifically encompasses naturally-occurring truncated or secreted forms of the specific PRO polypeptide (*e.g.*, an extracellular domain sequence), naturally-occurring variant forms (*e.g.*, alternatively spliced forms) and naturally-occurring allelic variants of the polypeptide. In various embodiments of the invention, the native sequence PRO polypeptides disclosed herein are mature or full-length native sequence polypeptides comprising the full-length amino acids sequences shown in the accompanying figures. Start and stop codons are shown in bold font and underlined in the figures. However, while the PRO polypeptide disclosed in the accompanying figures are shown to begin with methionine residues designated herein as amino acid position 1 in the figures, it is conceivable and possible that other methionine residues located either upstream or downstream from the amino acid position 1 in the figures may be employed as the starting amino acid residue for the PRO polypeptides.

The PRO polypeptide "extracellular domain" or "ECD" refers to a form of the PRO polypeptide which is essentially free of the transmembrane and cytoplasmic domains. Ordinarily, a PRO polypeptide ECD will have less than 1% of such transmembrane and/or cytoplasmic domains and preferably, will have less than 0.5% of such domains. It will be understood that any transmembrane domains identified for the PRO polypeptides of the present invention are identified pursuant to criteria routinely employed in the art for identifying that type of hydrophobic domain. The exact boundaries of a transmembrane domain may vary but most likely by no more than about 5 amino acids at either end of the domain as initially identified herein. Optionally, therefore, an extracellular domain of a PRO polypeptide may contain from about 5 or fewer amino acids on either side of the transmembrane domain/extracellular domain boundary as identified in the Examples or specification and such polypeptides, with or without the associated signal peptide, and nucleic acid encoding them, are contemplated by the present invention.

The approximate location of the "signal peptides" of the various PRO polypeptides disclosed herein are shown in the present specification and/or the accompanying figures. It is noted, however, that the C-terminal boundary of a signal peptide may vary, but most likely by no more than about 5 amino acids on either side of the signal peptide C-terminal boundary as initially identified herein, wherein the C-terminal boundary of the signal peptide may be identified pursuant to criteria routinely employed in the art for identifying that type of amino acid sequence element (*e.g.*, Nielsen et al., Prot. Eng. 10:1-6 (1997) and von Heinje et al., Nucl. Acids. Res. 14:4683-4690 (1986)). Moreover, it is also recognized that, in some cases, cleavage of a signal sequence from a secreted polypeptide is not entirely uniform, resulting in more than one secreted species. These mature polypeptides, where the signal peptide is cleaved within no more than about 5 amino acids on either side of the C-terminal boundary of the signal peptide as identified herein, and the polynucleotides encoding them, are contemplated by the present invention.

"PRO polypeptide variant" means an active PRO polypeptide as defined above or below having at least about 80% amino acid sequence identity with a full-length native sequence PRO polypeptide sequence as disclosed herein, a PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Such PRO polypeptide variants include, for instance, PRO

polypeptides wherein one or more amino acid residues are added, or deleted, at the N- or C-terminus of the full-length native amino acid sequence. Ordinarily, a PRO polypeptide variant will have at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to a full-length native sequence PRO polypeptide sequence as disclosed herein, a PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of a full-length PRO polypeptide sequence as disclosed herein. Ordinarily, PRO variant polypeptides are at least about 10 amino acids in length, alternatively at least about 20 amino acids in length, alternatively at least about 30 amino acids in length, alternatively at least about 40 amino acids in length, alternatively at least about 50 amino acids in length, alternatively at least about 60 amino acids in length, alternatively at least about 70 amino acids in length, alternatively at least about 80 amino acids in length, alternatively at least about 90 amino acids in length, alternatively at least about 100 amino acids in length, alternatively at least about 150 amino acids in length, alternatively at least about 200 amino acids in length, alternatively at least about 300 amino acids in length, or more.

"Percent (%) amino acid sequence identity" with respect to the PRO polypeptide sequences identified herein is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the specific PRO polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. For purposes herein, however, % amino acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through

Genentech, Inc., South San Francisco, California or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

$$100 \text{ times the fraction } X/Y$$

where X is the number of amino acid residues scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A. As examples of % amino acid sequence identity calculations using this method, Tables 2 and 3 demonstrate how to calculate the % amino acid sequence identity of the amino acid sequence designated "Comparison Protein" to the amino acid sequence designated "PRO", wherein "PRO" represents the amino acid sequence of a hypothetical PRO polypeptide of interest, "Comparison Protein" represents the amino acid sequence of a polypeptide against which the "PRO" polypeptide of interest is being compared, and "X", "Y" and "Z" each represent different hypothetical amino acid residues.

Unless specifically stated otherwise, all % amino acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program. However, % amino acid sequence identity values may also be obtained as described below by using the WU-BLAST-2 computer program (Altschul et al., Methods in Enzymology 266:460-480 (1996)). Most of the WU-BLAST-2 search parameters are set to the default values. Those not set to default values, i.e., the adjustable parameters, are set with the following values: overlap span = 1, overlap fraction = 0.125, word threshold (T) = 11, and scoring matrix = BLOSUM62. When WU-BLAST-2 is employed, a % amino acid sequence identity value is determined by dividing (a) the number of matching identical amino acid residues between the amino acid sequence of the PRO polypeptide of interest having a sequence derived from the native PRO polypeptide and the comparison amino acid sequence of interest (i.e., the sequence against which the PRO polypeptide of interest is being compared which may be a PRO variant polypeptide) as determined by WU-BLAST-2 by (b) the total number of amino acid residues of the PRO polypeptide of interest. For example, in the statement "a polypeptide comprising an the amino acid sequence A which has or having at least 80% amino acid sequence identity to the amino acid sequence B", the amino acid sequence A is the comparison amino acid sequence of interest and the amino acid sequence B is the amino acid sequence of the PRO polypeptide of interest.

Percent amino acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from <http://www.ncbi.nlm.nih.gov> or otherwise obtained from the

National Institute of Health, Bethesda, MD. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.

In situations where NCBI-BLAST2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

$$100 \text{ times the fraction } X/Y$$

where X is the number of amino acid residues scored as identical matches by the sequence alignment program NCBI-BLAST2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A.

"PRO variant polynucleotide" or "PRO variant nucleic acid sequence" means a nucleic acid molecule which encodes an active PRO polypeptide as defined below and which has at least about 80% nucleic acid sequence identity with a nucleotide acid sequence encoding a full-length native sequence PRO polypeptide sequence as disclosed herein, a full-length native sequence PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Ordinarily, a PRO variant polynucleotide will have at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity with a nucleic acid sequence encoding a full-length native sequence PRO polypeptide sequence as disclosed herein, a full-length native sequence PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal sequence, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Variants do not encompass the native nucleotide sequence.

Ordinarily, PRO variant polynucleotides are at least about 30 nucleotides in length, alternatively at least about 60 nucleotides in length, alternatively at least about 90 nucleotides in length, alternatively at least about 120 nucleotides in length, alternatively at least about 150 nucleotides in length, alternatively at least about 180 nucleotides in length, alternatively at least about 210 nucleotides in length, alternatively at least about 240 nucleotides in length, alternatively at least about 270 nucleotides in length, alternatively at least about 300 nucleotides in length, alternatively at least about 450 nucleotides in length, alternatively at least about 600 nucleotides in length, alternatively at least about 900 nucleotides in length, or more.

"Percent (%) nucleic acid sequence identity" with respect to PRO-encoding nucleic acid sequences identified herein is defined as the percentage of nucleotides in a candidate sequence that are identical with the nucleotides in the PRO nucleic acid sequence of interest, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent nucleic acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. For purposes herein, however, % nucleic acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, California or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for nucleic acid sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

$$100 \text{ times the fraction } W/Z$$

where W is the number of nucleotides scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C. As examples of % nucleic acid sequence identity calculations, Tables 4 and 5, demonstrate how to calculate the % nucleic acid sequence identity of the nucleic acid sequence designated "Comparison DNA" to the nucleic acid sequence designated "PRO-DNA", wherein "PRO-DNA" represents a hypothetical PRO-encoding nucleic acid sequence of interest, "Comparison DNA" represents the nucleotide sequence of a nucleic acid molecule against which the "PRO-DNA" nucleic acid molecule of interest is being compared, and "N", "L" and "V" each represent

different hypothetical nucleotides.

Unless specifically stated otherwise, all % nucleic acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program. However, % nucleic acid sequence identity values may also be obtained as described below by using the WU-BLAST-2 computer program (Altschul et al., Methods in Enzymology 266:460-480 (1996)). Most of the WU-BLAST-2 search parameters are set to the default values. Those not set to default values, i.e., the adjustable parameters, are set with the following values: overlap span = 1, overlap fraction = 0.125, word threshold (T) = 11, and scoring matrix = BLOSUM62. When WU-BLAST-2 is employed, a % nucleic acid sequence identity value is determined by dividing (a) the number of matching identical nucleotides between the nucleic acid sequence of the PRO polypeptide-encoding nucleic acid molecule of interest having a sequence derived from the native sequence PRO polypeptide-encoding nucleic acid and the comparison nucleic acid molecule of interest (i.e., the sequence against which the PRO polypeptide-encoding nucleic acid molecule of interest is being compared which may be a variant PRO polynucleotide) as determined by WU-BLAST-2 by (b) the total number of nucleotides of the PRO polypeptide-encoding nucleic acid molecule of interest. For example, in the statement "an isolated nucleic acid molecule comprising a nucleic acid sequence A which has or having at least 80% nucleic acid sequence identity to the nucleic acid sequence B", the nucleic acid sequence A is the comparison nucleic acid molecule of interest and the nucleic acid sequence B is the nucleic acid sequence of the PRO polypeptide-encoding nucleic acid molecule of interest.

Percent nucleic acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from <http://www.ncbi.nlm.nih.gov> or otherwise obtained from the National Institute of Health, Bethesda, MD. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.

In situations where NCBI-BLAST2 is employed for sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

100 times the fraction W/Z

where W is the number of nucleotides scored as identical matches by the sequence alignment program NCBI-BLAST2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C.

In other embodiments, PRO variant polynucleotides are nucleic acid molecules that encode an active PRO polypeptide and which are capable of hybridizing, preferably under stringent hybridization and wash conditions,

to nucleotide sequences encoding a full-length PRO polypeptide as disclosed herein. PRO variant polypeptides may be those that are encoded by a PRO variant polynucleotide.

"Isolated," when used to describe the various polypeptides disclosed herein, means polypeptide that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would typically interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. In preferred embodiments, the polypeptide will be purified (1) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or, preferably, silver stain. Isolated polypeptide includes polypeptide *in situ* within recombinant cells, since at least one component of the PRO polypeptide natural environment will not be present. Ordinarily, however, isolated polypeptide will be prepared by at least one purification step.

An "isolated" PRO polypeptide-encoding nucleic acid or other polypeptide-encoding nucleic acid is a nucleic acid molecule that is identified and separated from at least one contaminant nucleic acid molecule with which it is ordinarily associated in the natural source of the polypeptide-encoding nucleic acid. An isolated polypeptide-encoding nucleic acid molecule is other than in the form or setting in which it is found in nature. Isolated polypeptide-encoding nucleic acid molecules therefore are distinguished from the specific polypeptide-encoding nucleic acid molecule as it exists in natural cells. However, an isolated polypeptide-encoding nucleic acid molecule includes polypeptide-encoding nucleic acid molecules contained in cells that ordinarily express the polypeptide where, for example, the nucleic acid molecule is in a chromosomal location different from that of natural cells.

The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

The term "antibody" is used in the broadest sense and specifically covers, for example, single anti-PRO monoclonal antibodies (including agonist, antagonist, and neutralizing antibodies), anti-PRO antibody compositions with polypeptopic specificity, single chain anti-PRO antibodies, and fragments of anti-PRO antibodies (see below). The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially

homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally-occurring mutations that may be present in minor amounts.

"Stringency" of hybridization reactions is readily determinable by one of ordinary skill in the art, and generally is an empirical calculation dependent upon probe length, washing temperature, and salt concentration. In general, longer probes require higher temperatures for proper annealing, while shorter probes need lower temperatures. Hybridization generally depends on the ability of denatured DNA to reanneal when complementary strands are present in an environment below their melting temperature. The higher the degree of desired homology between the probe and hybridizable sequence, the higher the relative temperature which can be used. As a result, it follows that higher relative temperatures would tend to make the reaction conditions more stringent, while lower temperatures less so. For additional details and explanation of stringency of hybridization reactions, see Ausubel et al., Current Protocols in Molecular Biology, Wiley Interscience Publishers, (1995).

"Stringent conditions" or "high stringency conditions", as defined herein, may be identified by those that: (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50°C; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (v/v) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50mM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42°C; or (3) employ 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2 x SSC (sodium chloride/sodium citrate) and 50% formamide at 55°C, followed by a high-stringency wash consisting of 0.1 x SSC containing EDTA at 55°C.

"Moderately stringent conditions" may be identified as described by Sambrook et al., Molecular Cloning: A Laboratory Manual, New York: Cold Spring Harbor Press, 1989, and include the use of washing solution and hybridization conditions (e.g., temperature, ionic strength and %SDS) less stringent than those described above. An example of moderately stringent conditions is overnight incubation at 37°C in a solution comprising: 20% formamide, 5 x SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5 x Denhardt's solution, 10% dextran sulfate, and 20 mg/ml denatured sheared salmon sperm DNA, followed by washing the filters in 1 x SSC at about 37-50°C. The skilled artisan will recognize how to adjust the temperature, ionic strength, etc. as necessary to accommodate factors such as probe length and the like.

The term "epitope tagged" when used herein refers to a chimeric polypeptide comprising a PRO polypeptide fused to a "tag polypeptide". The tag polypeptide has enough residues to provide an epitope against which an antibody can be made, yet is short enough such that it does not interfere with activity of the polypeptide to which it is fused. The tag polypeptide preferably also is fairly unique so that the antibody does not substantially cross-react with other epitopes. Suitable tag polypeptides generally have at least six amino acid residues and usually between about 8 and 50 amino acid residues (preferably, between about 10 and 20 amino acid residues).

As used herein, the term "immunoadhesin" designates antibody-like molecules which combine the binding specificity of a heterologous protein (an "adhesin") with the effector functions of immunoglobulin constant domains. Structurally, the immunoadhesins comprise a fusion of an amino acid sequence with the desired binding

specificity which is other than the antigen recognition and binding site of an antibody (i.e., is "heterologous"), and an immunoglobulin constant domain sequence. The adhesin part of an immunoadhesin molecule typically is a contiguous amino acid sequence comprising at least the binding site of a receptor or a ligand. The immunoglobulin constant domain sequence in the immunoadhesin may be obtained from any immunoglobulin, such as IgG-1, IgG-2, IgG-3, or IgG-4 subtypes, IgA (including IgA-1 and IgA-2), IgE, IgD or IgM.

5 "Active" or "activity" for the purposes herein refers to form(s) of a PRO polypeptide which retain a biological and/or an immunological activity of native or naturally-occurring PRO, wherein "biological" activity refers to a biological function (either inhibitory or stimulatory) caused by a native or naturally-occurring PRO other than the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring PRO and an "immunological" activity refers to the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring PRO.

10 The term "antagonist" is used in the broadest sense, and includes any molecule that partially or fully blocks, inhibits, or neutralizes a biological activity of a native PRO polypeptide disclosed herein. In a similar manner, the term "agonist" is used in the broadest sense and includes any molecule that mimics a biological activity of a native PRO polypeptide disclosed herein. Suitable agonist or antagonist molecules specifically include agonist or antagonist antibodies or antibody fragments, fragments or amino acid sequence variants of native PRO polypeptides, peptides, antisense oligonucleotides, small organic molecules, etc. Methods for identifying agonists or antagonists of a PRO polypeptide may comprise contacting a PRO polypeptide with a candidate agonist or antagonist molecule and measuring a detectable change in one or more biological activities normally associated with the PRO polypeptide.

20 "Treatment" refers to both therapeutic treatment and prophylactic or preventative measures, wherein the object is to prevent or slow down (lessen) the targeted pathologic condition or disorder. Those in need of treatment include those already with the disorder as well as those prone to have the disorder or those in whom the disorder is to be prevented.

25 "Chronic" administration refers to administration of the agent(s) in a continuous mode as opposed to an acute mode, so as to maintain the initial therapeutic effect (activity) for an extended period of time. "Intermittent" administration is treatment that is not consecutively done without interruption, but rather is cyclic in nature.

"Mammal" for purposes of treatment refers to any animal classified as a mammal, including humans, domestic and farm animals, and zoo, sports, or pet animals, such as dogs, cats, cattle, horses, sheep, pigs, goats, rabbits, etc. Preferably, the mammal is human.

30 Administration "in combination with" one or more further therapeutic agents includes simultaneous (concurrent) and consecutive administration in any order.

"Carriers" as used herein include pharmaceutically acceptable carriers, excipients, or stabilizers which are nontoxic to the cell or mammal being exposed thereto at the dosages and concentrations employed. Often the physiologically acceptable carrier is an aqueous pH buffered solution. Examples of physiologically acceptable carriers include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptide; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine,

asparagine, arginine or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEEN™, polyethylene glycol (PEG), and PLURONICS™.

5 "Antibody fragments" comprise a portion of an intact antibody, preferably the antigen binding or variable region of the intact antibody. Examples of antibody fragments include Fab, Fab', F(ab')₂, and Fv fragments; diabodies; linear antibodies (Zapata et al., Protein Eng. 8(10): 1057-1062 [1995]); single-chain antibody molecules; and multispecific antibodies formed from antibody fragments.

Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, each with a single antigen-binding site, and a residual "Fc" fragment, a designation reflecting the ability to
10 crystallize readily. Pepsin treatment yields an F(ab')₂ fragment that has two antigen-combining sites and is still capable of cross-linking antigen.

"Fv" is the minimum antibody fragment which contains a complete antigen-recognition and -binding site. This region consists of a dimer of one heavy- and one light-chain variable domain in tight, non-covalent association. It is in this configuration that the three CDRs of each variable domain interact to define an antigen-
15 binding site on the surface of the V_H-V_L dimer. Collectively, the six CDRs confer antigen-binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

The Fab fragment also contains the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. Fab fragments differ from Fab' fragments by the addition of a few residues at the
20 carboxy terminus of the heavy chain CH1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group. F(ab')₂ antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

The "light chains" of antibodies (immunoglobulins) from any vertebrate species can be assigned to one
25 of two clearly distinct types, called kappa and lambda, based on the amino acid sequences of their constant domains.

Depending on the amino acid sequence of the constant domain of their heavy chains, immunoglobulins can be assigned to different classes. There are five major classes of immunoglobulins: IgA, IgD, IgE, IgG, and IgM, and several of these may be further divided into subclasses (isotypes), e.g., IgG1, IgG2, IgG3, IgG4, IgA,
30 and IgA2.

"Single-chain Fv" or "sFv" antibody fragments comprise the V_H and V_L domains of antibody, wherein these domains are present in a single polypeptide chain. Preferably, the Fv polypeptide further comprises a polypeptide linker between the V_H and V_L domains which enables the sFv to form the desired structure for antigen binding. For a review of sFv, see Pluckthun in The Pharmacology of Monoclonal Antibodies, vol. 113,
35 Rosenberg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994).

The term "diabodies" refers to small antibody fragments with two antigen-binding sites, which fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) in the same

polypeptide chain (V_H - V_L). By using a linker that is too short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites. Diabodies are described more fully in, for example, EP 404,097; WO 93/11161; and Hollinger et al., Proc. Natl. Acad. Sci. USA, 90:6444-6448 (1993).

5 An "isolated" antibody is one which has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials which would interfere with diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In preferred embodiments, the antibody will be purified (1) to greater than 95% by weight of antibody as determined by the Lowry method, and most preferably more than 99% by weight, (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence
10 by use of a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE under reducing or nonreducing conditions using Coomassie blue or, preferably, silver stain. Isolated antibody includes the antibody in situ within recombinant cells since at least one component of the antibody's natural environment will not be present. Ordinarily, however, isolated antibody will be prepared by at least one purification step.

15 An antibody that "specifically binds to" or is "specific for" a particular polypeptide or an epitope on a particular polypeptide is one that binds to that particular polypeptide or epitope on a particular polypeptide without substantially binding to any other polypeptide or polypeptide epitope.

The word "label" when used herein refers to a detectable compound or composition which is conjugated directly or indirectly to the antibody so as to generate a "labeled" antibody. The label may be detectable by itself (e.g. radioisotope labels or fluorescent labels) or, in the case of an enzymatic label, may catalyze chemical
20 alteration of a substrate compound or composition which is detectable.

By "solid phase" is meant a non-aqueous matrix to which the antibody of the present invention can adhere. Examples of solid phases encompassed herein include those formed partially or entirely of glass (e.g., controlled pore glass), polysaccharides (e.g., agarose), polyacrylamides, polystyrene, polyvinyl alcohol and silicones. In certain embodiments, depending on the context, the solid phase can comprise the well of an assay
25 plate; in others it is a purification column (e.g., an affinity chromatography column). This term also includes a discontinuous solid phase of discrete particles, such as those described in U.S. Patent No. 4,275,149.

A "liposome" is a small vesicle composed of various types of lipids, phospholipids and/or surfactant which is useful for delivery of a drug (such as a PRO polypeptide or antibody thereto) to a mammal. The components of the liposome are commonly arranged in a bilayer formation, similar to the lipid arrangement of
30 biological membranes.

A "small molecule" is defined herein to have a molecular weight below about 500 Daltons.

An "effective amount" of a polypeptide disclosed herein or an agonist or antagonist thereof is an amount sufficient to carry out a specifically stated purpose. An "effective amount" may be determined empirically and in a routine manner, in relation to the stated purpose.

Table 1

```

/*
 *
 * C-C increased from 12 to 15
 * Z is average of EQ
5  * B is average of ND
 * match with stop is _M; stop-stop = 0; J (joker) match = 0
 */
#define _M      -8      /* value of a match with a stop */

10 int _day[26][26] = {
/*   A B C D E F G H I J K L M N O P Q R S T U V W X Y Z */
/* A */ { 2, 0, -2, 0, 0, -4, 1, -1, -1, 0, -1, -2, -1, 0, _M, 1, 0, -2, 1, 1, 0, 0, -6, 0, -3, 0},
/* B */ { 0, 3, -4, 3, 2, -5, 0, 1, -2, 0, 0, -3, -2, 2, _M, -1, 1, 0, 0, 0, 0, -2, -5, 0, -3, 1},
/* C */ {-2, -4, 15, -5, -5, -4, -3, -3, -2, 0, -5, -6, -5, -4, _M, -3, -5, -4, 0, -2, 0, -2, -8, 0, 0, -5},
15 /* D */ { 0, 3, -5, 4, 3, -6, 1, 1, -2, 0, 0, -4, -3, 2, _M, -1, 2, -1, 0, 0, 0, -2, -7, 0, -4, 2},
/* E */ { 0, 2, -5, 3, 4, -5, 0, 1, -2, 0, 0, -3, -2, 1, _M, -1, 2, -1, 0, 0, 0, -2, -7, 0, -4, 3},
/* F */ {-4, -5, -4, -6, -5, 9, -5, -2, 1, 0, -5, 2, 0, -4, _M, -5, -5, -4, -3, -3, 0, -1, 0, 0, 7, -5},
/* G */ { 1, 0, -3, 1, 0, -5, 5, -2, -3, 0, -2, -4, -3, 0, _M, -1, -1, -3, 1, 0, 0, -1, -7, 0, -5, 0},
/* H */ {-1, 1, -3, 1, 1, -2, -2, 6, -2, 0, 0, -2, -2, 2, _M, 0, 3, 2, -1, -1, 0, -2, -3, 0, 0, 2},
20 /* I */ {-1, -2, -2, -2, -2, 1, -3, -2, 5, 0, -2, 2, 2, -2, _M, -2, -2, -2, -1, 0, 0, 4, -5, 0, -1, -2},
/* J */ { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* K */ {-1, 0, -5, 0, 0, -5, -2, 0, -2, 0, 5, -3, 0, 1, _M, -1, 1, 3, 0, 0, 0, -2, -3, 0, -4, 0},
/* L */ {-2, -3, -6, -4, -3, 2, -4, -2, 2, 0, -3, 6, 4, -3, _M, -3, -2, -3, -3, -1, 0, 2, -2, 0, -1, -2},
/* M */ {-1, -2, -5, -3, -2, 0, -3, -2, 2, 0, 0, 4, 6, -2, _M, -2, -1, 0, -2, -1, 0, 2, -4, 0, -2, -1},
25 /* N */ { 0, 2, -4, 2, 1, -4, 0, 2, -2, 0, 1, -3, -2, 2, _M, -1, 1, 0, 1, 0, 0, -2, -4, 0, -2, 1},
/* O */ { _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, 0, _M, _M, _M, _M, _M, _M, _M, _M, _M},
/* P */ { 1, -1, -3, -1, -1, -5, -1, 0, -2, 0, -1, -3, -2, -1, _M, 6, 0, 0, 1, 0, 0, -1, -6, 0, -5, 0},
/* Q */ { 0, 1, -5, 2, 2, -5, -1, 3, -2, 0, 1, -2, -1, 1, _M, 0, 4, 1, -1, -1, 0, -2, -5, 0, -4, 3},
/* R */ {-2, 0, -4, -1, -1, -4, -3, 2, -2, 0, 3, -3, 0, 0, _M, 0, 1, 6, 0, -1, 0, -2, 2, 0, -4, 0},
30 /* S */ { 1, 0, 0, 0, 0, -3, 1, -1, -1, 0, 0, -3, -2, 1, _M, 1, -1, 0, 2, 1, 0, -1, -2, 0, -3, 0},
/* T */ { 1, 0, -2, 0, 0, -3, 0, -1, 0, 0, 0, -1, -1, 0, _M, 0, -1, -1, 1, 3, 0, 0, -5, 0, -3, 0},
/* U */ { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* V */ { 0, -2, -2, -2, -2, -1, -1, -2, 4, 0, -2, 2, 2, -2, _M, -1, -2, -2, -1, 0, 0, 4, -6, 0, -2, -2},
35 /* W */ {-6, -5, -8, -7, -7, 0, -7, -3, -5, 0, -3, -2, -4, -4, _M, -6, -5, 2, -2, -5, 0, -6, 17, 0, 0, -6},
/* X */ { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* Y */ {-3, -3, 0, -4, -4, 7, -5, 0, -1, 0, -4, -1, -2, -2, _M, -5, -4, -4, -3, -3, 0, -2, 0, 0, 10, -4},
/* Z */ { 0, 1, -5, 2, 3, -5, 0, 2, -2, 0, 0, -2, -1, 1, _M, 0, 3, 0, 0, 0, 0, -2, -6, 0, -4, 4}
};

40

45

50

55

```

Table 1 (cont')

```

/*
*/
#include <stdio.h>
#include <ctype.h>

5
#define MAXJMP      16      /* max jumps in a diag */
#define MAXGAP      24      /* don't continue to penalize gaps larger than this */
#define JMPS        1024    /* max jmps in an path */
10
#define MX          4       /* save if there's at least MX-1 bases since last jmp */

#define DMAT         3      /* value of matching bases */
#define DMIS         0      /* penalty for mismatched bases */
#define DINS0        8      /* penalty for a gap */
15
#define DINS1        1      /* penalty per base */
#define PINS0        8      /* penalty for a gap */
#define PINS1        4      /* penalty per residue */

struct jmp {
20
    short            n[MAXJMP]; /* size of jmp (neg for del) */
    unsigned short   x[MAXJMP]; /* base no. of jmp in seq x */
}; /* limits seq to 2^16 -1 */

struct diag {
25
    int              score;      /* score at last jmp */
    long             offset;     /* offset of prev block */
    short            ijmp;       /* current jmp index */
    struct jmp        jp;        /* list of jmps */
};

30
struct path {
    int              spc;         /* number of leading spaces */
    short            n[JMPS]; /* size of jmp (gap) */
    int              x[JMPS]; /* loc of jmp (last elem before gap) */
35
};

char              *ofile;        /* output file name */
char              *namex[2];     /* seq names: getseqs() */
char              *prog;         /* prog name for err msgs */
40
char              *seqx[2];      /* seqs: getseqs() */
int               dmax;          /* best diag: nw() */
int               dmax0;         /* final diag */
int               dna;           /* set if dna: main() */
int               endgaps;       /* set if penalizing end gaps */
45
int               gapx, gapy;     /* total gaps in seqs */
int               len0, len1;    /* seq lens */
int               ngapx, ngapy;   /* total size of gaps */
int               smax;          /* max score: nw() */
int               *xbm;          /* bitmap for matching */
50
long              offset;        /* current offset in jmp file */
struct            diag           /* holds diagonals */
struct            path           /* holds path for seqs */
pp[2];

char              *calloc(), *malloc(), *index(), *strcpy();
55
char              *getseq(), *g_calloc();

```

60

Table 1 (cont')

```

/* Needleman-Wunsch alignment program
*
* usage: progs file1 file2
* where file1 and file2 are two dna or two protein sequences.
5  * The sequences can be in upper- or lower-case and may contain ambiguity
* Any lines beginning with ';', '>' or '<' are ignored
* Max file length is 65535 (limited by unsigned short x in the jmp struct)
* A sequence with 1/3 or more of its elements ACGTU is assumed to be DNA
* Output is in the file "align.out"
10 *
* The program may create a tmp file in /tmp to hold info about traceback.
* Original version developed under BSD 4.3 on a vax 8650
*/
#include "nw.h"
15 #include "day.h"

static _dbval[26] = {
    1,14,2,13,0,0,4,11,0,0,12,0,3,15,0,0,0,5,6,8,8,7,9,0,10,0
};
20
static _pbval[26] = {
    1, 2|(1<<('D'-'A'))|(1<<('N'-'A')), 4, 8, 16, 32, 64,
    128, 256, 0xFFFFFFFF, 1<<10, 1<<11, 1<<12, 1<<13, 1<<14,
    1<<15, 1<<16, 1<<17, 1<<18, 1<<19, 1<<20, 1<<21, 1<<22,
25 1<<23, 1<<24, 1<<25|(1<<('E'-'A'))|(1<<('Q'-'A'))
};

main(ac, av)
30     int    ac;
     char   *av[];
{
    prog = av[0];
    if (ac != 3) {
35         fprintf(stderr, "usage: %s file1 file2\n", prog);
        fprintf(stderr, "where file1 and file2 are two dna or two protein sequences.\n");
        fprintf(stderr, "The sequences can be in upper- or lower-case\n");
        fprintf(stderr, "Any lines beginning with ';' or '<' are ignored\n");
        fprintf(stderr, "Output is in the file \"align.out\"\n");
        exit(1);
40     }
    namex[0] = av[1];
    namex[1] = av[2];
    seqx[0] = getseq(namex[0], &len0);
    seqx[1] = getseq(namex[1], &len1);
45     xbm = (dna)? _dbval : _pbval;

    endgaps = 0;                /* 1 to penalize endgaps */
    ofile = "align.out";        /* output file */

50     nw();                    /* fill in the matrix, get the possible jumps */
    readjumps();                /* get the actual jumps */
    print();                    /* print stats, alignment */

55     cleanup(0);              /* unlink any tmp files */
}

```

Table 1 (cont')

```

/* do the alignment, return best score: main()
* dna: values in Fitch and Smith, PNAS, 80, 1382-1386, 1983
* pro: PAM 250 values
* When scores are equal, we prefer mismatches to any gap, prefer
5  * a new gap to extending an ongoing gap, and prefer a gap in seqx
  * to a gap in seq y.
  */
nw0
{
10  char      *px, *py;          /* seqs and ptrs */
    int      *ndely, *dely;     /* keep track of dely */
    int      ndelx, delx;       /* keep track of delx */
    int      *tmp;              /* for swapping row0, row1 */
    int      mis;               /* score for each type */
15  int      ins0, ins1;         /* insertion penalties */
    register id;                /* diagonal index */
    register ij;                /* jmp index */
    register *col0, *col1;      /* score for curr, last row */
    register xx, yy;            /* index into seqs */

20  dx = (struct diag *)g_calloc("to get diags", len0+len1+1, sizeof(struct diag));

    ndely = (int *)g_calloc("to get ndely", len1+1, sizeof(int));
    dely = (int *)g_calloc("to get dely", len1+1, sizeof(int));
25  col0 = (int *)g_calloc("to get col0", len1+1, sizeof(int));
    col1 = (int *)g_calloc("to get col1", len1+1, sizeof(int));
    ins0 = (dna)? DINS0 : PINS0;
    ins1 = (dna)? DINS1 : PINS1;

30  smax = -10000;
    if (endgaps) {
        for (col0[0] = dely[0] = -ins0, yy = 1; yy <= len1; yy++) {
            col0[yy] = dely[yy] = col0[yy-1] - ins1;
            ndely[yy] = yy;
35  }
        col0[0] = 0;          /* Waterman Bull Math Biol 84 */
    }
    else
        for (yy = 1; yy <= len1; yy++)
40  dely[yy] = -ins0;

    /* fill in match matrix
    */
45  for (px = seqx[0], xx = 1; xx <= len0; px++, xx++) {
        /* initialize first entry in col
        */
        if (endgaps) {
            if (xx == 1)
50  col1[0] = delx = -(ins0+ins1);
            else
                col1[0] = delx = col0[0] - ins1;
            ndelx = xx;
        }
        else {
55  col1[0] = 0;
            delx = -ins0;
            ndelx = 0;
        }
    }
60

```

Table 1 (cont')

...nw

```

for (py = seqx[1], yy = 1; yy <= len1; py++, yy++) {
  mis = col0[yy-1];
  if (dna)
    mis += (xbm[*px-'A']&xbm[*py-'A'])? DMAT : DMIS;
  else
    mis += _day[*px-'A'][*py-'A'];

  /* update penalty for del in x seq;
   * favor new del over ongoing del
   * ignore MAXGAP if weighting endgaps
   */
  if (endgaps || ndely[yy] < MAXGAP) {
    if (col0[yy] - ins0 >= dely[yy]) {
      dely[yy] = col0[yy] - (ins0+ins1);
      ndely[yy] = 1;
    } else {
      dely[yy] -= ins1;
      ndely[yy]++;
    }
  } else {
    if (col0[yy] - (ins0+ins1) >= dely[yy]) {
      dely[yy] = col0[yy] - (ins0+ins1);
      ndely[yy] = 1;
    } else
      ndely[yy]++;
  }

  /* update penalty for del in y seq;
   * favor new del over ongoing del
   */
  if (endgaps || ndelx < MAXGAP) {
    if (col1[yy-1] - ins0 >= delx) {
      delx = col1[yy-1] - (ins0+ins1);
      ndelx = 1;
    } else {
      delx -= ins1;
      ndelx++;
    }
  } else {
    if (col1[yy-1] - (ins0+ins1) >= delx) {
      delx = col1[yy-1] - (ins0+ins1);
      ndelx = 1;
    } else
      ndelx++;
  }

  /* pick the maximum score; we're favoring
   * mis over any del and delx over dely
   */

```

Table 1 (cont')

...nw

```

5      id = xx - yy + len1 - 1;
      if (mis >= delx && mis >= dely[yy])
          col1[yy] = mis;
      else if (delx >= dely[yy]) {
          col1[yy] = delx;
          ij = dx[id].ijmp;
          if (dx[id].jp.n[0] && (!dna || (ndelx >= MAXJMP
10      && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
              dx[id].ijmp++;
              if (++ij >= MAXJMP) {
                  writejumps(id);
                  ij = dx[id].ijmp = 0;
                  dx[id].offset = offset;
15      offset += sizeof(struct jmp) + sizeof(offset);
              }
          }
          dx[id].jp.n[ij] = ndelx;
          dx[id].jp.x[ij] = xx;
          dx[id].score = delx;
20      }
      else {
          col1[yy] = dely[yy];
          ij = dx[id].ijmp;
25      if (dx[id].jp.n[0] && (!dna || (ndely[yy] >= MAXJMP
          && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
              dx[id].ijmp++;
              if (++ij >= MAXJMP) {
                  writejumps(id);
                  ij = dx[id].ijmp = 0;
                  dx[id].offset = offset;
30      offset += sizeof(struct jmp) + sizeof(offset);
              }
          }
          dx[id].jp.n[ij] = -ndely[yy];
          dx[id].jp.x[ij] = xx;
          dx[id].score = dely[yy];
35      }
      if (xx == len0 && yy < len1) {
          /* last col
          */
          if (endgaps)
              col1[yy] -= ins0+ins1*(len1-yy);
          if (col1[yy] > smax) {
45      smax = col1[yy];
              dmax = id;
          }
      }
50      }
      if (endgaps && xx < len0)
          col1[yy-1] -= ins0+ins1*(len0-xx);
      if (col1[yy-1] > smax) {
          smax = col1[yy-1];
          dmax = id;
55      }
      tmp = col0; col0 = col1; col1 = tmp;
  }
  (void) free((char *)ndely);
  (void) free((char *)dely);
  (void) free((char *)col0);
60  (void) free((char *)col1);
      }

```

Table 1 (cont')

```

/*
 *
 * print() -- only routine visible outside this module
 *
5  * static:
 * getmat() -- trace back best path, count matches: print()
 * pr_align() -- print alignment of described in array p[]: print()
 * dumpblock() -- dump a block of lines with numbers, stars: pr_align()
 * nums() -- put out a number line: dumpblock()
10 * putline() -- put out a line (name, [num], seq, [num]): dumpblock()
 * stars() -- put a line of stars: dumpblock()
 * stripname() -- strip any path and prefix from a seqname
 */

15 #include "nw.h"

#define SPC      3
#define P_LINE  256 /* maximum output line */
#define P_SPC    3 /* space between name or num and seq */

20 extern _day[26][26];
int olen; /* set output line length */
FILE *fx; /* output file */

25 print()
{
    int lx, ly, firstgap, lastgap; /* overlap */

    if ((fx = fopen(ofile, "w")) == 0) {
30         fprintf(stderr, "%s: can't write %s\n", prog, ofile);
        cleanup(1);
    }
    fprintf(fx, "<first sequence: %s (length = %d)\n", namex[0], len0);
    fprintf(fx, "<second sequence: %s (length = %d)\n", namex[1], len1);
35     olen = 60;
    lx = len0;
    ly = len1;
    firstgap = lastgap = 0;
    if (dmax < len1 - 1) { /* leading gap in x */
40         pp[0].spc = firstgap = len1 - dmax - 1;
        ly -= pp[0].spc;
    }
    else if (dmax > len1 - 1) { /* leading gap in y */
45         pp[1].spc = firstgap = dmax - (len1 - 1);
        lx -= pp[1].spc;
    }
    if (dmax0 < len0 - 1) { /* trailing gap in x */
        lastgap = len0 - dmax0 - 1;
        lx -= lastgap;
50     }
    else if (dmax0 > len0 - 1) { /* trailing gap in y */
        lastgap = dmax0 - (len0 - 1);
        ly -= lastgap;
55     }
    getmat(lx, ly, firstgap, lastgap);
    pr_align();
}

60

```

print

Table 1 (cont')

```

/*
 * trace back the best path, count matches
 */
static
5  getmat(lx, ly, firstgap, lastgap)                                getmat
    int    lx, ly;                                /* "core" (minus endgaps) */
    int    firstgap, lastgap;                      /* leading trailing overlap */
{
    int          nm, i0, i1, siz0, siz1;
    char          outx[32];
    double        pct;
    register      n0, n1;
    register char  *p0, *p1;

    /* get total matches, score
    */
    i0 = i1 = siz0 = siz1 = 0;
    p0 = seqx[0] + pp[1].spc;
    p1 = seqx[1] + pp[0].spc;
    n0 = pp[1].spc + 1;
    n1 = pp[0].spc + 1;

    nm = 0;
    while ( *p0 && *p1 ) {
        if (siz0) {
            p1++;
            n1++;
            siz0--;
        }
        else if (siz1) {
            p0++;
            n0++;
            siz1--;
        }
        else {
            if (xbm[*p0-'A'] & xbm[*p1-'A'])
                nm++;
            if (n0++ == pp[0].x[i0])
                siz0 = pp[0].n[i0++];
            if (n1++ == pp[1].x[i1])
                siz1 = pp[1].n[i1++];
            p0++;
            p1++;
        }
    }

    /* pct homology:
    * if penalizing endgaps, base is the shorter seq
    * else, knock off overhangs and take shorter core
    */
    if (endgaps)
        lx = (len0 < len1)? len0 : len1;
    else
        lx = (lx < ly)? lx : ly;
    pct = 100.*((double)nm/((double)lx);
    fprintf(fx, "\n");
    fprintf(fx, "< %d match%s in an overlap of %d: %.2f percent similarity\n",
        nm, (nm == 1)? "" : "es", lx, pct);

```

Table 1 (cont')

```

fprintf(fx, "<gaps in first sequence: %d", gapx);
if (gapx) {
    (void) sprintf(outx, " (%d %s%s)",
        ngapx, (dna)? "base": "residue", (ngapx == 1)? "": "s");
5     fprintf(fx, "%s", outx);

    fprintf(fx, ", gaps in second sequence: %d", gapy);
    if (gapy) {
        (void) sprintf(outx, " (%d %s%s)",
10         ngapy, (dna)? "base": "residue", (ngapy == 1)? "": "s");
        fprintf(fx, "%s", outx);
    }
    if (dna)
        fprintf(fx,
15         "\n<score: %d (match = %d, mismatch = %d, gap penalty = %d + %d per base)\n",
            smax, DMAT, DMIS, DINS0, DINS1);
    else
        fprintf(fx,
20         "\n<score: %d (Dayhoff PAM 250 matrix, gap penalty = %d + %d per residue)\n",
            smax, PINS0, PINS1);
    if (endgaps)
        fprintf(fx,
25         "<endgaps penalized. left endgap: %d %s%s, right endgap: %d %s%s\n",
            firstgap, (dna)? "base": "residue", (firstgap == 1)? "": "s",
            lastgap, (dna)? "base": "residue", (lastgap == 1)? "": "s");
    else
        fprintf(fx, "<endgaps not penalized\n");
}

30 static nm; /* matches in core -- for checking */
static lmax; /* lengths of stripped file names */
static ij[2]; /* jmp index for a path */
static nc[2]; /* number at start of current line */
static ni[2]; /* current elem number -- for gapping */
35 static siz[2];
static char *ps[2]; /* ptr to current element */
static char *po[2]; /* ptr to next output char slot */
static char out[2][P_LINE]; /* output line */
static char star[P_LINE]; /* set by stars() */
40

/*
 * print alignment of described in struct path pp[]
 */
static
45 pr_align()
{
    int nn; /* char count */
    int more;
    register i;

50     for (i = 0, lmax = 0; i < 2; i++) {
        nn = stripname(nameex[i]);
        if (nn > lmax)
            lmax = nn;

55         nc[i] = 1;
        ni[i] = 1;
        siz[i] = ij[i] = 0;
        ps[i] = seqx[i];
60         po[i] = out[i];
    }

```

...getmat

pr_align

Table 1 (cont')

```

for (nn = nm = 0, more = 1; more; ) {
    for (i = more = 0; i < 2; i++) {
        /*
5         * do we have more of this sequence?
        */
        if (!*ps[i])
            continue;

10        more++;

        if (pp[i].spc) { /* leading space */
            *po[i]++ = ' ';
            pp[i].spc--;
15        }
        else if (siz[i]) { /* in a gap */
            *po[i]++ = '-';
            siz[i]--;
20        }
        else { /* we're putting a seq element
            */
            *po[i] = *ps[i];
            if (islower(*ps[i]))
                *ps[i] = toupper(*ps[i]);
25            po[i]++;
            ps[i]++;

            /*
30            * are we at next gap for this seq?
            */
            if (ni[i] == pp[i].x[ij[i]]) {
                /*
                * we need to merge all gaps
                * at this location
                */
35                siz[i] = pp[i].n[ij[i] + +];
                while (ni[i] == pp[i].x[ij[i]])
                    siz[i] += pp[i].n[ij[i] + +];
            }
            ni[i]++;
40        }
    }
    if (++nn == olen || !more && nn) {
        dumpblock();
        for (i = 0; i < 2; i++)
            po[i] = out[i];
        nn = 0;
45    }
}

50 }

/*
 * dump a block of lines, including numbers, stars: pr_align()
 */
55 static
dumpblock()
{
    register i;

60    for (i = 0; i < 2; i++)
        *po[i]-- = '\0';

```

...pr_align

dumpblock

Table 1 (cont')

...dumpblock

```

5      (void) putc('\n', fx);
      for (i = 0; i < 2; i++) {
          if (*out[i] && (*out[i] != ' ' || *(po[i]) != ' ')) {
              if (i == 0)
                  nums(i);
              if (i == 0 && *out[1])
                  stars();
10         putline(i);
              if (i == 0 && *out[1])
                  fprintf(fx, star);
              if (i == 1)
                  nums(i);
15         }
      }
}

/*
20  * put out a number line: dumpblock()
  */
static
nums(ix)
25  {
    int    ix;        /* index in out[] holding seq line */

    char    nline[P_LINE];
    register i, j;
    register char *pn, *px, *py;

30     for (pn = nline, i = 0; i < lmax+P_SPC; i++, pn++)
        *pn = ' ';
    for (i = nc[ix], py = out[ix]; *py; py++, pn++) {
        if (*py == ' ' || *py == '-')
            *pn = ' ';
35         else {
            if (i%10 == 0 || (i == 1 && nc[ix] != 1)) {
                j = (i < 0)? -i : i;
                for (px = pn; j /= 10, px--)
                    *px = j%10 + '0';
40                 if (i < 0)
                    *px = '-';
            }
            else
                *pn = ' ';
45             *pn = ' ';
            *pn = ' ';
        }
    }
    *pn = '\0';
    nc[ix] = i;
50     for (pn = nline; *pn; pn++)
        (void) putc(*pn, fx);
    (void) putc('\n', fx);
}

55  /*
  * put out a line (name, [num], seq, [num]): dumpblock()
  */
static
putline(ix)
60  int    ix;        {

```

nums

putline

Table 1 (cont')

...putline

```

5.      int          i;
      register char  *px;

      for (px = name[ix], i = 0; *px && *px != ':'; px++, i++)
          (void) putc(*px, fx);
      for (; i < lmax+P_SPC; i++)
          (void) putc(' ', fx);
10
      /* these count from 1:
      * ni[] is current element (from 1)
      * nc[] is number at start of current line
      */
15      for (px = out[ix]; *px; px++)
          (void) putc(*px&0x7F, fx);
      (void) putc('\n', fx);
      }

20      /*
      * put a line of stars (seqs always in out[0], out[1]): dumpblock()
      */
      static
25      stars()
      {
          int          i;
          register char *p0, *p1, cx, *px;

30          if (!(*out[0] || (*out[0] == ' ' && *(p0[0]) == ' ') ||
              !*out[1] || (*out[1] == ' ' && *(p0[1]) == ' '))
              return;
          px = star;
          for (i = lmax+P_SPC; i; i--)
35              *px++ = ' ';

          for (p0 = out[0], p1 = out[1]; *p0 && *p1; p0++, p1++) {
              if (isalpha(*p0) && isalpha(*p1)) {
40                  if (xbm[*p0-'A']&xbm[*p1-'A']) {
                      cx = '*';
                      nm++;
                  }
                  else if (!dna && _day[*p0-'A'][*p1-'A'] > 0)
45                      cx = '.';
                  else
                      cx = ' ';
              }
              else
50                  cx = ' ';
              *px++ = cx;
          }
          *px++ = '\n';
          *px = '\0';
55      }

```

stars

Table 1 (cont')

```
/*
 * strip path or prefix from pn, return len: pr_align()
 */
static
5 stripname(pn)                                stripname
    char    *pn;    /* file name (may be path) */
    {
        register char    *px, *py;
10         py = 0;
        for (px = pn; *px; px++)
            if (*px == '/')
                py = px + 1;
        if (py)
15         (void) strcpy(pn, py);
        return(strlen(pn));
    }
20
25
30
35
40
45
50
55
60
```

Table 1 (cont')

```

/*
 * cleanup() -- cleanup any tmp file
 * getseq() -- read in seq, set dna, len, maxlen
 * g_calloc() -- calloc() with error checkin
5  * readjumps() -- get the good jumps; from tmp file if necessary
 * writejumps() -- write a filled array of jumps to a tmp file: nw()
 */
#include "nw.h"
#include <sys/file.h>

10 char    *jname = "/tmp/homgXXXXXX";    /* tmp file for jumps */
FILE    *fj;

int      cleanup();                      /* cleanup tmp file */
15 long    lseek();

/*
 * remove any tmp file if we blow
 */
20 cleanup(i)                                cleanup
    int    i;
{
    if (fj)
        (void) unlink(jname);
25    exit(i);
}

/*
 * read, return ptr to seq, set dna, len, maxlen
 * skip lines starting with ';', '<', or '>'
 * seq in upper or lower case
 */
30 char    *
getseq(file, len)                                getseq
    char    *file;    /* file name */
    int     *len;     /* seq len */
{
    char    line[1024], *pseq;
    register char    *px, *py;
    int     natgc, tlen;
    FILE    *fp;

    if ((fp = fopen(file, "r")) == 0) {
        fprintf(stderr, "%s: can't read %s\n", prog, file);
45    exit(1);
    }
    tlen = natgc = 0;
    while (fgets(line, 1024, fp)) {
        if (*line == ';' || *line == '<' || *line == '>')
            continue;
50        for (px = line; *px != '\n'; px++)
            if (isupper(*px) || islower(*px))
                tlen++;
    }
    if ((pseq = malloc((unsigned)(tlen+6))) == 0) {
        fprintf(stderr, "%s: malloc() failed to get %d bytes for %s\n", prog, tlen+6, file);
55    exit(1);
    }
    pseq[0] = pseq[1] = pseq[2] = pseq[3] = '\0';
60

```

Table 1 (cont')

...getseq

```

py = pseq + 4;
*len = tlen;
rewind(fp);
5
while (fgets(line, 1024, fp)) {
    if (*line == ';' || *line == '<' || *line == '>')
        continue;
    for (px = line; *px != '\n'; px++) {
10        if (isupper(*px))
            *py++ = *px;
        else if (islower(*px))
            *py++ = toupper(*px);
        if (index("ATGCU", *(py-1)))
15            natgc++;
    }
}
*py++ = '\0';
*py = '\0';
20 (void) fclose(fp);
dna = natgc > (tlen/3);
return(pseq+4);
}

25 char *
g_alloc(msg, nx, sz)
    char *msg;          /* program, calling routine */
    int nx, sz;          /* number and size of elements */
{
30     char *px, *calloc();

    if ((px = calloc((unsigned)nx, (unsigned)sz)) == 0) {
        if (*msg) {
35             fprintf(stderr, "%s: g_alloc() failed %s (n=%d, sz=%d)\n", prog, msg, nx, sz);
            exit(1);
        }
    }
    return(px);
}

40 /*
 * get final jmps from dx[] or tmp file, set pp[], reset dmax: main()
 */
readjmps()
45 {
    int fd = -1;
    int siz, i0, i1;
    register i, j, xx;

50     if (fj) {
        (void) fclose(fj);
        if ((fd = open(jname, O_RDONLY, 0)) < 0) {
            fprintf(stderr, "%s: can't open() %s\n", prog, jname);
            cleanup(1);
55         }
    }
    for (i = i0 = i1 = 0, dmax0 = dmax, xx = len0; i++) {
        while (1) {
60             for (j = dx[dmax].ijmp; j >= 0 && dx[dmax].jp.x[j] >= xx; j--)
                ;

```

g_alloc

readjmps

Table 1 (cont')

...readjumps

```

5      if (j < 0 && dx[dmax].offset && fj) {
        (void) lseek(fd, dx[dmax].offset, 0);
        (void) read(fd, (char *)&dx[dmax].jp, sizeof(struct jmp));
        (void) read(fd, (char *)&dx[dmax].offset, sizeof(dx[dmax].offset));
        dx[dmax].ijmp = MAXJMP-1;
      }
      else
10         break;
    }
    if (i >= JMPS) {
        fprintf(stderr, "%s: too many gaps in alignment\n", prog);
        cleanup(1);
    }
15    if (j >= 0) {
        siz = dx[dmax].jp.n[j];
        xx = dx[dmax].jp.x[j];
        dmax += siz;
        if (siz < 0) { /* gap in second seq */
20            pp[1].n[i1] = -siz;
            xx += siz;
            /* id = xx - yy + len1 - 1
             */
            pp[1].x[i1] = xx - dmax + len1 - 1;
            gapy++;
            ngapy -= siz;
            /* ignore MAXGAP when doing endgaps */
            siz = (-siz < MAXGAP || endgaps)? -siz : MAXGAP;
            i1++;
30        }
        else if (siz > 0) { /* gap in first seq */
            pp[0].n[i0] = siz;
            pp[0].x[i0] = xx;
            gapx++;
            ngapx += siz;
            /* ignore MAXGAP when doing endgaps */
            siz = (siz < MAXGAP || endgaps)? siz : MAXGAP;
            i0++;
40        }
    }
    else
        break;
}

45    /* reverse the order of jumps
    */
    for (j = 0, i0--; j < i0; j++, i0--) {
        i = pp[0].n[j]; pp[0].n[j] = pp[0].n[i0]; pp[0].n[i0] = i;
        i = pp[0].x[j]; pp[0].x[j] = pp[0].x[i0]; pp[0].x[i0] = i;
50    }
    for (j = 0, i1--; j < i1; j++, i1--) {
        i = pp[1].n[j]; pp[1].n[j] = pp[1].n[i1]; pp[1].n[i1] = i;
        i = pp[1].x[j]; pp[1].x[j] = pp[1].x[i1]; pp[1].x[i1] = i;
55    }
    if (fd >= 0)
        (void) close(fd);
    if (fj) {
        (void) unlink(jname);
        fj = 0;
        offset = 0;
60    }
}

```

Table 1 (cont')

```

/*
 * write a filled jmp struct offset of the prev one (if any): nw()
 */
5  writejumps(ix)                                writejumps
    int    ix;
    {
        char    *mktemp();
10         if (!fj) {
            if (mktemp(jname) < 0) {
                fprintf(stderr, "%s: can't mktemp() %s\n", prog, jname);
                cleanup(1);
            }
15         if ((fj = fopen(jname, "w")) == 0) {
            fprintf(stderr, "%s: can't write %s\n", prog, jname);
            exit(1);
        }
20         (void) fwrite((char *)&dx[ix].jp, sizeof(struct jmp), 1, fj);
        (void) fwrite((char *)&dx[ix].offset, sizeof(dx[ix].offset), 1, fj);
    }
}
25
30
35
40
45
50
55
60

```

Table 2

PRO	XXXXXXXXXXXXXXXXXX	(Length = 15 amino acids)
Comparison Protein	XXXXXXYYYYYYY	(Length = 12 amino acids)

5 % amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) =

10 5 divided by 15 = 33.3%

Table 3

PRO	XXXXXXXXXX	(Length = 10 amino acids)
15 Comparison Protein	XXXXXXYYYYYYZZYZ	(Length = 15 amino acids)

% amino acid sequence identity =

20 (the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) =

5 divided by 10 = 50%

Table 4

25 PRO-DNA	NNNNNNNNNNNNNN	(Length = 14 nucleotides)
Comparison DNA	NNNNNNLLLLLLLLLL	(Length = 16 nucleotides)

% nucleic acid sequence identity =

30 (the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) =

6 divided by 14 = 42.9%

35

Table 5

PRO-DNA	NNNNNNNNNNNN	(Length = 12 nucleotides)
Comparison DNA	NNNNLLLVV	(Length = 9 nucleotides)

5 % nucleic acid sequence identity =

(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) =

10 4 divided by 12 = 33.3%

II. Compositions and Methods of the Invention

A. Full-Length PRO Polypeptides

15 The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO polypeptides. In particular, cDNAs encoding various PRO polypeptides have been identified and isolated, as disclosed in further detail in the Examples below. It is noted that proteins produced in separate expression rounds may be given different PRO numbers but the UNQ number is unique for any given DNA and the encoded protein, and will not be changed. However, for sake of simplicity, in the present specification the protein encoded by the full length native nucleic acid molecules disclosed herein
20 as well as all further native homologues and variants included in the foregoing definition of PRO, will be referred to as "PRO/number", regardless of their origin or mode of preparation.

As disclosed in the Examples below, various cDNA clones have been deposited with the ATCC. The actual nucleotide sequences of those clones can readily be determined by the skilled artisan by sequencing of the deposited clone using routine methods in the art. The predicted amino acid sequence can be determined from the
25 nucleotide sequence using routine skill. For the PRO polypeptides and encoding nucleic acids described herein, Applicants have identified what is believed to be the reading frame best identifiable with the sequence information available at the time.

B. PRO Polypeptide Variants

30 In addition to the full-length native sequence PRO polypeptides described herein, it is contemplated that PRO variants can be prepared. PRO variants can be prepared by introducing appropriate nucleotide changes into the PRO DNA, and/or by synthesis of the desired PRO polypeptide. Those skilled in the art will appreciate that amino acid changes may alter post-translational processes of the PRO, such as changing the number or position of glycosylation sites or altering the membrane anchoring characteristics.

35 Variations in the native full-length sequence PRO or in various domains of the PRO described herein, can be made, for example, using any of the techniques and guidelines for conservative and non-conservative

mutations set forth, for instance, in U.S. Patent No. 5,364,934. Variations may be a substitution, deletion or insertion of one or more codons encoding the PRO that results in a change in the amino acid sequence of the PRO as compared with the native sequence PRO. Optionally the variation is by substitution of at least one amino acid with any other amino acid in one or more of the domains of the PRO. Guidance in determining which amino acid residue may be inserted, substituted or deleted without adversely affecting the desired activity may be found by
5 comparing the sequence of the PRO with that of homologous known protein molecules and minimizing the number of amino acid sequence changes made in regions of high homology. Amino acid substitutions can be the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, such as the replacement of a leucine with a serine, i.e., conservative amino acid replacements. Insertions or deletions may optionally be in the range of about 1 to 5 amino acids. The variation allowed may be determined by
10 systematically making insertions, deletions or substitutions of amino acids in the sequence and testing the resulting variants for activity exhibited by the full-length or mature native sequence.

PRO polypeptide fragments are provided herein. Such fragments may be truncated at the N-terminus or C-terminus, or may lack internal residues, for example, when compared with a full length native protein. Certain fragments lack amino acid residues that are not essential for a desired biological activity of the PRO polypeptide.
15

PRO fragments may be prepared by any of a number of conventional techniques. Desired peptide fragments may be chemically synthesized. An alternative approach involves generating PRO fragments by enzymatic digestion, e.g., by treating the protein with an enzyme known to cleave proteins at sites defined by particular amino acid residues, or by digesting the DNA with suitable restriction enzymes and isolating the desired
20 fragment. Yet another suitable technique involves isolating and amplifying a DNA fragment encoding a desired polypeptide fragment, by polymerase chain reaction (PCR). Oligonucleotides that define the desired termini of the DNA fragment are employed at the 5' and 3' primers in the PCR. Preferably, PRO polypeptide fragments share at least one biological and/or immunological activity with the native PRO polypeptide disclosed herein.

In particular embodiments, conservative substitutions of interest are shown in Table 6 under the heading
25 of preferred substitutions. If such substitutions result in a change in biological activity, then more substantial changes, denominated exemplary substitutions in Table 6, or as further described below in reference to amino acid classes, are introduced and the products screened.

Table 6

	<u>Original Residue</u>	<u>Exemplary Substitutions</u>	<u>Preferred Substitutions</u>
5	Ala (A)	val; leu; ile	val
	Arg (R)	lys; gln; asn	lys
	Asn (N)	gln; his; lys; arg	gln
	Asp (D)	glu	glu
	Cys (C)	ser	ser
10	Gln (Q)	asn	asn
	Glu (E)	asp	asp
	Gly (G)	pro; ala	ala
	His (H)	asn; gln; lys; arg	arg
	Ile (I)	leu; val; met; ala; phe;	
15		norleucine	leu
	Leu (L)	norleucine; ile; val;	
		met; ala; phe	ile
	Lys (K)	arg; gln; asn	arg
	Met (M)	leu; phe; ile	leu
20	Phe (F)	leu; val; ile; ala; tyr	leu
	Pro (P)	ala	ala
	Ser (S)	thr	thr
	Thr (T)	ser	ser
	Trp (W)	tyr; phe	tyr
25	Tyr (Y)	trp; phe; thr; ser	phe
	Val (V)	ile; leu; met; phe;	
		ala; norleucine	leu

30 Substantial modifications in function or immunological identity of the PRO polypeptide are accomplished by selecting substitutions that differ significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Naturally occurring residues are divided into groups based on common side-chain properties:

- 35 (1) hydrophobic: norleucine, met, ala, val, leu, ile;
 (2) neutral hydrophilic: cys, ser, thr;
 (3) acidic: asp, glu;
 (4) basic: asn, gln, his, lys, arg;
 (5) residues that influence chain orientation: gly, pro; and
 40 (6) aromatic: trp, tyr, phe.

Non-conservative substitutions will entail exchanging a member of one of these classes for another class. Such substituted residues also may be introduced into the conservative substitution sites or, more preferably, into the remaining (non-conserved) sites.

45 The variations can be made using methods known in the art such as oligonucleotide-mediated (site-directed) mutagenesis, alanine scanning, and PCR mutagenesis. Site-directed mutagenesis [Carter et al., Nucl. Acids Res., 13:4331 (1986); Zoller et al., Nucl. Acids Res., 10:6487 (1987)], cassette mutagenesis [Wells et al.,

Gene, 34:315 (1985)], restriction selection mutagenesis [Wells et al., Philos. Trans. R. Soc. London SerA, 317:415 (1986)] or other known techniques can be performed on the cloned DNA to produce the PRO variant DNA.

Scanning amino acid analysis can also be employed to identify one or more amino acids along a contiguous sequence. Among the preferred scanning amino acids are relatively small, neutral amino acids. Such amino acids include alanine, glycine, serine, and cysteine. Alanine is typically a preferred scanning amino acid among this group because it eliminates the side-chain beyond the beta-carbon and is less likely to alter the main-chain conformation of the variant [Cunningham and Wells, Science, 244: 1081-1085 (1989)]. Alanine is also typically preferred because it is the most common amino acid. Further, it is frequently found in both buried and exposed positions [Creighton, The Proteins, (W.H. Freeman & Co., N.Y.); Chothia, J. Mol. Biol., 150:1 (1976)]. If alanine substitution does not yield adequate amounts of variant, an isoteric amino acid can be used.

C. Modifications of PRO

Covalent modifications of PRO are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a PRO polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C- terminal residues of the PRO. Derivatization with bifunctional agents is useful, for instance, for crosslinking PRO to a water-insoluble support matrix or surface for use in the method for purifying anti-PRO antibodies, and vice-versa. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propioimide.

Other modifications include deamidation of glutamyl and asparaginy residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the α -amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, Proteins: Structure and Molecular Properties, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the PRO polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence PRO (either by removing the underlying glycosylation site or by deleting the glycosylation by chemical and/or enzymatic means), and/or adding one or more glycosylation sites that are not present in the native sequence PRO. In addition, the phrase includes qualitative changes in the glycosylation of the native proteins, involving a change in the nature and proportions of the various carbohydrate moieties present.

Addition of glycosylation sites to the PRO polypeptide may be accomplished by altering the amino acid sequence. The alteration may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native sequence PRO (for O-linked glycosylation sites). The PRO amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding

the PRO polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the PRO polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, CRC Crit. Rev. Biochem., pp. 259-306 (1981).

Removal of carbohydrate moieties present on the PRO polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al., Arch. Biochem. Biophys., 259:52 (1987) and by Edge et al., Anal. Biochem., 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura et al., Meth. Enzymol., 138:350 (1987).

Another type of covalent modification of PRO comprises linking the PRO polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol (PEG), polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

The PRO of the present invention may also be modified in a way to form a chimeric molecule comprising PRO fused to another, heterologous polypeptide or amino acid sequence.

In one embodiment, such a chimeric molecule comprises a fusion of the PRO with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl- terminus of the PRO. The presence of such epitope-tagged forms of the PRO can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the PRO to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field et al., Mol. Cell. Biol., 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., Molecular and Cellular Biology, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., Protein Engineering, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., BioTechnology, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., Science, 255:192-194 (1992)]; an α -tubulin epitope peptide [Skinner et al., J. Biol. Chem., 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., Proc. Natl. Acad. Sci. USA, 87:6393-6397 (1990)].

In an alternative embodiment, the chimeric molecule may comprise a fusion of the PRO with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule (also referred to as an "immunoadhesin"), such a fusion could be to the Fc region of an IgG molecule. The Ig fusions preferably include the substitution of a soluble (transmembrane domain deleted or inactivated) form of a PRO polypeptide in place of at least one variable region within an Ig molecule. In a particularly preferred embodiment, the immunoglobulin fusion includes the hinge, CH2 and CH3, or the hinge, CH1, CH2 and CH3 regions of an IgG1 molecule. For the production of immunoglobulin fusions see also US Patent No. 5,428,130 issued June 27,

1995.

D. Preparation of PRO

The description below relates primarily to production of PRO by culturing cells transformed or transfected with a vector containing PRO nucleic acid. It is, of course, contemplated that alternative methods, which are well known in the art, may be employed to prepare PRO. For instance, the PRO sequence, or portions thereof, may be produced by direct peptide synthesis using solid-phase techniques [see, e.g., Stewart et al., Solid-Phase Peptide Synthesis, W.H. Freeman Co., San Francisco, CA (1969); Merrifield, J. Am. Chem. Soc., 85:2149-2154 (1963)]. *In vitro* protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be accomplished, for instance, using an Applied Biosystems Peptide Synthesizer (Foster City, CA) using manufacturer's instructions. Various portions of the PRO may be chemically synthesized separately and combined using chemical or enzymatic methods to produce the full-length PRO.

1. Isolation of DNA Encoding PRO

DNA encoding PRO may be obtained from a cDNA library prepared from tissue believed to possess the PRO mRNA and to express it at a detectable level. Accordingly, human PRO DNA can be conveniently obtained from a cDNA library prepared from human tissue, such as described in the Examples. The PRO-encoding gene may also be obtained from a genomic library or by known synthetic procedures (e.g., automated nucleic acid synthesis).

Libraries can be screened with probes (such as antibodies to the PRO or oligonucleotides of at least about 20-80 bases) designed to identify the gene of interest or the protein encoded by it. Screening the cDNA or genomic library with the selected probe may be conducted using standard procedures, such as described in Sambrook et al., Molecular Cloning: A Laboratory Manual (New York: Cold Spring Harbor Laboratory Press, 1989). An alternative means to isolate the gene encoding PRO is to use PCR methodology [Sambrook et al., supra; Dieffenbach et al., PCR Primer: A Laboratory Manual (Cold Spring Harbor Laboratory Press, 1995)].

The Examples below describe techniques for screening a cDNA library. The oligonucleotide sequences selected as probes should be of sufficient length and sufficiently unambiguous that false positives are minimized. The oligonucleotide is preferably labeled such that it can be detected upon hybridization to DNA in the library being screened. Methods of labeling are well known in the art, and include the use of radiolabels like ³²P-labeled ATP, biotinylation or enzyme labeling. Hybridization conditions, including moderate stringency and high stringency, are provided in Sambrook et al., supra.

Sequences identified in such library screening methods can be compared and aligned to other known sequences deposited and available in public databases such as GenBank or other private sequence databases. Sequence identity (at either the amino acid or nucleotide level) within defined regions of the molecule or across the full-length sequence can be determined using methods known in the art and as described herein.

Nucleic acid having protein coding sequence may be obtained by screening selected cDNA or genomic libraries using the deduced amino acid sequence disclosed herein for the first time, and, if necessary, using conventional primer extension procedures as described in Sambrook et al., supra, to detect precursors and

processing intermediates of mRNA that may not have been reverse-transcribed into cDNA.

2. Selection and Transformation of Host Cells

Host cells are transfected or transformed with expression or cloning vectors described herein for PRO production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences. The culture conditions, such as media, temperature, pH and the like, can be selected by the skilled artisan without undue experimentation. In general, principles, protocols, and practical techniques for maximizing the productivity of cell cultures can be found in Mammalian Cell Biotechnology: a Practical Approach, M. Butler, ed. (IRL Press, 1991) and Sambrook et al., supra.

Methods of eukaryotic cell transfection and prokaryotic cell transformation are known to the ordinarily skilled artisan, for example, CaCl_2 , CaPO_4 , liposome-mediated and electroporation. Depending on the host cell used, transformation is performed using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described in Sambrook et al., supra, or electroporation is generally used for prokaryotes. Infection with *Agrobacterium tumefaciens* is used for transformation of certain plant cells, as described by Shaw et al., Gene, 23:315 (1983) and WO 89/05859 published 29 June 1989. For mammalian cells without such cell walls, the calcium phosphate precipitation method of Graham and van der Eb, Virology, 52:456-457 (1978) can be employed. General aspects of mammalian cell host system transfections have been described in U.S. Patent No. 4,399,216. Transformations into yeast are typically carried out according to the method of Van Solingen et al., J. Bact., 130:946 (1977) and Hsiao et al., Proc. Natl. Acad. Sci. (USA), 76:3829 (1979). However, other methods for introducing DNA into cells, such as by nuclear microinjection, electroporation, bacterial protoplast fusion with intact cells, or polycations, e.g., polybrene, polyornithine, may also be used. For various techniques for transforming mammalian cells, see Keown et al., Methods in Enzymology, 185:527-537 (1990) and Mansour et al., Nature, 336:348-352 (1988).

Suitable host cells for cloning or expressing the DNA in the vectors herein include prokaryote, yeast, or higher eukaryote cells. Suitable prokaryotes include but are not limited to eubacteria, such as Gram-negative or Gram-positive organisms, for example, Enterobacteriaceae such as *E. coli*. Various *E. coli* strains are publicly available, such as *E. coli* K12 strain MM294 (ATCC 31,446); *E. coli* X1776 (ATCC 31,537); *E. coli* strain W3110 (ATCC 27,325) and K5 772 (ATCC 53,635). Other suitable prokaryotic host cells include Enterobacteriaceae such as *Escherichia*, e.g., *E. coli*, *Enterobacter*, *Erwinia*, *Klebsiella*, *Proteus*, *Salmonella*, e.g., *Salmonella typhimurium*, *Serratia*, e.g., *Serratia marcescans*, and *Shigella*, as well as *Bacilli* such as *B. subtilis* and *B. licheniformis* (e.g., *B. licheniformis* 41P disclosed in DD 266,710 published 12 April 1989), *Pseudomonas* such as *P. aeruginosa*, and *Streptomyces*. These examples are illustrative rather than limiting. Strain W3110 is one particularly preferred host or parent host because it is a common host strain for recombinant DNA product fermentations. Preferably, the host cell secretes minimal amounts of proteolytic enzymes. For example, strain W3110 may be modified to effect a genetic mutation in the genes encoding proteins endogenous to the host, with examples of such hosts including *E. coli* W3110 strain 1A2, which has the complete genotype *tonA*; *E. coli* W3110 strain 9E4, which has the complete genotype *tonA ptr3*; *E. coli* W3110 strain 27C7 (ATCC

55,244), which has the complete genotype *tonA pir3 phoA E15 (argF-lac)169 degP ompT kar^r*; *E. coli* W3110 strain 37D6, which has the complete genotype *tonA pir3 phoA E15 (argF-lac)169 degP ompT rbs7 ilvG kar^r*; *E. coli* W3110 strain 40B4, which is strain 37D6 with a non-kanamycin resistant *degP* deletion mutation; and an *E. coli* strain having mutant periplasmic protease disclosed in U.S. Patent No. 4,946,783 issued 7 August 1990. Alternatively, *in vitro* methods of cloning, e.g., PCR or other nucleic acid polymerase reactions, are suitable.

5 In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for PRO-encoding vectors. *Saccharomyces cerevisiae* is a commonly used lower eukaryotic host microorganism. Others include *Schizosaccharomyces pombe* (Beach and Nurse, Nature, 290: 140 [1981]; EP 139,383 published 2 May 1985); *Kluyveromyces* hosts (U.S. Patent No. 4,943,529; Fleer et al., Bio/Technology, 9:968-975 (1991)) such as, e.g., *K. lactis* (MW98-8C, CBS683, CBS4574; Louvencourt et al., J. Bacteriol., 154(2):737-742 [1983]), *K. fragilis* (ATCC 12,424), *K. bulgaricus* (ATCC 16,045), *K. wickerhamii* (ATCC 24,178), *K. waltii* (ATCC 56,500), *K. drosophilae* (ATCC 36,906; Van den Berg et al., Bio/Technology, 8:135 (1990)), *K. thermotolerans*, and *K. marxianus*; *yarrowia* (EP 402,226); *Pichia pastoris* (EP 183,070; Sreekrishna et al., J. Basic Microbiol., 28:265-278 [1988]); *Candida*; *Trichoderma reesia* (EP 244,234); *Neurospora crassa* (Case et al., Proc. Natl. Acad. Sci. USA, 76:5259-5263 [1979]); *Schwanniomyces* such as *Schwanniomyces occidentalis* (EP 394,538 published 31 October 1990); and filamentous fungi such as, e.g., *Neurospora*, *Penicillium*, *Tolypocladium* (WO 91/00357 published 10 January 1991), and *Aspergillus* hosts such as *A. nidulans* (Ballance et al., Biochem. Biophys. Res. Commun., 112:284-289 [1983]; Tilburn et al., Gene, 26:205-221 [1983]; Yelton et al., Proc. Natl. Acad. Sci. USA, 81: 1470-1474 [1984]) and *A. niger* (Kelly and Hynes, EMBO J., 4:475-479 [1985]). Methylophilic yeasts are suitable herein and include, but are not limited to, yeast capable of growth on methanol selected from the genera consisting of *Hansenula*, *Candida*, *Kloeckera*, *Pichia*, *Saccharomyces*, *Torulopsis*, and *Rhodotorula*. A list of specific species that are exemplary of this class of yeasts may be found in C. Anthony, The Biochemistry of Methylophilic Yeasts, 269 (1982).

Suitable host cells for the expression of glycosylated PRO are derived from multicellular organisms. Examples of invertebrate cells include insect cells such as *Drosophila* S2 and *Spodoptera* Sf9, as well as plant cells. Examples of useful mammalian host cell lines include Chinese hamster ovary (CHO) and COS cells. More specific examples include monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham et al., J. Gen Virol., 36:59 (1977)); Chinese hamster ovary cells/-DHFR (CHO, Urlaub and Chasin, Proc. Natl. Acad. Sci. USA, 77:4216 (1980)); mouse sertoli cells (TM4, Mather, Biol. Reprod., 23:243-251 (1980)); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2, HB 8065); and mouse mammary tumor (MMT 060562, ATCC CCL51). The selection of the appropriate host cell is deemed to be within the skill in the art.

3. Selection and Use of a Replicable Vector

35 The nucleic acid (e.g., cDNA or genomic DNA) encoding PRO may be inserted into a replicable vector for cloning (amplification of the DNA) or for expression. Various vectors are publicly available. The vector may, for example, be in the form of a plasmid, cosmid, viral particle, or phage. The appropriate nucleic acid sequence may be inserted into the vector by a variety of procedures. In general, DNA is inserted into an

appropriate restriction endonuclease site(s) using techniques known in the art. Vector components generally include, but are not limited to, one or more of a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination sequence. Construction of suitable vectors containing one or more of these components employs standard ligation techniques which are known to the skilled artisan.

5 The PRO may be produced recombinantly not only directly, but also as a fusion polypeptide with a heterologous polypeptide, which may be a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature protein or polypeptide. In general, the signal sequence may be a component of the vector, or it may be a part of the PRO-encoding DNA that is inserted into the vector. The signal sequence may be a prokaryotic signal sequence selected, for example, from the group of the alkaline phosphatase,
10 penicillinase, lpp, or heat-stable enterotoxin II leaders. For yeast secretion the signal sequence may be, e.g., the yeast invertase leader, alpha factor leader (including *Saccharomyces* and *Kluyveromyces* α -factor leaders, the latter described in U.S. Patent No. 5,010,182), or acid phosphatase leader, the *C. albicans* glucoamylase leader (EP 362,179 published 4 April 1990), or the signal described in WO 90/13646 published 15 November 1990. In mammalian cell expression, mammalian signal sequences may be used to direct secretion of the protein, such as
15 signal sequences from secreted polypeptides of the same or related species, as well as viral secretory leaders.

Both expression and cloning vectors contain a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. Such sequences are well known for a variety of bacteria, yeast, and viruses. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria, the 2μ plasmid origin is suitable for yeast, and various viral origins (SV40, polyoma, adenovirus, VSV or BPV) are useful for
20 cloning vectors in mammalian cells.

Expression and cloning vectors will typically contain a selection gene, also termed a selectable marker. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g., ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, e.g., the gene encoding D-alanine racemase for *Bacilli*.

25 An example of suitable selectable markers for mammalian cells are those that enable the identification of cells competent to take up the PRO-encoding nucleic acid, such as DHFR or thymidine kinase. An appropriate host cell when wild-type DHFR is employed is the CHO cell line deficient in DHFR activity, prepared and propagated as described by Urlaub et al., Proc. Natl. Acad. Sci. USA, 77:4216 (1980). A suitable selection gene for use in yeast is the *trp1* gene present in the yeast plasmid YRp7 [Stinchcomb et al., Nature, 282:39 (1979);
30 Kingsman et al., Gene, 7:141 (1979); Tschemper et al., Gene, 10:157 (1980)]. The *trp1* gene provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example, ATCC No. 44076 or PEP4-1 [Jones, Genetics, 85:12 (1977)].

Expression and cloning vectors usually contain a promoter operably linked to the PRO-encoding nucleic acid sequence to direct mRNA synthesis. Promoters recognized by a variety of potential host cells are well
35 known. Promoters suitable for use with prokaryotic hosts include the β -lactamase and lactose promoter systems [Chang et al., Nature, 275:615 (1978); Goeddel et al., Nature, 281:544 (1979)], alkaline phosphatase, a tryptophan (*trp*) promoter system [Goeddel, Nucleic Acids Res., 8:4057 (1980); EP 36,776], and hybrid

promoters such as the tac promoter [deBoer et al., Proc. Natl. Acad. Sci. USA, 80:21-25 (1983)]. Promoters for use in bacterial systems also will contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding PRO.

5 Examples of suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase [Hitzeman et al., J. Biol. Chem., 255:2073 (1980)] or other glycolytic enzymes [Hess et al., J. Adv. Enzyme Reg., 7:149 (1968); Holland, Biochemistry, 17:4900 (1978)], such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase.

10 Other yeast promoters, which are inducible promoters having the additional advantage of transcription controlled by growth conditions, are the promoter regions for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, metallothionein, glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Suitable vectors and promoters for use in yeast expression are further described in EP 73,657.

15 PRO transcription from vectors in mammalian host cells is controlled, for example, by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus (UK 2,211,504 published 5 July 1989), adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and Simian Virus 40 (SV40), from heterologous mammalian promoters, e.g., the actin promoter or an immunoglobulin promoter, and from heat-shock promoters, provided such promoters are compatible with the host cell systems.

20 Transcription of a DNA encoding the PRO by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp, that act on a promoter to increase its transcription. Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin, α -fetoprotein, and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. The enhancer may be spliced into the vector at a position 5' or 3' to the PRO coding sequence, but is preferably located at a site 5' from the promoter.

25 Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) will also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5' and, occasionally 3', untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the mRNA encoding PRO.

30 Still other methods, vectors, and host cells suitable for adaptation to the synthesis of PRO in recombinant vertebrate cell culture are described in Gething et al., Nature, 293:620-625 (1981); Mantei et al., Nature, 281:40-46 (1979); EP 117,060; and EP 117,058.

4. Detecting Gene Amplification/Expression

Gene amplification and/or expression may be measured in a sample directly, for example, by conventional Southern blotting, Northern blotting to quantitate the transcription of mRNA [Thomas, Proc. Natl. Acad. Sci. USA, 77:5201-5205 (1980)], dot blotting (DNA analysis), or *in situ* hybridization, using an appropriately labeled probe, based on the sequences provided herein. Alternatively, antibodies may be employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. The antibodies in turn may be labeled and the assay may be carried out where the duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected.

Gene expression, alternatively, may be measured by immunological methods, such as immunohistochemical staining of cells or tissue sections and assay of cell culture or body fluids, to quantitate directly the expression of gene product. Antibodies useful for immunohistochemical staining and/or assay of sample fluids may be either monoclonal or polyclonal, and may be prepared in any mammal. Conveniently, the antibodies may be prepared against a native sequence PRO polypeptide or against a synthetic peptide based on the DNA sequences provided herein or against exogenous sequence fused to PRO DNA and encoding a specific antibody epitope.

5. Purification of Polypeptide

Forms of PRO may be recovered from culture medium or from host cell lysates. If membrane-bound, it can be released from the membrane using a suitable detergent solution (e.g. Triton-X 100) or by enzymatic cleavage. Cells employed in expression of PRO can be disrupted by various physical or chemical means, such as freeze-thaw cycling, sonication, mechanical disruption, or cell lysing agents.

It may be desired to purify PRO from recombinant cell proteins or polypeptides. The following procedures are exemplary of suitable purification procedures: by fractionation on an ion-exchange column; ethanol precipitation; reverse phase HPLC; chromatography on silica or on a cation-exchange resin such as DEAE; chromatofocusing; SDS-PAGE; ammonium sulfate precipitation; gel filtration using, for example, Sephadex G-75; protein A Sepharose columns to remove contaminants such as IgG; and metal chelating columns to bind epitope-tagged forms of the PRO. Various methods of protein purification may be employed and such methods are known in the art and described for example in Deutscher, Methods in Enzymology, 182 (1990); Scopes, Protein Purification: Principles and Practice, Springer-Verlag, New York (1982). The purification step(s) selected will depend, for example, on the nature of the production process used and the particular PRO produced.

E. Uses for PRO

Nucleotide sequences (or their complement) encoding PRO have various applications in the art of molecular biology, including uses as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. PRO nucleic acid will also be useful for the preparation of PRO polypeptides by the recombinant techniques described herein.

The full-length native sequence PRO gene, or portions thereof, may be used as hybridization probes for a cDNA library to isolate the full-length PRO cDNA or to isolate still other cDNAs (for instance, those encoding

naturally-occurring variants of PRO or PRO from other species) which have a desired sequence identity to the native PRO sequence disclosed herein. Optionally, the length of the probes will be about 20 to about 50 bases. The hybridization probes may be derived from at least partially novel regions of the full length native nucleotide sequence wherein those regions may be determined without undue experimentation or from genomic sequences including promoters, enhancer elements and introns of native sequence PRO. By way of example, a screening method will comprise isolating the coding region of the PRO gene using the known DNA sequence to synthesize a selected probe of about 40 bases. Hybridization probes may be labeled by a variety of labels, including radionucleotides such as ^{32}P or ^{35}S , or enzymatic labels such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems. Labeled probes having a sequence complementary to that of the PRO gene of the present invention can be used to screen libraries of human cDNA, genomic DNA or mRNA to determine which members of such libraries the probe hybridizes to. Hybridization techniques are described in further detail in the Examples below.

Any EST sequences disclosed in the present application may similarly be employed as probes, using the methods disclosed herein.

Other useful fragments of the PRO nucleic acids include antisense or sense oligonucleotides comprising a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target PRO mRNA (sense) or PRO DNA (antisense) sequences. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment of the coding region of PRO DNA. Such a fragment generally comprises at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, for example, Stein and Cohen (Cancer Res. 48:2659, 1988) and van der Krol et al. (BioTechniques 6:958, 1988).

Binding of antisense or sense oligonucleotides to target nucleic acid sequences results in the formation of duplexes that block transcription or translation of the target sequence by one of several means, including enhanced degradation of the duplexes, premature termination of transcription or translation, or by other means. The antisense oligonucleotides thus may be used to block expression of PRO proteins. Antisense or sense oligonucleotides further comprise oligonucleotides having modified sugar-phosphodiester backbones (or other sugar linkages, such as those described in WO 91/06629) and wherein such sugar linkages are resistant to endogenous nucleases. Such oligonucleotides with resistant sugar linkages are stable *in vivo* (i.e., capable of resisting enzymatic degradation) but retain sequence specificity to be able to bind to target nucleotide sequences.

Other examples of sense or antisense oligonucleotides include those oligonucleotides which are covalently linked to organic moieties, such as those described in WO 90/10048, and other moieties that increases affinity of the oligonucleotide for a target nucleic acid sequence, such as poly-(L-lysine). Further still, intercalating agents, such as ellipticine, and alkylating agents or metal complexes may be attached to sense or antisense oligonucleotides to modify binding specificities of the antisense or sense oligonucleotide for the target nucleotide sequence.

Antisense or sense oligonucleotides may be introduced into a cell containing the target nucleic acid sequence by any gene transfer method, including, for example, CaPO_4 -mediated DNA transfection, electroporation, or by using gene transfer vectors such as Epstein-Barr virus. In a preferred procedure, an

antisense or sense oligonucleotide is inserted into a suitable retroviral vector. A cell containing the target nucleic acid sequence is contacted with the recombinant retroviral vector, either *in vivo* or *ex vivo*. Suitable retroviral vectors include, but are not limited to, those derived from the murine retrovirus M-MuLV, N2 (a retrovirus derived from M-MuLV), or the double copy vectors designated DCT5A, DCT5B and DCT5C (see WO 90/13641).

5 Sense or antisense oligonucleotides also may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or
10 receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell.

Alternatively, a sense or an antisense oligonucleotide may be introduced into a cell containing the target nucleic acid sequence by formation of an oligonucleotide-lipid complex, as described in WO 90/10448. The sense or antisense oligonucleotide-lipid complex is preferably dissociated within the cell by an endogenous lipase.

15 Antisense or sense RNA or DNA molecules are generally at least about 5 bases in length, about 10 bases in length, about 15 bases in length, about 20 bases in length, about 25 bases in length, about 30 bases in length, about 35 bases in length, about 40 bases in length, about 45 bases in length, about 50 bases in length, about 55 bases in length, about 60 bases in length, about 65 bases in length, about 70 bases in length, about 75 bases in length, about 80 bases in length, about 85 bases in length, about 90 bases in length, about 95 bases in length, about 100 bases in length, or more.

20 The probes may also be employed in PCR techniques to generate a pool of sequences for identification of closely related PRO coding sequences.

Nucleotide sequences encoding a PRO can also be used to construct hybridization probes for mapping the gene which encodes that PRO and for the genetic analysis of individuals with genetic disorders. The nucleotide sequences provided herein may be mapped to a chromosome and specific regions of a chromosome
25 using known techniques, such as *in situ* hybridization, linkage analysis against known chromosomal markers, and hybridization screening with libraries.

When the coding sequences for PRO encode a protein which binds to another protein (example, where the PRO is a receptor), the PRO can be used in assays to identify the other proteins or molecules involved in the binding interaction. By such methods, inhibitors of the receptor/ligand binding interaction can be identified.
30 Proteins involved in such binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction. Also, the receptor PRO can be used to isolate correlative ligand(s). Screening assays can be designed to find lead compounds that mimic the biological activity of a native PRO or a receptor for PRO. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates. Small molecules
35 contemplated include synthetic organic or inorganic compounds. The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays and cell based assays, which are well characterized in the art.

Nucleic acids which encode PRO or its modified forms can also be used to generate either transgenic animals or "knock out" animals which, in turn, are useful in the development and screening of therapeutically useful reagents. A transgenic animal (e.g., a mouse or rat) is an animal having cells that contain a transgene, which transgene was introduced into the animal or an ancestor of the animal at a prenatal, e.g., an embryonic stage. A transgene is a DNA which is integrated into the genome of a cell from which a transgenic animal
5 develops. In one embodiment, cDNA encoding PRO can be used to clone genomic DNA encoding PRO in accordance with established techniques and the genomic sequences used to generate transgenic animals that contain cells which express DNA encoding PRO. Methods for generating transgenic animals, particularly animals such as mice or rats, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009. Typically, particular cells would be targeted for PRO transgene incorporation with
10 tissue-specific enhancers. Transgenic animals that include a copy of a transgene encoding PRO introduced into the germ line of the animal at an embryonic stage can be used to examine the effect of increased expression of DNA encoding PRO. Such animals can be used as tester animals for reagents thought to confer protection from, for example, pathological conditions associated with its overexpression. In accordance with this facet of the invention, an animal is treated with the reagent and a reduced incidence of the pathological condition, compared
15 to untreated animals bearing the transgene, would indicate a potential therapeutic intervention for the pathological condition.

Alternatively, non-human homologues of PRO can be used to construct a PRO "knock out" animal which has a defective or altered gene encoding PRO as a result of homologous recombination between the endogenous gene encoding PRO and altered genomic DNA encoding PRO introduced into an embryonic stem cell of the
20 animal. For example, cDNA encoding PRO can be used to clone genomic DNA encoding PRO in accordance with established techniques. A portion of the genomic DNA encoding PRO can be deleted or replaced with another gene, such as a gene encoding a selectable marker which can be used to monitor integration. Typically, several kilobases of unaltered flanking DNA (both at the 5' and 3' ends) are included in the vector [see e.g., Thomas and Capecchi, *Cell*, 51:503 (1987) for a description of homologous recombination vectors]. The vector
25 is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced DNA has homologously recombined with the endogenous DNA are selected [see e.g., Li et al., *Cell*, 69:915 (1992)]. The selected cells are then injected into a blastocyst of an animal (e.g., a mouse or rat) to form aggregation chimeras [see e.g., Bradley, in *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, E. J. Robertson, ed. (IRL, Oxford, 1987), pp. 113-152]. A chimeric embryo can then be implanted into a suitable
30 pseudopregnant female foster animal and the embryo brought to term to create a "knock out" animal. Progeny harboring the homologously recombined DNA in their germ cells can be identified by standard techniques and used to breed animals in which all cells of the animal contain the homologously recombined DNA. Knockout animals can be characterized for instance, for their ability to defend against certain pathological conditions and for their development of pathological conditions due to absence of the PRO polypeptide.

35 Nucleic acid encoding the PRO polypeptides may also be used in gene therapy. In gene therapy applications, genes are introduced into cells in order to achieve *in vivo* synthesis of a therapeutically effective genetic product, for example for replacement of a defective gene. "Gene therapy" includes both conventional

gene therapy where a lasting effect is achieved by a single treatment, and the administration of gene therapeutic agents, which involves the one time or repeated administration of a therapeutically effective DNA or mRNA. Antisense RNAs and DNAs can be used as therapeutic agents for blocking the expression of certain genes *in vivo*. It has already been shown that short antisense oligonucleotides can be imported into cells where they act as inhibitors, despite their low intracellular concentrations caused by their restricted uptake by the cell membrane.

5 (Zamecnik *et al.*, Proc. Natl. Acad. Sci. USA 83:4143-4146 [1986]). The oligonucleotides can be modified to enhance their uptake, e.g. by substituting their negatively charged phosphodiester groups by uncharged groups.

There are a variety of techniques available for introducing nucleic acids into viable cells. The techniques vary depending upon whether the nucleic acid is transferred into cultured cells *in vitro*, or *in vivo* in the cells of the intended host. Techniques suitable for the transfer of nucleic acid into mammalian cells *in vitro* include the use of liposomes, electroporation, microinjection, cell fusion, DEAE-dextran, the calcium phosphate precipitation method, etc. The currently preferred *in vivo* gene transfer techniques include transfection with viral (typically retroviral) vectors and viral coat protein-liposome mediated transfection (Dzau *et al.*, Trends in Biotechnology 11, 205-210 [1993]). In some situations it is desirable to provide the nucleic acid source with an agent that targets the target cells, such as an antibody specific for a cell surface membrane protein or the target cell, a ligand for a receptor on the target cell, etc. Where liposomes are employed, proteins which bind to a cell surface membrane protein associated with endocytosis may be used for targeting and/or to facilitate uptake, e.g. capsid proteins or fragments thereof tropic for a particular cell type, antibodies for proteins which undergo internalization in cycling, proteins that target intracellular localization and enhance intracellular half-life. The technique of receptor-mediated endocytosis is described, for example, by Wu *et al.*, J. Biol. Chem. 262, 4429-4432 (1987); and Wagner *et al.*, Proc. Natl. Acad. Sci. USA 87, 3410-3414 (1990). For review of gene marking and gene therapy protocols see Anderson *et al.*, Science 256, 808-813 (1992).

10
15
20

The PRO polypeptides described herein may also be employed as molecular weight markers for protein electrophoresis purposes and the isolated nucleic acid sequences may be used for recombinantly expressing those markers.

25 The nucleic acid molecules encoding the PRO polypeptides or fragments thereof described herein are useful for chromosome identification. In this regard, there exists an ongoing need to identify new chromosome markers, since relatively few chromosome marking reagents, based upon actual sequence data are presently available. Each PRO nucleic acid molecule of the present invention can be used as a chromosome marker.

30 The PRO polypeptides and nucleic acid molecules of the present invention may also be used diagnostically for tissue typing, wherein the PRO polypeptides of the present invention may be differentially expressed in one tissue as compared to another, preferably in a diseased tissue as compared to a normal tissue of the same tissue type. PRO nucleic acid molecules will find use for generating probes for PCR, Northern analysis, Southern analysis and Western analysis.

35 The PRO polypeptides described herein may also be employed as therapeutic agents. The PRO polypeptides of the present invention can be formulated according to known methods to prepare pharmaceutically useful compositions, whereby the PRO product hereof is combined in admixture with a pharmaceutically acceptable carrier vehicle. Therapeutic formulations are prepared for storage by mixing the active ingredient

having the desired degree of purity with optional physiologically acceptable carriers, excipients or stabilizers (Remington's Pharmaceutical Sciences 16th edition, Osol, A. Ed. (1980)), in the form of lyophilized formulations or aqueous solutions. Acceptable carriers, excipients or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone, amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEENTM, PLURONICSTM or PEG.

10 The formulations to be used for *in vivo* administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes, prior to or following lyophilization and reconstitution.

Therapeutic compositions herein generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

15 The route of administration is in accord with known methods, e.g. injection or infusion by intravenous, intraperitoneal, intracerebral, intramuscular, intraocular, intraarterial or intralesional routes, topical administration, or by sustained release systems.

Dosages and desired drug concentrations of pharmaceutical compositions of the present invention may vary depending on the particular use envisioned. The determination of the appropriate dosage or route of administration is well within the skill of an ordinary physician. Animal experiments provide reliable guidance for the determination of effective doses for human therapy. Interspecies scaling of effective doses can be performed following the principles laid down by Mordenti, J. and Chappell, W. "The use of interspecies scaling in toxicokinetics" In *Toxicokinetics and New Drug Development*, Yacobi et al., Eds., Pergamon Press, New York 1989, pp. 42-96.

20 When *in vivo* administration of a PRO polypeptide or agonist or antagonist thereof is employed, normal dosage amounts may vary from about 10 ng/kg to up to 100 mg/kg of mammal body weight or more per day, preferably about 1 μ g/kg/day to 10 mg/kg/day, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature; see, for example, U.S. Pat. Nos. 4,657,760; 5,206,344; or 5,225,212. It is anticipated that different formulations will be effective for different treatment compounds and different disorders, that administration targeting one organ or tissue, for example, may necessitate delivery in a manner different from that to another organ or tissue.

30 Where sustained-release administration of a PRO polypeptide is desired in a formulation with release characteristics suitable for the treatment of any disease or disorder requiring administration of the PRO polypeptide, microencapsulation of the PRO polypeptide is contemplated. Microencapsulation of recombinant proteins for sustained release has been successfully performed with human growth hormone (rhGH), interferon- (rhIFN-), interleukin-2, and MN rgp120. Johnson et al., *Nat. Med.*, 2:795-799 (1996); Yasuda, *Biomed. Ther.*, 27:1221-1223 (1993); Hora et al., *Bio/Technology*, 8:755-758 (1990); Cleland, "Design and Production of Single Immunization Vaccines Using Polylactide Polyglycolide Microsphere Systems," in *Vaccine Design: The Subunit*

and Adjuvant Approach, Powell and Newman, eds, (Plenum Press: New York, 1995), pp. 439-462; WO 97/03692, WO 96/40072, WO 96/07399; and U.S. Pat. No. 5,654,010.

The sustained-release formulations of these proteins were developed using poly-lactic-coglycolic acid (PLGA) polymer due to its biocompatibility and wide range of biodegradable properties. The degradation products of PLGA; lactic and glycolic acids, can be cleared quickly within the human body. Moreover, the degradability of this polymer can be adjusted from months to years depending on its molecular weight and composition. Lewis, "Controlled release of bioactive agents from lactide/glycolide polymer," in: M. Chasin and R. Langer (Eds.), Biodegradable Polymers as Drug Delivery Systems (Marcel Dekker: New York, 1990), pp. 1-41.

This invention encompasses methods of screening compounds to identify those that mimic the PRO polypeptide (agonists) or prevent the effect of the PRO polypeptide (antagonists). Screening assays for antagonist drug candidates are designed to identify compounds that bind or complex with the PRO polypeptides encoded by the genes identified herein, or otherwise interfere with the interaction of the encoded polypeptides with other cellular proteins. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates.

The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays, and cell-based assays, which are well characterized in the art.

All assays for antagonists are common in that they call for contacting the drug candidate with a PRO polypeptide encoded by a nucleic acid identified herein under conditions and for a time sufficient to allow these two components to interact.

In binding assays, the interaction is binding and the complex formed can be isolated or detected in the reaction mixture. In a particular embodiment, the PRO polypeptide encoded by the gene identified herein or the drug candidate is immobilized on a solid phase, e.g., on a microtiter plate, by covalent or non-covalent attachments. Non-covalent attachment generally is accomplished by coating the solid surface with a solution of the PRO polypeptide and drying. Alternatively, an immobilized antibody, e.g., a monoclonal antibody, specific for the PRO polypeptide to be immobilized can be used to anchor it to a solid surface. The assay is performed by adding the non-immobilized component, which may be labeled by a detectable label, to the immobilized component, e.g., the coated surface containing the anchored component. When the reaction is complete, the non-reacted components are removed, e.g., by washing, and complexes anchored on the solid surface are detected. When the originally non-immobilized component carries a detectable label, the detection of label immobilized on the surface indicates that complexing occurred. Where the originally non-immobilized component does not carry a label, complexing can be detected, for example, by using a labeled antibody specifically binding the immobilized complex.

If the candidate compound interacts with but does not bind to a particular PRO polypeptide encoded by a gene identified herein, its interaction with that polypeptide can be assayed by methods well known for detecting protein-protein interactions. Such assays include traditional approaches, such as, e.g., cross-linking, co-immunoprecipitation, and co-purification through gradients or chromatographic columns. In addition, protein-protein interactions can be monitored by using a yeast-based genetic system described by Fields and co-workers (Fields and Song, Nature (London), 340:245-246 (1989); Chien et al., Proc. Natl. Acad. Sci. USA, 88:9578-9582

(1991)) as disclosed by Chevray and Nathans, Proc. Natl. Acad. Sci. USA, 89: 5789-5793 (1991). Many transcriptional activators, such as yeast GAL4, consist of two physically discrete modular domains, one acting as the DNA-binding domain, the other one functioning as the transcription-activation domain. The yeast expression system described in the foregoing publications (generally referred to as the "two-hybrid system") takes advantage of this property, and employs two hybrid proteins, one in which the target protein is fused to the DNA-binding domain of GAL4, and another, in which candidate activating proteins are fused to the activation domain. The expression of a GAL1-*lacZ* reporter gene under control of a GAL4-activated promoter depends on reconstitution of GAL4 activity via protein-protein interaction. Colonies containing interacting polypeptides are detected with a chromogenic substrate for β -galactosidase. A complete kit (MATCHMAKER™) for identifying protein-protein interactions between two specific proteins using the two-hybrid technique is commercially available from Clontech. This system can also be extended to map protein domains involved in specific protein interactions as well as to pinpoint amino acid residues that are crucial for these interactions.

Compounds that interfere with the interaction of a gene encoding a PRO polypeptide identified herein and other intra- or extracellular components can be tested as follows: usually a reaction mixture is prepared containing the product of the gene and the intra- or extracellular component under conditions and for a time allowing for the interaction and binding of the two products. To test the ability of a candidate compound to inhibit binding, the reaction is run in the absence and in the presence of the test compound. In addition, a placebo may be added to a third reaction mixture, to serve as positive control. The binding (complex formation) between the test compound and the intra- or extracellular component present in the mixture is monitored as described hereinabove. The formation of a complex in the control reaction(s) but not in the reaction mixture containing the test compound indicates that the test compound interferes with the interaction of the test compound and its reaction partner.

To assay for antagonists, the PRO polypeptide may be added to a cell along with the compound to be screened for a particular activity and the ability of the compound to inhibit the activity of interest in the presence of the PRO polypeptide indicates that the compound is an antagonist to the PRO polypeptide. Alternatively, antagonists may be detected by combining the PRO polypeptide and a potential antagonist with membrane-bound PRO polypeptide receptors or recombinant receptors under appropriate conditions for a competitive inhibition assay. The PRO polypeptide can be labeled, such as by radioactivity, such that the number of PRO polypeptide molecules bound to the receptor can be used to determine the effectiveness of the potential antagonist. The gene encoding the receptor can be identified by numerous methods known to those of skill in the art, for example, ligand panning and FACS sorting. Coligan et al., Current Protocols in Immun., 1(2): Chapter 5 (1991). Preferably, expression cloning is employed wherein polyadenylated RNA is prepared from a cell responsive to the PRO polypeptide and a cDNA library created from this RNA is divided into pools and used to transfect COS cells or other cells that are not responsive to the PRO polypeptide. Transfected cells that are grown on glass slides are exposed to labeled PRO polypeptide. The PRO polypeptide can be labeled by a variety of means including iodination or inclusion of a recognition site for a site-specific protein kinase. Following fixation and incubation, the slides are subjected to autoradiographic analysis. Positive pools are identified and sub-pools are prepared and re-transfected using an interactive sub-pooling and re-screening process, eventually yielding a single

clone that encodes the putative receptor.

As an alternative approach for receptor identification, labeled PRO polypeptide can be photoaffinity-linked with cell membrane or extract preparations that express the receptor molecule. Cross-linked material is resolved by PAGE and exposed to X-ray film. The labeled complex containing the receptor can be excised, resolved into peptide fragments, and subjected to protein micro-sequencing. The amino acid sequence obtained from micro-sequencing would be used to design a set of degenerate oligonucleotide probes to screen a cDNA library to identify the gene encoding the putative receptor.

In another assay for antagonists, mammalian cells or a membrane preparation expressing the receptor would be incubated with labeled PRO polypeptide in the presence of the candidate compound. The ability of the compound to enhance or block this interaction could then be measured.

More specific examples of potential antagonists include an oligonucleotide that binds to the fusions of immunoglobulin with PRO polypeptide, and, in particular, antibodies including, without limitation, poly- and monoclonal antibodies and antibody fragments, single-chain antibodies, anti-idiotypic antibodies, and chimeric or humanized versions of such antibodies or fragments, as well as human antibodies and antibody fragments. Alternatively, a potential antagonist may be a closely related protein, for example, a mutated form of the PRO polypeptide that recognizes the receptor but imparts no effect, thereby competitively inhibiting the action of the PRO polypeptide.

Another potential PRO polypeptide antagonist is an antisense RNA or DNA construct prepared using antisense technology, where, e.g., an antisense RNA or DNA molecule acts to block directly the translation of mRNA by hybridizing to targeted mRNA and preventing protein translation. Antisense technology can be used to control gene expression through triple-helix formation or antisense DNA or RNA, both of which methods are based on binding of a polynucleotide to DNA or RNA. For example, the 5' coding portion of the polynucleotide sequence, which encodes the mature PRO polypeptides herein, is used to design an antisense RNA oligonucleotide of from about 10 to 40 base pairs in length. A DNA oligonucleotide is designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res., 6:3073 (1979); Cooney et al., Science, 241: 456 (1988); Dervan et al., Science, 251:1360 (1991)), thereby preventing transcription and the production of the PRO polypeptide. The antisense RNA oligonucleotide hybridizes to the mRNA *in vivo* and blocks translation of the mRNA molecule into the PRO polypeptide (antisense - Okano, Neurochem., 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression (CRC Press: Boca Raton, FL, 1988). The oligonucleotides described above can also be delivered to cells such that the antisense RNA or DNA may be expressed *in vivo* to inhibit production of the PRO polypeptide. When antisense DNA is used, oligodeoxyribonucleotides derived from the translation-initiation site, e.g., between about -10 and +10 positions of the target gene nucleotide sequence, are preferred.

Potential antagonists include small molecules that bind to the active site, the receptor binding site, or growth factor or other relevant binding site of the PRO polypeptide, thereby blocking the normal biological activity of the PRO polypeptide. Examples of small molecules include, but are not limited to, small peptides or peptide-like molecules, preferably soluble peptides, and synthetic non-peptidyl organic or inorganic compounds.

Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA.

Ribozymes act by sequence-specific hybridization to the complementary target RNA, followed by endonucleolytic cleavage. Specific ribozyme cleavage sites within a potential RNA target can be identified by known techniques. For further details see, e.g., Rossi, Current Biology, 4:469-471 (1994), and PCT publication No. WO 97/33551 (published September 18, 1997).

5 Nucleic acid molecules in triple-helix formation used to inhibit transcription should be single-stranded and composed of deoxynucleotides. The base composition of these oligonucleotides is designed such that it promotes triple-helix formation via Hoogsteen base-pairing rules, which generally require sizeable stretches of purines or pyrimidines on one strand of a duplex. For further details see, e.g., PCT publication No. WO 97/33551, *supra*.

10 These small molecules can be identified by any one or more of the screening assays discussed hereinabove and/or by any other screening techniques well known for those skilled in the art.

Diagnostic and therapeutic uses of the herein disclosed molecules may also be based upon the positive functional assay hits disclosed and described below.

F. Anti-PRO Antibodies

15 The present invention further provides anti-PRO antibodies. Exemplary antibodies include polyclonal, monoclonal, humanized, bispecific, and heteroconjugate antibodies.

1. Polyclonal Antibodies

20 The anti-PRO antibodies may comprise polyclonal antibodies. Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include the PRO polypeptide or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).
25 The immunization protocol may be selected by one skilled in the art without undue experimentation.

30 2. Monoclonal Antibodies

The anti-PRO antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically
35 bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*.

The immunizing agent will typically include the PRO polypeptide or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or

lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies [Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63].

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against PRO. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an *in vitro* binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980).

After the desired hybridoma cells are identified, the clones may be subcloned by limiting dilution procedures and grown by standard methods [Goding, supra]. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells may be grown *in vivo* as ascites in a mammal.

The monoclonal antibodies secreted by the subclones may be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies may also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also may be modified, for example, by substituting the coding

sequence for human heavy and light chain constant domains in place of the homologous murine sequences [U.S. Patent No. 4,816,567; Morrison et al., supra] or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

5 The antibodies may be monovalent antibodies. Methods for preparing monovalent antibodies are well known in the art. For example, one method involves recombinant expression of immunoglobulin light chain and modified heavy chain. The heavy chain is truncated generally at any point in the Fc region so as to prevent heavy chain crosslinking. Alternatively, the relevant cysteine residues are substituted with another amino acid residue or are deleted so as to prevent crosslinking.

10 *In vitro* methods are also suitable for preparing monovalent antibodies. Digestion of antibodies to produce fragments thereof, particularly, Fab fragments, can be accomplished using routine techniques known in the art.

3. Human and Humanized Antibodies

15 The anti-PRO antibodies of the invention may further comprise humanized antibodies or human antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a
20 complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially
25 all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-329 (1988); and Presta, Curr. Op. Struct. Biol.,
30 2:593-596 (1992)].

Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization can be essentially performed following the method of Winter and co-workers
35 [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeven et al., Science, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (U.S. Patent No.

4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries [Hoogenboom and Winter, *J. Mol. Biol.*, 227:381 (1991); Marks et al., *J. Mol. Biol.*, 222:581 (1991)]. The techniques of Cole et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies (Cole et al., *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, p. 77 (1985) and Boerner et al., *J. Immunol.*, 147(1):86-95 (1991)]. Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks *et al.*, *Bio/Technology* 10, 779-783 (1992); Lonberg *et al.*, *Nature* 368 856-859 (1994); Morrison, *Nature* 368, 812-13 (1994); Fishwild *et al.*, *Nature Biotechnology* 14, 845-51 (1996); Neuberger, *Nature Biotechnology* 14, 826 (1996); Lonberg and Huszar, *Intern. Rev. Immunol.* 13 65-93 (1995).

The antibodies may also be affinity matured using known selection and/or mutagenesis methods as described above. Preferred affinity matured antibodies have an affinity which is five times, more preferably 10 times, even more preferably 20 or 30 times greater than the starting antibody (generally murine, humanized or human) from which the matured antibody is prepared.

4. Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for the PRO, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities [Milstein and Cuello, *Nature*, 305:537-539 (1983)]. Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker et al., *EMBO J.*, 10:3655-3659 (1991).

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least

one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. F(ab')₂ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan *et al.*, Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate F(ab')₂ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Fab' fragments may be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby *et al.*, J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody F(ab')₂ molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling *in vitro* to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various technique for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny *et al.*, J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger *et al.*, Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary

V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber *et al.*, J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt *et al.*, J. Immunol. 147:60 (1991).

- 5 Exemplary bispecific antibodies may bind to two different epitopes on a given PRO polypeptide herein. Alternatively, an anti-PRO polypeptide arm may be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular PRO polypeptide. Bispecific antibodies may also be used to localize cytotoxic agents to cells which express a particular PRO polypeptide. These antibodies possess a PRO-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the PRO polypeptide and further binds tissue factor (TF).
- 10

5. Heteroconjugate Antibodies

- 15 Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells [U.S. Patent No. 4,676,980], and for treatment of HIV infection [WO 91/00360; WO 92/200373; EP 03089]. It is contemplated that the antibodies may be prepared *in vitro* using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins may be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.
- 20

6. Effector Function Engineering

- 25 It may be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) may be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated may have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron *et al.*, J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity may also be prepared using heterobifunctional cross-linkers as described in Wolff *et al.* Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and may thereby have enhanced complement lysis and ADCC capabilities. See Stevenson *et al.*, Anti-Cancer Drug Design, 3: 219-230 (1989).
- 30

35

7. Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent

such as a chemotherapeutic agent, toxin (*e.g.*, an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (*i.e.*, a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, *Aleurites fordii* proteins, dianthin proteins, *Phytolaca americana* proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ^{212}Bi , ^{131}I , ^{131}In , ^{90}Y , and ^{186}Re .

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta *et al.*, Science, **238**: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody may be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (*e.g.*, avidin) that is conjugated to a cytotoxic agent (*e.g.*, a radionucleotide).

8. Immunoliposomes

The antibodies disclosed herein may also be formulated as immunoliposomes. Liposomes containing the antibody are prepared by methods known in the art, such as described in Epstein *et al.*, Proc. Natl. Acad. Sci. USA, **82**: 3688 (1985); Hwang *et al.*, Proc. Natl. Acad. Sci. USA, **77**: 4030 (1980); and U.S. Pat. Nos. 4,485,045 and 4,544,545. Liposomes with enhanced circulation time are disclosed in U.S. Patent No. 5,013,556.

Particularly useful liposomes can be generated by the reverse-phase evaporation method with a lipid composition comprising phosphatidylcholine, cholesterol, and PEG-derivatized phosphatidylethanolamine (PEG-PE). Liposomes are extruded through filters of defined pore size to yield liposomes with the desired diameter. Fab' fragments of the antibody of the present invention can be conjugated to the liposomes as described in Martin *et al.*, J. Biol. Chem., **257**: 286-288 (1982) via a disulfide-interchange reaction. A chemotherapeutic agent (such as Doxorubicin) is optionally contained within the liposome. See Gabizon *et al.*, J. National Cancer Inst., **81**(19): 1484 (1989).

9. Pharmaceutical Compositions of Antibodies

Antibodies specifically binding a PRO polypeptide identified herein, as well as other molecules identified

by the screening assays disclosed hereinbefore, can be administered for the treatment of various disorders in the form of pharmaceutical compositions.

If the PRO polypeptide is intracellular and whole antibodies are used as inhibitors, internalizing antibodies are preferred. However, lipofections or liposomes can also be used to deliver the antibody, or an antibody fragment, into cells. Where antibody fragments are used, the smallest inhibitory fragment that specifically binds to the binding domain of the target protein is preferred. For example, based upon the variable-region sequences of an antibody, peptide molecules can be designed that retain the ability to bind the target protein sequence. Such peptides can be synthesized chemically and/or produced by recombinant DNA technology. See, *e.g.*, Marasco *et al.*, Proc. Natl. Acad. Sci. USA, 90: 7889-7893 (1993). The formulation herein may also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. Alternatively, or in addition, the composition may comprise an agent that enhances its function, such as, for example, a cytotoxic agent, cytokine, chemotherapeutic agent, or growth-inhibitory agent. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.

The active ingredients may also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacrylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles, and nanocapsules) or in macroemulsions. Such techniques are disclosed in Remington's Pharmaceutical Sciences, *supra*.

The formulations to be used for *in vivo* administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes.

Sustained-release preparations may be prepared. Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, *e.g.*, films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and γ ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOTTM (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid. While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods. When encapsulated antibodies remain in the body for a long time, they may denature or aggregate as a result of exposure to moisture at 37°C, resulting in a loss of biological activity and possible changes in immunogenicity. Rational strategies can be devised for stabilization depending on the mechanism involved. For example, if the aggregation mechanism is discovered to be intermolecular S-S bond formation through thio-disulfide interchange, stabilization may be achieved by modifying sulfhydryl residues, lyophilizing from acidic solutions, controlling moisture content, using appropriate additives, and developing specific polymer matrix compositions.

G. Uses for anti-PRO Antibodies

The anti-PRO antibodies of the invention have various utilities. For example, anti-PRO antibodies may be used in diagnostic assays for PRO, *e.g.*, detecting its expression (and in some cases, differential expression) in specific cells, tissues, or serum. Various diagnostic assay techniques known in the art may be used, such as competitive binding assays, direct or indirect sandwich assays and immunoprecipitation assays conducted in either heterogeneous or homogeneous phases [Zola, Monoclonal Antibodies: A Manual of Techniques, CRC Press, Inc. (1987) pp. 147-158]. The antibodies used in the diagnostic assays can be labeled with a detectable moiety. The detectable moiety should be capable of producing, either directly or indirectly, a detectable signal. For example, the detectable moiety may be a radioisotope, such as ^3H , ^{14}C , ^{32}P , ^{35}S , or ^{125}I , a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, beta-galactosidase or horseradish peroxidase. Any method known in the art for conjugating the antibody to the detectable moiety may be employed, including those methods described by Hunter et al., Nature, 144:945 (1962); David et al., Biochemistry, 13:1014 (1974); Pain et al., J. Immunol. Meth., 40:219 (1981); and Nygren, J. Histochem. and Cytochem., 30:407 (1982).

Anti-PRO antibodies also are useful for the affinity purification of PRO from recombinant cell culture or natural sources. In this process, the antibodies against PRO are immobilized on a suitable support, such as Sephadex resin or filter paper, using methods well known in the art. The immobilized antibody then is contacted with a sample containing the PRO to be purified, and thereafter the support is washed with a suitable solvent that will remove substantially all the material in the sample except the PRO, which is bound to the immobilized antibody. Finally, the support is washed with another suitable solvent that will release the PRO from the antibody.

The following examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way.

All patent and literature references cited in the present specification are hereby incorporated by reference in their entirety.

EXAMPLES

Commercially available reagents referred to in the examples were used according to manufacturer's instructions unless otherwise indicated. The source of those cells identified in the following examples, and throughout the specification, by ATCC accession numbers is the American Type Culture Collection, Manassas, VA.

EXAMPLE 1: Extracellular Domain Homology Screening to Identify Novel Polypeptides and cDNA Encoding Therefor

The extracellular domain (ECD) sequences (including the secretion signal sequence, if any) from about 950 known secreted proteins from the Swiss-Prot public database were used to search EST databases. The EST databases included public databases (*e.g.*, Dayhoff, GenBank), and proprietary databases (*e.g.* LIFESEQTM, Incyte Pharmaceuticals, Palo Alto, CA). The search was performed using the computer program BLAST or

BLAST-2 (Altschul *et al.*, Methods in Enzymology, 266:460-480 (1996)) as a comparison of the ECD protein sequences to a 6 frame translation of the EST sequences. Those comparisons with a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into consensus DNA sequences with the program "phrap" (Phil Green, University of Washington, Seattle, WA).

5 Using this extracellular domain homology screen, consensus DNA sequences were assembled relative to the other identified EST sequences using phrap. In addition, the consensus DNA sequences obtained were often (but not always) extended using repeated cycles of BLAST or BLAST-2 and phrap to extend the consensus sequence as far as possible using the sources of EST sequences discussed above.

10 Based upon the consensus sequences obtained as described above, oligonucleotides were then synthesized and used to identify by PCR a cDNA library that contained the sequence of interest and for use as probes to isolate a clone of the full-length coding sequence for a PRO polypeptide. Forward and reverse PCR primers generally range from 20 to 30 nucleotides and are often designed to give a PCR product of about 100-1000 bp in length. The probe sequences are typically 40-55 bp in length. In some cases, additional oligonucleotides are synthesized when the consensus sequence is greater than about 1-1.5kbp. In order to screen several libraries for a full-length clone, DNA from the libraries was screened by PCR amplification, as per Ausubel *et al.*, Current
15 Protocols in Molecular Biology, with the PCR primer pair. A positive library was then used to isolate clones encoding the gene of interest using the probe oligonucleotide and one of the primer pairs.

The cDNA libraries used to isolate the cDNA clones were constructed by standard methods using commercially available reagents such as those from Invitrogen, San Diego, CA. The cDNA was primed with oligo dT containing a NotI site, linked with blunt to SalI hemikinased adaptors, cleaved with NotI, sized
20 appropriately by gel electrophoresis, and cloned in a defined orientation into a suitable cloning vector (such as pRKB or pRKD; pRK5B is a precursor of pRK5D that does not contain the SfiI site; *see*, Holmes *et al.*, Science, 253:1278-1280 (1991)) in the unique XhoI and NotI sites.

EXAMPLE 2: Isolation of cDNA clones by Amylase Screening

25 1. Preparation of oligo dT primed cDNA library

mRNA was isolated from a human tissue of interest using reagents and protocols from Invitrogen, San Diego, CA (Fast Track 2). This RNA was used to generate an oligo dT primed cDNA library in the vector pRK5D using reagents and protocols from Life Technologies, Gaithersburg, MD (Super Script Plasmid System). In this procedure, the double stranded cDNA was sized to greater than 1000 bp and the SalI/NotI linked cDNA
30 was cloned into XhoI/NotI cleaved vector. pRK5D is a cloning vector that has an sp6 transcription initiation site followed by an SfiI restriction enzyme site preceding the XhoI/NotI cDNA cloning sites.

2. Preparation of random primed cDNA library

35 A secondary cDNA library was generated in order to preferentially represent the 5' ends of the primary cDNA clones. Sp6 RNA was generated from the primary library (described above), and this RNA was used to generate a random primed cDNA library in the vector pSST-AMY.0 using reagents and protocols from Life Technologies (Super Script Plasmid System, referenced above). In this procedure the double stranded cDNA was

sized to 500-1000 bp, linked with blunt to NotI adaptors, cleaved with SfiI, and cloned into SfiI/NotI cleaved vector. pSST-AMY.0 is a cloning vector that has a yeast alcohol dehydrogenase promoter preceding the cDNA cloning sites and the mouse amylase sequence (the mature sequence without the secretion signal) followed by the yeast alcohol dehydrogenase terminator, after the cloning sites. Thus, cDNAs cloned into this vector that are fused in frame with amylase sequence will lead to the secretion of amylase from appropriately transfected yeast colonies.

3. Transformation and Detection

DNA from the library described in paragraph 2 above was chilled on ice to which was added electrocompetent DH10B bacteria (Life Technologies, 20 ml). The bacteria and vector mixture was then electroporated as recommended by the manufacturer. Subsequently, SOC media (Life Technologies, 1 ml) was added and the mixture was incubated at 37°C for 30 minutes. The transformants were then plated onto 20 standard 150 mm LB plates containing ampicillin and incubated for 16 hours (37°C). Positive colonies were scraped off the plates and the DNA was isolated from the bacterial pellet using standard protocols, *e.g.* CsCl-gradient. The purified DNA was then carried on to the yeast protocols below.

The yeast methods were divided into three categories: (1) Transformation of yeast with the plasmid/cDNA combined vector; (2) Detection and isolation of yeast clones secreting amylase; and (3) PCR amplification of the insert directly from the yeast colony and purification of the DNA for sequencing and further analysis.

The yeast strain used was HD56-5A (ATCC-90785). This strain has the following genotype: MAT⁺, ura3-52, leu2-3, leu2-112, his3-11, his3-15, MAL⁺, SUC⁺, GAL⁺. Preferably, yeast mutants can be employed that have deficient post-translational pathways. Such mutants may have translocation deficient alleles in *sec71*, *sec72*, *sec62*, with truncated *sec71* being most preferred. Alternatively, antagonists (including antisense nucleotides and/or ligands) which interfere with the normal operation of these genes, other proteins implicated in this post translation pathway (*e.g.*, SEC61p, SEC72p, SEC62p, SEC63p, TDJ1p or SSA1p-4p) or the complex formation of these proteins may also be preferably employed in combination with the amylase-expressing yeast.

Transformation was performed based on the protocol outlined by Gietz *et al.*, Nucl. Acid. Res., 20:1425 (1992). Transformed cells were then inoculated from agar into YEPD complex media broth (100 ml) and grown overnight at 30°C. The YEPD broth was prepared as described in Kaiser *et al.*, Methods in Yeast Genetics, Cold Spring Harbor Press, Cold Spring Harbor, NY, p. 207 (1994). The overnight culture was then diluted to about 2×10^6 cells/ml (approx. OD₆₀₀=0.1) into fresh YEPD broth (500 ml) and regrown to 1×10^7 cells/ml (approx. OD₆₀₀=0.4-0.5).

The cells were then harvested and prepared for transformation by transfer into GS3 rotor bottles in a Sorval GS3 rotor at 5,000 rpm for 5 minutes, the supernatant discarded, and then resuspended into sterile water, and centrifuged again in 50 ml falcon tubes at 3,500 rpm in a Beckman GS-6KR centrifuge. The supernatant was discarded and the cells were subsequently washed with LiAc/TE (10 ml, 10 mM Tris-HCl, 1 mM EDTA pH 7.5, 100 mM Li₂OOCCH₃), and resuspended into LiAc/TE (2.5 ml).

Transformation took place by mixing the prepared cells (100 μ l) with freshly denatured single stranded

salmon testes DNA (Lofstrand Labs, Gaithersburg, MD) and transforming DNA (1 μ g, vol. < 10 μ l) in microfuge tubes. The mixture was mixed briefly by vortexing, then 40% PEG/TE (600 μ l, 40% polyethylene glycol-4000, 10 mM Tris-HCl, 1 mM EDTA, 100 mM Li₂OOCCH₃, pH 7.5) was added. This mixture was gently mixed and incubated at 30°C while agitating for 30 minutes. The cells were then heat shocked at 42°C for 15 minutes, and the reaction vessel centrifuged in a microfuge at 12,000 rpm for 5-10 seconds, decanted and resuspended into TE (500 μ l, 10 mM Tris-HCl, 1 mM EDTA pH 7.5) followed by recentrifugation. The cells were then diluted into TE (1 ml) and aliquots (200 μ l) were spread onto the selective media previously prepared in 150 mm growth plates (VWR).

Alternatively, instead of multiple small reactions, the transformation was performed using a single, large scale reaction, wherein reagent amounts were scaled up accordingly.

The selective media used was a synthetic complete dextrose agar lacking uracil (SCD-Ura) prepared as described in Kaiser *et al.*, Methods in Yeast Genetics, Cold Spring Harbor Press, Cold Spring Harbor, NY, p. 208-210 (1994). Transformants were grown at 30°C for 2-3 days.

The detection of colonies secreting amylase was performed by including red starch in the selective growth media. Starch was coupled to the red dye (Reactive Red-120, Sigma) as per the procedure described by Biely *et al.*, Anal. Biochem., 172:176-179 (1988). The coupled starch was incorporated into the SCD-Ura agar plates at a final concentration of 0.15% (w/v), and was buffered with potassium phosphate to a pH of 7.0 (50-100 mM final concentration).

The positive colonies were picked and streaked across fresh selective media (onto 150 mm plates) in order to obtain well isolated and identifiable single colonies. Well isolated single colonies positive for amylase secretion were detected by direct incorporation of red starch into buffered SCD-Ura agar. Positive colonies were determined by their ability to break down starch resulting in a clear halo around the positive colony visualized directly.

4. Isolation of DNA by PCR Amplification

When a positive colony was isolated, a portion of it was picked by a toothpick and diluted into sterile water (30 μ l) in a 96 well plate. At this time, the positive colonies were either frozen and stored for subsequent analysis or immediately amplified. An aliquot of cells (5 μ l) was used as a template for the PCR reaction in a 25 μ l volume containing: 0.5 μ l KlenTaq (Clontech, Palo Alto, CA); 4.0 μ l 10 mM dNTP's (Perkin Elmer-Cetus); 2.5 μ l KlenTaq buffer (Clontech); 0.25 μ l forward oligo 1; 0.25 μ l reverse oligo 2; 12.5 μ l distilled water. The sequence of the forward oligonucleotide 1 was:

5'-TGTAACGACGCGCCAGTTAAATAGACCTGCAATTATTAATCT-3' (SEQ ID NO:611)

The sequence of reverse oligonucleotide 2 was:

5'-CAGGAAACAGCTATGACCACCTGCACACCTGCAAATCCATT-3' (SEQ ID NO:612)

PCR was then performed as follows:

- | | | |
|----|--------------|------------------|
| a. | Denature | 92°C, 5 minutes |
| b. | 3 cycles of: | |
| | Denature | 92°C, 30 seconds |
| | Anneal | 59°C, 30 seconds |

		Extend	72°C, 60 seconds
5	c.	3 cycles of:	
		Denature	92°C, 30 seconds
		Anneal	57°C, 30 seconds
		Extend	72°C, 60 seconds
	d.	25 cycles of:	
		Denature	92°C, 30 seconds
		Anneal	55°C, 30 seconds
		Extend	72°C, 60 seconds
10	e.	Hold	4°C

The underlined regions of the oligonucleotides annealed to the ADH promoter region and the amylase region, respectively, and amplified a 307 bp region from vector pSST-AMY.0 when no insert was present. Typically, the first 18 nucleotides of the 5' end of these oligonucleotides contained annealing sites for the sequencing primers. Thus, the total product of the PCR reaction from an empty vector was 343 bp. However, signal sequence-fused cDNA resulted in considerably longer nucleotide sequences.

Following the PCR, an aliquot of the reaction (5 μ l) was examined by agarose gel electrophoresis in a 1% agarose gel using a Tris-Borate-EDTA (TBE) buffering system as described by Sambrook *et al.*, *supra*. Clones resulting in a single strong PCR product larger than 400 bp were further analyzed by DNA sequencing after purification with a 96 Qiaquick PCR clean-up column (Qiagen Inc., Chatsworth, CA).

EXAMPLE 3: Isolation of cDNA Clones Using Signal Algorithm Analysis

Various polypeptide-encoding nucleic acid sequences were identified by applying a proprietary signal sequence finding algorithm developed by Genentech, Inc. (South San Francisco, CA) upon ESTs as well as clustered and assembled EST fragments from public (*e.g.*, GenBank) and/or private (LIFESEQ®, Incyte Pharmaceuticals, Inc., Palo Alto, CA) databases. The signal sequence algorithm computes a secretion signal score based on the character of the DNA nucleotides surrounding the first and optionally the second methionine codon(s) (ATG) at the 5'-end of the sequence or sequence fragment under consideration. The nucleotides following the first ATG must code for at least 35 unambiguous amino acids without any stop codons. If the first ATG has the required amino acids, the second is not examined. If neither meets the requirement, the candidate sequence is not scored. In order to determine whether the EST sequence contains an authentic signal sequence, the DNA and corresponding amino acid sequences surrounding the ATG codon are scored using a set of seven sensors (evaluation parameters) known to be associated with secretion signals. Use of this algorithm resulted in the identification of numerous polypeptide-encoding nucleic acid sequences.

EXAMPLE 4: Isolation of cDNA clones Encoding Human PRO Polypeptides

Using the techniques described in Examples 1 to 3 above, numerous full-length cDNA clones were identified as encoding PRO polypeptides as disclosed herein. These cDNAs were then deposited under the terms of the Budapest Treaty with the American Type Culture Collection, 10801 University Blvd., Manassas, VA 20110-2209, USA (ATCC) as shown in Table 7 below.

Table 7

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA16435-1208	209930	June 2, 1998
	DNA23318-1211	209787	April 21, 1998
	DNA23322-1393	203400	October 27, 1998
5	DNA23334-1392	209918	June 2, 1998
	DNA26843-1389	203099	August 4, 1998
	DNA 26844-1394	209926	June 2, 1998
	DNA30867-1335	209807	April 28, 1998
	DNA33470-1175	209398	October 17, 1997
10	DNA34436-1238	209523	December 10, 1997
	DNA35557-1137	209255	September 16, 1997
	DNA35599-1168	209373	October 16, 1997
	DNA35668-1171	209371	October 16, 1997
	DNA36992-1168	209382	October 16, 1997
15	DNA39423-1182	209387	October 17, 1997
	DNA39427-1179	209395	October 17, 1997
	DNA39510-1181	209392	October 17, 1997
	DNA39518-1247	209529	December 10, 1997
	DNA39975-1210	209783	April 21, 1998
20	DNA39976-1215	209524	December 10, 1997
	DNA39979-1213	209789	April 21, 1998
	DNA40594-1233	209617	February 5, 1998
	DNA40603-1232	209486	November 21, 1997
	DNA40604-1187	209394	October 17, 1997
25	DNA40625-1189	209788	April 21, 1998
	DNA41225-1217	209491	November 21, 1997
	DNA41379-1236	209488	November 21, 1997
	DNA41386-1316	209703	March 26, 1998
	DNA44161-1434	209907	May 27, 1998
30	DNA44179-1362	209851	May 6, 1998
	DNA44192-1246	209531	December 10, 1997
	DNA44694-1500	203114	August 11, 1998
	DNA45234-1277	209654	March 5, 1998
	DNA45409-2511	203579	January 12, 1999
35	DNA45415-1318	209810	April 28, 1998
	DNA45417-1432	209910	May 27, 1998
	DNA45493-1349	209805	April 28, 1998

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA46776-1284	209721	March 31, 1998
	DNA48296-1292	209668	March 11, 1998
	DNA48306-1291	209911	May 27, 1998
5	DNA48328-1355	209843	May 6, 1998
	DNA48329-1290	209785	April 21, 1998
	DNA48334-1435	209924	June 2, 1998
	DNA49141-1431	203003	June 23, 1998
	DNA49624-1279	209655	March 5, 1998
10	DNA49647-1398	209919	June 2, 1998
	DNA49819-1439	209931	June 2, 1998
	DNA50911-1288	209714	March 31, 1998
	DNA50914-1289	209722	March 31, 1998
	DNA50919-1361	209848	May 6, 1998
15	DNA50980-1286	209717	March 31, 1998
	DNA52185-1370	209861	May 14, 1998
	DNA53906-1368	209747	April 7, 1998
	DNA53912-1457	209870	May 14, 1998
	DNA53913-1490	203162	August 25, 1998
20	DNA53977-1371	209862	May 14, 1998
	DNA53978-1443	209983	June 16, 1998
	DNA53996-1442	209921	June 2, 1998
	DNA54002-1367	209754	April 7, 1998
	DNA55737-1345	209753	April 7, 1998
25	DNA56050-1455	203011	June 23, 1998
	DNA56052-1454	203026	June 23, 1998
	DNA56107-1415	203405	October 27, 1998
	DNA56110-1437	203113	August 11, 1998
	DNA56406-1704	203478	November 17, 1998
30	DNA56409-1377	209882	May 20, 1998
	DNA56410-1414	209923	June 2, 1998
	DNA56436-1448	209902	May 27, 1998
	DNA56529-1647	203293	September 29, 1998
	DNA56855-1447	203004	June 23, 1998
35	DNA56859-1445	203019	June 23, 1998
	DNA56860-1510	209952	June 9, 1998
	DNA56865-1491	203022	June 23, 1998

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA56868-1478	203024	June 23, 1998
	DNA56869-1545	203161	August 25, 1998
	DNA56870-1492	209925	June 2, 1998
5	DNA57039-1402	209777	April 14, 1998
	DNA57253-1382	209867	May 14, 1998
	DNA57254-1477	203289	September 29, 1998
	DNA57699-1412	203020	June 23, 1998
	DNA57704-1452	209953	June 9, 1998
10	DNA57710-1451	203048	July 1, 1998
	DNA57827-1493	203045	July 1, 1998
	DNA57844-1410	203010	June 23, 1998
	DNA58723-1588	203133	August 18, 1998
	DNA58727-1474	203171	September 1, 1998
15	DNA58730-1607	203221	September 15, 1998
	DNA58732-1650	203290	September 29, 1998
	DNA58737-1473	203136	August 18, 1998
	DNA58743-1609	203154	August 25, 1998
	DNA58747-1384	209868	May 14, 1998
20	DNA58828-1519	203172	September 1, 1998
	DNA58846-1409	209957	June 9, 1998
	DNA58848-1472	209955	June 9, 1998
	DNA58849-1494	209958	June 9, 1998
	DNA58850-1495	209956	June 9, 1998
25	DNA58852-1637	203271	September 22, 1998
	DNA58853-1423	203016	June 23, 1998
	DNA58855-1422	203018	June 23, 1998
	DNA59211-1450	209960	June 9, 1998
	DNA59212-1627	203245	September 9, 1998
30	DNA59213-1487	209959	June 9, 1998
	DNA59219-1613	203220	September 15, 1998
	DNA59497-1496	209941	June 4, 1998
	DNA59602-1436	203051	July 1, 1998
	DNA59603-1419	209944	June 9, 1998
35	DNA59605-1418	203005	June 23, 1998
	DNA59607-1497	209946	June 9, 1998
	DNA59610-1556	209990	June 16, 1998

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA59612-1466	209947	June 9, 1998
	DNA59613-1417	203007	June 23, 1998
	DNA59616-1465	209991	June 16, 1998
5	DNA59619-1464	203041	July 1, 1998
	DNA59625-1498	209992	June 16, 1998
	DNA59817-1703	203470	November 17, 1998
	DNA59827-1426	203089	August 4, 1998
	DNA59828-1608	203158	August 25, 1998
10	DNA59837-2545	203658	February 9, 1999
	DNA59844-2542	203650	February 9, 1999
	DNA59853-1505	209985	June 16, 1998
	DNA59854-1459	209974	June 16, 1998
	DNA59855-1485	209987	June 16, 1998
15	DNA60278-1530	203170	September 1, 1998
	DNA60283-1484	203043	July 1, 1998
	DNA60608-1577	203126	August 18, 1998
	DNA60611-1524	203175	September 1, 1998
	DNA60619-1482	209993	June 16, 1998
20	DNA60625-1507	209975	June 16, 1998
	DNA60629-1481	209979	June 16, 1998
	DNA60740-1615	203456	November 3, 1998
	DNA61608-1606	203239	September 9, 1998
	DNA61755-1554	203112	August 11, 1998
25	DNA62809-1531	203237	September 9, 1998
	DNA62812-1594	203248	September 9, 1998
	DNA62813-2544	203655	February 9, 1999
	DNA62845-1684	203361	October 20, 1998
	DNA64849-1604	203468	November 17, 1998
30	DNA64852-1589	203127	August 18, 1998
	DNA64863-1573	203251	September 9, 1998
	DNA64881-1602	203240	September 9, 1998
	DNA64902-1667	203317	October 6, 1998
	DNA64952-1568	203222	September 15, 1998
35	DNA65403-1565	203230	September 15, 1998
	DNA65413-1534	203234	September 15, 1998
	DNA65423-1595	203227	September 15, 1998

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA66304-1546	203321	October 6, 1998
	DNA66308-1537	203159	August 25, 1998
	DNA66511-1563	203228	September 15, 1998
5	DNA66512-1564	203218	September 15, 1998
	DNA66519-1535	203236	September 15, 1998
	DNA66521-1583	203225	September 15, 1998
	DNA66658-1584	203229	September 15, 1998
	DNA66660-1585	203279	September 22, 1998
10	DNA66669-1597	203272	September 22, 1998
	DNA66674-1599	203281	September 22, 1998
	DNA68836-1656	203455	November 3, 1998
	DNA68862-2546	203652	February 9, 1999
	DNA68866-1644	203283	September 22, 1998
15	DNA68869-1610	203164	August 25, 1998
	DNA68871-1638	203280	September 22, 1998
	DNA68879-1631	203274	September 22, 1998
	DNA68880-1676	203319	October 6, 1998
	DNA68882-1677	203318	October 6, 1998
20	DNA68883-1691	203535	December 15, 1998
	DNA68885-1678	203311	October 6, 1998
	DNA71180-1655	203403	October 27, 1998
	DNA71184-1634	203266	September 22, 1998
	DNA71213-1659	203401	October 27, 1998
25	DNA71234-1651	203402	October 27, 1998
	DNA71269-1621	203284	September 22, 1998
	DNA71277-1636	203285	September 22, 1998
	DNA71286-1687	203357	October 20, 1998
	DNA71883-1660	203475	November 17, 1998
30	DNA73401-1633	203273	September 22, 1998
	DNA73492-1671	203324	October 6, 1998
	DNA73730-1679	203320	October 6, 1998
	DNA73734-1680	203363	October 20, 1998
	DNA73735-1681	203356	October 20, 1998
35	DNA73742-1662	203316	October 6, 1998
	DNA73746-1654	203411	October 27, 1998
	DNA73760-1672	203314	October 6, 1998

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA76393-1664	203323	October 6, 1998
	DNA76398-1699	203474	November 17, 1998
	DNA76399-1700	203472	November 17, 1998
5	DNA76522-2500	203469	November 17, 1998
	DNA76533-1689	203410	October 27, 1998
	DNA77303-2502	203479	November 17, 1998
	DNA77626-1705	203536	December 15, 1998
	DNA77648-1688	203408	October 27, 1998
10	DNA81754-2532	203542	December 15, 1998
	DNA81757-2512	203543	December 15, 1998
	DNA82302-2529	203534	December 15, 1998
	DNA82340-2530	203547	December 22, 1998
	DNA87991-2540	203656	February 9, 1999
15	DNA92238-2539	203602	January 20, 1999
	DNA115291-2681	PTA-202	June 8, 1999
	DNA23336-2861	PTA-1673	April 11, 2000
	DNA30862-1396	209920	June 2, 1998
	DNA30871-1157	209380	October 16, 1997
20	DNA32279-1131	209259	September 16, 1997
	DNA33206-1165	209372	October 16, 1997
	DNA35673-1201	209418	October 28, 1997
	DNA47361-1154-2	209431	November 7, 1997
	DNA49631-1328	209806	April 28, 1998
25	DNA52594-1270	209679	March 17, 1998
	DNA55800-1263	209680	March 17, 1998
	DNA56531-1648	203286	September 29, 1998
	DNA56965-1356	209842	May 6, 1998
	DNA57037-1444	209903	May 27, 1998
30	DNA57695-1340	203006	June 23, 1998
	DNA57834-1339	209954	June 9, 1998
	DNA57841-1522	203458	November 3, 1998
	DNA58847-1383	209879	May 20, 1998
	DNA59493-1420	203050	July 1, 1998
35	DNA59586-1520	203288	September 29, 1998
	DNA59608-2577	203870	March 23, 1999
	DNA59849-1504	209986	June 16, 1998

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA60292-1506	203540	December 15, 1998
	DNA62377-1381-1	203552	December 22, 1998
	DNA62880-1513	203097	August 4, 1998
5	DNA66672-1586	203265	September 22, 1998
	DNA67962-1649	203291	September 29, 1998
	DNA69555-2867	PTA-1632	April 4, 2000
	DNA71162-2764	PTA-860	October 19, 1999
	DNA71290-1630	203275	September 22, 1998
10	DNA76401-1683	203360	October 20, 1998
	DNA76541-1675	203409	October 27, 1998
	DNA76788-2526	203551	December 22, 1998
	DNA77623-2524	203546	December 22, 1998
	DNA80136-2503	203541	December 15, 1998
15	DNA83568-2692	PTA-386	July 20, 1999
	DNA84210-2576	203818	March 2, 1999
	DNA86576-2595	203868	March 23, 1999
	DNA87976-2593	203888	March 30, 1999
	DNA92256-2596	203891	March 30, 1999
20	DNA92289-2598	PTA-131	May 25, 1999
	DNA96850-2705	PTA-479	August 3, 1999
	DNA96855-2629	PTA-18	May 4, 1999
	DNA96857-2636	PTA-17	May 4, 1999
	DNA96860-2700	PTA-478	August 3, 1999
25	DNA96861-2844	PTA-1436	March 2, 2000
	DNA96866-2698	PTA-491	August 3, 1999
	DNA96870-2676	PTA-254	June 22, 1999
	DNA96872-2674	PTA-550	August 17, 1999
	DNA96878-2626	PTA-23	May 4, 1999
30	DNA96879-2619	203967	April 27, 1999
	DNA96889-2641	PTA-119	May 25, 1999
	DNA96893-2621	PTA-12	May 4, 1999
	DNA96897-2688	PTA-379	July 20, 1999
	DNA98564-2643	PTA-125	May 25, 1999
35	DNA107443-2718	PTA-490	August 3, 1999
	DNA107786-2723	PTA-474	August 3, 1999
	DNA108682-2712	PTA-486	August 3, 1999

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA108684-2761	PTA-653	September 14, 1999
	DNA108701-2749	PTA-554	August 17, 1999
	DNA108720-2717	PTA-511	August 10, 1999
5	DNA108726-2729	PTA-514	August 10, 1999
	DNA108728-2760	PTA-654	September 14, 1999
	DNA108738-2767	PTA-862	October 19, 1999
	DNA108743-2722	PTA-508	August 10, 1999
	DNA108758-2759	PTA-655	September 14, 1999
10	DNA108765-2758	PTA-657	September 14, 1999
	DNA108783-2747	PTA-616	August 31, 1999
	DNA108789-2748	PTA-547	August 17, 1999
	DNA108806-2724	PTA-610	August 31, 1999
	DNA108936-2719	PTA-519	August 10, 1999
15	DNA119510-2771	PTA-947	November 9, 1999
	DNA119517-2778	PTA-951	November 16, 1999
	DNA119535-2756	PTA-613	August 31, 1999
	DNA119537-2777	PTA-956	November 16, 1999
	DNA119714-2851	PTA-1537	March 21, 2000
20	DNA125170-2780	PTA-953	November 16, 1999
	DNA129594-2841	PTA-1481	March 14, 2000
	DNA129793-2857	PTA-1733	April 18, 2000
	DNA130809-2769	PTA-949	November 9, 1999
	DNA131639-2874	PTA-1784	April 25, 2000
25	DNA131649-2855	PTA-1482	March 14, 2000
	DNA131652-2876	PTA-1628	April 4, 2000
	DNA131658-2875	PTA-1671	April 11, 2000
	DNA132162-2770	PTA-950	November 9, 1999
	DNA136110-2763	PTA-652	September 14, 1999
30	DNA139592-2866	PTA-1587	March 28, 2000
	DNA139608-2856	PTA-1581	March 28, 2000
	DNA143292-2848	PTA-1778	April 25, 2000
	DNA144844-2843	PTA-1536	March 21, 2000
	DNA144857-2845	PTA-1589	March 28, 2000
35	DNA145841-2868	PTA-1678	April 11, 2000
	DNA148004-2882	PTA-1779	April 25, 2000
	DNA149893-2873	PTA-1672	April 11, 2000

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA149930-2884	PTA-1668	April 11, 2000
	DNA150157-2898	PTA-1777	April 25, 2000
	DNA150163-2842	PTA-1533	March 21, 2000
5	DNA153579-2894	PTA-1729	April 18, 2000
	DNA164625-2890	PTA-1535	March 21, 2000
	DNA57838-1337	203014	June 23, 1998
	DNA59777-1480	203111	August 11, 1998
	DNA66675-1587	203282	September 22, 1998
10	DNA76532-1702	203473	November 17, 1998
	DNA105849-2704	PTA-473	August 3, 1999
	DNA83500-2506	203391	October 29, 1998

These deposits were made under the provisions of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure and the Regulations thereunder (Budapest Treaty). This assures maintenance of a viable culture of the deposit for 30 years from the date of deposit. The deposits will be made available by ATCC under the terms of the Budapest Treaty, and subject to an agreement between Genentech, Inc. and ATCC, which assures permanent and unrestricted availability of the progeny of the culture of the deposit to the public upon issuance of the pertinent U.S. patent or upon laying open to the public of any U.S. or foreign patent application, whichever comes first, and assures availability of the progeny to one determined by the U.S. Commissioner of Patents and Trademarks to be entitled thereto according to 35 USC § 122 and the Commissioner's rules pursuant thereto (including 37 CFR § 1.14 with particular reference to 886 OG 638).

The assignee of the present application has agreed that if a culture of the materials on deposit should die or be lost or destroyed when cultivated under suitable conditions, the materials will be promptly replaced on notification with another of the same. Availability of the deposited material is not to be construed as a license to practice the invention in contravention of the rights granted under the authority of any government in accordance with its patent laws.

30 EXAMPLE 5: Use of PRO as a hybridization probe

The following method describes use of a nucleotide sequence encoding PRO as a hybridization probe.

DNA comprising the coding sequence of full-length or mature PRO as disclosed herein is employed as a probe to screen for homologous DNAs (such as those encoding naturally-occurring variants of PRO) in human tissue cDNA libraries or human tissue genomic libraries.

35 Hybridization and washing of filters containing either library DNAs is performed under the following high stringency conditions. Hybridization of radiolabeled PRO-derived probe to the filters is performed in a solution of 50% formamide, 5x SSC, 0.1% SDS, 0.1% sodium pyrophosphate, 50 mM sodium phosphate, pH

6.8, 2x Denhardt's solution, and 10% dextran sulfate at 42°C for 20 hours. Washing of the filters is performed in an aqueous solution of 0.1x SSC and 0.1% SDS at 42°C.

DNAs having a desired sequence identity with the DNA encoding full-length native sequence PRO can then be identified using standard techniques known in the art.

5 EXAMPLE 6: Expression of PRO in *E. coli*

This example illustrates preparation of an unglycosylated form of PRO by recombinant expression in *E. coli*.

The DNA sequence encoding PRO is initially amplified using selected PCR primers. The primers should contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector. A variety of expression vectors may be employed. An example of a suitable vector is pBR322 (derived from *E. coli*; see Bolivar et al., Gene, 2:95 (1977)) which contains genes for ampicillin and tetracycline resistance. The vector is digested with restriction enzyme and dephosphorylated. The PCR amplified sequences are then ligated into the vector. The vector will preferably include sequences which encode for an antibiotic resistance gene, a trp promoter, a polyhis leader (including the first six STII codons, polyhis sequence, and enterokinase cleavage site), the PRO coding region, lambda transcriptional terminator, and an argU gene.

The ligation mixture is then used to transform a selected *E. coli* strain using the methods described in Sambrook et al., supra. Transformants are identified by their ability to grow on LB plates and antibiotic resistant colonies are then selected. Plasmid DNA can be isolated and confirmed by restriction analysis and DNA sequencing.

Selected clones can be grown overnight in liquid culture medium such as LB broth supplemented with antibiotics. The overnight culture may subsequently be used to inoculate a larger scale culture. The cells are then grown to a desired optical density, during which the expression promoter is turned on.

After culturing the cells for several more hours, the cells can be harvested by centrifugation. The cell pellet obtained by the centrifugation can be solubilized using various agents known in the art, and the solubilized PRO protein can then be purified using a metal chelating column under conditions that allow tight binding of the protein.

PRO may be expressed in *E. coli* in a poly-His tagged form, using the following procedure. The DNA encoding PRO is initially amplified using selected PCR primers. The primers will contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector, and other useful sequences providing for efficient and reliable translation initiation, rapid purification on a metal chelation column, and proteolytic removal with enterokinase. The PCR-amplified, poly-His tagged sequences are then ligated into an expression vector, which is used to transform an *E. coli* host based on strain 52 (W3110 fuhA(tonA) lon galE rpoHts(htpRts) clpP(lacIq)). Transformants are first grown in LB containing 50 mg/ml carbenicillin at 30°C with shaking until an O.D.600 of 3-5 is reached. Cultures are then diluted 50-100 fold into CRAP media (prepared by mixing 3.57 g (NH₄)₂SO₄, 0.71 g sodium citrate•2H₂O, 1.07 g KCl, 5.36 g Difco yeast extract, 5.36 g Sheffield hycase SF in 500 mL water, as well as 110 mM MPOS, pH 7.3, 0.55% (w/v) glucose and 7 mM MgSO₄) and grown for approximately 20-30 hours at 30°C with shaking. Samples are removed to verify

expression by SDS-PAGE analysis, and the bulk culture is centrifuged to pellet the cells. Cell pellets are frozen until purification and refolding.

5 *E. coli* paste from 0.5 to 1 L fermentations (6-10 g pellets) is resuspended in 10 volumes (w/v) in 7 M guanidine, 20 mM Tris, pH 8 buffer. Solid sodium sulfite and sodium tetrathionate is added to make final concentrations of 0.1M and 0.02 M, respectively, and the solution is stirred overnight at 4°C. This step results in a denatured protein with all cysteine residues blocked by sulfitolization. The solution is centrifuged at 40,000 rpm in a Beckman Ultracentrifuge for 30 min. The supernatant is diluted with 3-5 volumes of metal chelate column buffer (6 M guanidine, 20 mM Tris, pH 7.4) and filtered through 0.22 micron filters to clarify. The clarified extract is loaded onto a 5 ml Qiagen Ni-NTA metal chelate column equilibrated in the metal chelate column buffer. The column is washed with additional buffer containing 50 mM imidazole (Calbiochem, Utrol
10 grade), pH 7.4. The protein is eluted with buffer containing 250 mM imidazole. Fractions containing the desired protein are pooled and stored at 4°C. Protein concentration is estimated by its absorbance at 280 nm using the calculated extinction coefficient based on its amino acid sequence.

The proteins are refolded by diluting the sample slowly into freshly prepared refolding buffer consisting of: 20 mM Tris, pH 8.6, 0.3 M NaCl, 2.5 M urea, 5 mM cysteine, 20 mM glycine and 1 mM EDTA. Refolding
15 volumes are chosen so that the final protein concentration is between 50 to 100 micrograms/ml. The refolding solution is stirred gently at 4°C for 12-36 hours. The refolding reaction is quenched by the addition of TFA to a final concentration of 0.4% (pH of approximately 3). Before further purification of the protein, the solution is filtered through a 0.22 micron filter and acetonitrile is added to 2-10% final concentration. The refolded protein is chromatographed on a Poros R1/H reversed phase column using a mobile buffer of 0.1% TFA with elution with a gradient of acetonitrile from 10 to 80%. Aliquots of fractions with A280 absorbance are analyzed
20 on SDS polyacrylamide gels and fractions containing homogeneous refolded protein are pooled. Generally, the properly refolded species of most proteins are eluted at the lowest concentrations of acetonitrile since those species are the most compact with their hydrophobic interiors shielded from interaction with the reversed phase resin. Aggregated species are usually eluted at higher acetonitrile concentrations. In addition to resolving misfolded
25 forms of proteins from the desired form, the reversed phase step also removes endotoxin from the samples.

Fractions containing the desired folded PRO polypeptide are pooled and the acetonitrile removed using a gentle stream of nitrogen directed at the solution. Proteins are formulated into 20 mM Hepes, pH 6.8 with 0.14 M sodium chloride and 4% mannitol by dialysis or by gel filtration using G25 Superfine (Pharmacia) resins equilibrated in the formulation buffer and sterile filtered.

30 Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

EXAMPLE 7: Expression of PRO in mammalian cells

This example illustrates preparation of a potentially glycosylated form of PRO by recombinant expression in mammalian cells.

35 The vector, pRK5 (see EP 307,247, published March 15, 1989), is employed as the expression vector. Optionally, the PRO DNA is ligated into pRK5 with selected restriction enzymes to allow insertion of the PRO DNA using ligation methods such as described in Sambrook et al., supra. The resulting vector is called pRK5-

PRO.

In one embodiment, the selected host cells may be 293 cells. Human 293 cells (ATCC CCL 1573) are grown to confluence in tissue culture plates in medium such as DMEM supplemented with fetal calf serum and optionally, nutrient components and/or antibiotics. About 10 μ g pRK5-PRO DNA is mixed with about 1 μ g DNA encoding the VA RNA gene [Thimmappaya et al., *Cell*, 31:543 (1982)] and dissolved in 500 μ l of 1 mM Tris-HCl, 0.1 mM EDTA, 0.227 M CaCl_2 . To this mixture is added, dropwise, 500 μ l of 50 mM HEPES (pH 7.35), 280 mM NaCl, 1.5 mM NaPO_4 , and a precipitate is allowed to form for 10 minutes at 25°C. The precipitate is suspended and added to the 293 cells and allowed to settle for about four hours at 37°C. The culture medium is aspirated off and 2 ml of 20% glycerol in PBS is added for 30 seconds. The 293 cells are then washed with serum free medium, fresh medium is added and the cells are incubated for about 5 days.

Approximately 24 hours after the transfections, the culture medium is removed and replaced with culture medium (alone) or culture medium containing 200 $\mu\text{Ci/ml}$ ^{35}S -cysteine and 200 $\mu\text{Ci/ml}$ ^{35}S -methionine. After a 12 hour incubation, the conditioned medium is collected, concentrated on a spin filter, and loaded onto a 15% SDS gel. The processed gel may be dried and exposed to film for a selected period of time to reveal the presence of PRO polypeptide. The cultures containing transfected cells may undergo further incubation (in serum free medium) and the medium is tested in selected bioassays.

In an alternative technique, PRO may be introduced into 293 cells transiently using the dextran sulfate method described by Somparyrac et al., *Proc. Natl. Acad. Sci.*, 12:7575 (1981). 293 cells are grown to maximal density in a spinner flask and 700 μ g pRK5-PRO DNA is added. The cells are first concentrated from the spinner flask by centrifugation and washed with PBS. The DNA-dextran precipitate is incubated on the cell pellet for four hours. The cells are treated with 20% glycerol for 90 seconds, washed with tissue culture medium, and re-introduced into the spinner flask containing tissue culture medium, 5 $\mu\text{g/ml}$ bovine insulin and 0.1 $\mu\text{g/ml}$ bovine transferrin. After about four days, the conditioned media is centrifuged and filtered to remove cells and debris. The sample containing expressed PRO can then be concentrated and purified by any selected method, such as dialysis and/or column chromatography.

In another embodiment, PRO can be expressed in CHO cells. The pRK5-PRO can be transfected into CHO cells using known reagents such as CaPO_4 or DEAE-dextran. As described above, the cell cultures can be incubated, and the medium replaced with culture medium (alone) or medium containing a radiolabel such as ^{35}S -methionine. After determining the presence of PRO polypeptide, the culture medium may be replaced with serum free medium. Preferably, the cultures are incubated for about 6 days, and then the conditioned medium is harvested. The medium containing the expressed PRO can then be concentrated and purified by any selected method.

Epitope-tagged PRO may also be expressed in host CHO cells. The PRO may be subcloned out of the pRK5 vector. The subclone insert can undergo PCR to fuse in frame with a selected epitope tag such as a poly-his tag into a Baculovirus expression vector. The poly-his tagged PRO insert can then be subcloned into a SV40 driven vector containing a selection marker such as DHFR for selection of stable clones. Finally, the CHO cells can be transfected (as described above) with the SV40 driven vector. Labeling may be performed, as described above, to verify expression. The culture medium containing the expressed poly-His tagged PRO can then be

concentrated and purified by any selected method, such as by Ni^{2+} -chelate affinity chromatography.

PRO may also be expressed in CHO and/or COS cells by a transient expression procedure or in CHO cells by another stable expression procedure.

Stable expression in CHO cells is performed using the following procedure. The proteins are expressed as an IgG construct (immunoadhesin), in which the coding sequences for the soluble forms (e.g. extracellular domains) of the respective proteins are fused to an IgG1 constant region sequence containing the hinge, CH2 and CH2 domains and/or is a poly-His tagged form.

Following PCR amplification, the respective DNAs are subcloned in a CHO expression vector using standard techniques as described in Ausubel et al., Current Protocols of Molecular Biology, Unit 3.16, John Wiley and Sons (1997). CHO expression vectors are constructed to have compatible restriction sites 5' and 3' of the DNA of interest to allow the convenient shuttling of cDNA's. The vector used expression in CHO cells is as described in Lucas et al., Nucl. Acids Res. 24:9 (1774-1779 (1996), and uses the SV40 early promoter/enhancer to drive expression of the cDNA of interest and dihydrofolate reductase (DHFR). DHFR expression permits selection for stable maintenance of the plasmid following transfection.

Twelve micrograms of the desired plasmid DNA is introduced into approximately 10 million CHO cells using commercially available transfection reagents Superfect[®] (Qiagen), Dosper[®] or Fugene[®] (Boehringer Mannheim). The cells are grown as described in Lucas et al., supra. Approximately 3×10^7 cells are frozen in an ampule for further growth and production as described below.

The ampules containing the plasmid DNA are thawed by placement into water bath and mixed by vortexing. The contents are pipetted into a centrifuge tube containing 10 mLs of media and centrifuged at 1000 rpm for 5 minutes. The supernatant is aspirated and the cells are resuspended in 10 mL of selective media (0.2 μm filtered PS20 with 5% 0.2 μm diafiltered fetal bovine serum). The cells are then aliquoted into a 100 mL spinner containing 90 mL of selective media. After 1-2 days, the cells are transferred into a 250 mL spinner filled with 150 mL selective growth medium and incubated at 37°C. After another 2-3 days; 250 mL, 500 mL and 2000 mL spinners are seeded with 3×10^5 cells/mL. The cell media is exchanged with fresh media by centrifugation and resuspension in production medium. Although any suitable CHO media may be employed, a production medium described in U.S. Patent No. 5,122,469, issued June 16, 1992 may actually be used. A 3L production spinner is seeded at 1.2×10^6 cells/mL. On day 0, the cell number pH is determined. On day 1, the spinner is sampled and sparging with filtered air is commenced. On day 2, the spinner is sampled, the temperature shifted to 33°C, and 30 mL of 500 g/L glucose and 0.6 mL of 10% antifoam (e.g., 35% polydimethylsiloxane emulsion, Dow Corning 365 Medical Grade Emulsion) taken. Throughout the production, the pH is adjusted as necessary to keep it at around 7.2. After 10 days, or until the viability dropped below 70%, the cell culture is harvested by centrifugation and filtering through a 0.22 μm filter. The filtrate was either stored at 4°C or immediately loaded onto columns for purification.

For the poly-His tagged constructs, the proteins are purified using a Ni-NTA column (Qiagen). Before purification, imidazole is added to the conditioned media to a concentration of 5 mM. The conditioned media is pumped onto a 6 ml Ni-NTA column equilibrated in 20 mM Hepes, pH 7.4, buffer containing 0.3 M NaCl and 5 mM imidazole at a flow rate of 4-5 mL/min. at 4°C. After loading, the column is washed with additional

equilibration buffer and the protein eluted with equilibration buffer containing 0.25 M imidazole. The highly purified protein is subsequently desalted into a storage buffer containing 10 mM Hepes, 0.14 M NaCl and 4% mannitol, pH 6.8, with a 25 ml G25 Superfine (Pharmacia) column and stored at -80°C.

Immunoadhesin (Fc-containing) constructs are purified from the conditioned media as follows. The conditioned medium is pumped onto a 5 ml Protein A column (Pharmacia) which had been equilibrated in 20 mM Na phosphate buffer, pH 6.8. After loading, the column is washed extensively with equilibration buffer before elution with 100 mM citric acid, pH 3.5. The eluted protein is immediately neutralized by collecting 1 ml fractions into tubes containing 275 μ L of 1 M Tris buffer, pH 9. The highly purified protein is subsequently desalted into storage buffer as described above for the poly-His tagged proteins. The homogeneity is assessed by SDS polyacrylamide gels and by N-terminal amino acid sequencing by Edman degradation.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

EXAMPLE 8: Expression of PRO in Yeast

The following method describes recombinant expression of PRO in yeast.

First, yeast expression vectors are constructed for intracellular production or secretion of PRO from the ADH2/GAPDH promoter. DNA encoding PRO and the promoter is inserted into suitable restriction enzyme sites in the selected plasmid to direct intracellular expression of PRO. For secretion, DNA encoding PRO can be cloned into the selected plasmid, together with DNA encoding the ADH2/GAPDH promoter, a native PRO signal peptide or other mammalian signal peptide, or, for example, a yeast alpha-factor or invertase secretory signal/leader sequence, and linker sequences (if needed) for expression of PRO.

Yeast cells, such as yeast strain AB110, can then be transformed with the expression plasmids described above and cultured in selected fermentation media. The transformed yeast supernatants can be analyzed by precipitation with 10% trichloroacetic acid and separation by SDS-PAGE, followed by staining of the gels with Coomassie Blue stain.

Recombinant PRO can subsequently be isolated and purified by removing the yeast cells from the fermentation medium by centrifugation and then concentrating the medium using selected cartridge filters. The concentrate containing PRO may further be purified using selected column chromatography resins.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

EXAMPLE 9: Expression of PRO in Baculovirus-Infected Insect Cells

The following method describes recombinant expression of PRO in Baculovirus-infected insect cells.

The sequence coding for PRO is fused upstream of an epitope tag contained within a baculovirus expression vector. Such epitope tags include poly-his tags and immunoglobulin tags (like Fc regions of IgG). A variety of plasmids may be employed, including plasmids derived from commercially available plasmids such as pVL1393 (Novagen). Briefly, the sequence encoding PRO or the desired portion of the coding sequence of PRO such as the sequence encoding the extracellular domain of a transmembrane protein or the sequence encoding the mature protein if the protein is extracellular is amplified by PCR with primers complementary to the 5' and 3' regions. The 5' primer may incorporate flanking (selected) restriction enzyme sites. The product is then

digested with those selected restriction enzymes and subcloned into the expression vector.

Recombinant baculovirus is generated by co-transfecting the above plasmid and BaculoGold™ virus DNA (Pharmingen) into *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711) using lipofectin (commercially available from GIBCO-BRL). After 4 - 5 days of incubation at 28°C, the released viruses are harvested and used for further amplifications. Viral infection and protein expression are performed as described by O'Reilley et al.,

5 Baculovirus expression vectors: A Laboratory Manual, Oxford: Oxford University Press (1994).

Expressed poly-his tagged PRO can then be purified, for example, by Ni²⁺-chelate affinity chromatography as follows. Extracts are prepared from recombinant virus-infected Sf9 cells as described by Rupert et al., Nature, 362:175-179 (1993). Briefly, Sf9 cells are washed, resuspended in sonication buffer (25 mL Hepes, pH 7.9; 12.5 mM MgCl₂; 0.1 mM EDTA; 10% glycerol; 0.1% NP-40; 0.4 M KCl), and sonicated
10 twice for 20 seconds on ice. The sonicates are cleared by centrifugation, and the supernatant is diluted 50-fold in loading buffer (50 mM phosphate, 300 mM NaCl, 10% glycerol, pH 7.8) and filtered through a 0.45 µm filter. A Ni²⁺-NTA agarose column (commercially available from Qiagen) is prepared with a bed volume of 5 mL, washed with 25 mL of water and equilibrated with 25 mL of loading buffer. The filtered cell extract is loaded onto the column at 0.5 mL per minute. The column is washed to baseline A₂₈₀ with loading buffer, at which point
15 fraction collection is started. Next, the column is washed with a secondary wash buffer (50 mM phosphate; 300 mM NaCl, 10% glycerol, pH 6.0), which elutes nonspecifically bound protein. After reaching A₂₈₀ baseline again, the column is developed with a 0 to 500 mM Imidazole gradient in the secondary wash buffer. One mL fractions are collected and analyzed by SDS-PAGE and silver staining or Western blot with Ni²⁺-NTA-conjugated to alkaline phosphatase (Qiagen). Fractions containing the eluted His₁₀-tagged PRO are pooled and dialyzed
20 against loading buffer.

Alternatively, purification of the IgG tagged (or Fc tagged) PRO can be performed using known chromatography techniques, including for instance, Protein A or protein G column chromatography.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

25 EXAMPLE 10: Preparation of Antibodies that Bind PRO

This example illustrates preparation of monoclonal antibodies which can specifically bind PRO.

Techniques for producing the monoclonal antibodies are known in the art and are described, for instance, in Goding, supra. Immunogens that may be employed include purified PRO, fusion proteins containing PRO, and cells expressing recombinant PRO on the cell surface. Selection of the immunogen can be made by the skilled
30 artisan without undue experimentation.

Mice, such as Balb/c, are immunized with the PRO immunogen emulsified in complete Freund's adjuvant and injected subcutaneously or intraperitoneally in an amount from 1-100 micrograms. Alternatively, the immunogen is emulsified in MPL-TDM adjuvant (Ribi Immunochemical Research, Hamilton, MT) and injected into the animal's hind foot pads. The immunized mice are then boosted 10 to 12 days later with additional
35 immunogen emulsified in the selected adjuvant. Thereafter, for several weeks, the mice may also be boosted with additional immunization injections. Serum samples may be periodically obtained from the mice by retro-orbital bleeding for testing in ELISA assays to detect anti-PRO antibodies.

After a suitable antibody titer has been detected, the animals "positive" for antibodies can be injected with a final intravenous injection of PRO. Three to four days later, the mice are sacrificed and the spleen cells are harvested. The spleen cells are then fused (using 35% polyethylene glycol) to a selected murine myeloma cell line such as P3X63AgU.1, available from ATCC, No. CRL 1597. The fusions generate hybridoma cells which can then be plated in 96 well tissue culture plates containing HAT (hypoxanthine, aminopterin, and thymidine) medium to inhibit proliferation of non-fused cells, myeloma hybrids, and spleen cell hybrids.

The hybridoma cells will be screened in an ELISA for reactivity against PRO. Determination of "positive" hybridoma cells secreting the desired monoclonal antibodies against PRO is within the skill in the art.

The positive hybridoma cells can be injected intraperitoneally into syngeneic Balb/c mice to produce ascites containing the anti-PRO monoclonal antibodies. Alternatively, the hybridoma cells can be grown in tissue culture flasks or roller bottles. Purification of the monoclonal antibodies produced in the ascites can be accomplished using ammonium sulfate precipitation, followed by gel exclusion chromatography. Alternatively, affinity chromatography based upon binding of antibody to protein A or protein G can be employed.

EXAMPLE 11: Purification of PRO Polypeptides Using Specific Antibodies

Native or recombinant PRO polypeptides may be purified by a variety of standard techniques in the art of protein purification. For example, pro-PRO polypeptide, mature PRO polypeptide, or pre-PRO polypeptide is purified by immunoaffinity chromatography using antibodies specific for the PRO polypeptide of interest. In general, an immunoaffinity column is constructed by covalently coupling the anti-PRO polypeptide antibody to an activated chromatographic resin.

Polyclonal immunoglobulins are prepared from immune sera either by precipitation with ammonium sulfate or by purification on immobilized Protein A (Pharmacia LKB Biotechnology, Piscataway, N.J.). Likewise, monoclonal antibodies are prepared from mouse ascites fluid by ammonium sulfate precipitation or chromatography on immobilized Protein A. Partially purified immunoglobulin is covalently attached to a chromatographic resin such as CnBr-activated SEPHAROSE™ (Pharmacia LKB Biotechnology). The antibody is coupled to the resin, the resin is blocked, and the derivative resin is washed according to the manufacturer's instructions.

Such an immunoaffinity column is utilized in the purification of PRO polypeptide by preparing a fraction from cells containing PRO polypeptide in a soluble form. This preparation is derived by solubilization of the whole cell or of a subcellular fraction obtained via differential centrifugation by the addition of detergent or by other methods well known in the art. Alternatively, soluble PRO polypeptide containing a signal sequence may be secreted in useful quantity into the medium in which the cells are grown.

A soluble PRO polypeptide-containing preparation is passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of PRO polypeptide (*e.g.*, high ionic strength buffers in the presence of detergent). Then, the column is eluted under conditions that disrupt antibody/PRO polypeptide binding (*e.g.*, a low pH buffer such as approximately pH 2-3, or a high concentration of a chaotrope such as urea or thiocyanate ion), and PRO polypeptide is collected.

EXAMPLE 12: Drug Screening

This invention is particularly useful for screening compounds by using PRO polypeptides or binding fragment thereof in any of a variety of drug screening techniques. The PRO polypeptide or fragment employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the PRO polypeptide or fragment. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between PRO polypeptide or a fragment and the agent being tested. Alternatively, one can examine the diminution in complex formation between the PRO polypeptide and its target cell or target receptors caused by the agent being tested.

Thus, the present invention provides methods of screening for drugs or any other agents which can affect a PRO polypeptide-associated disease or disorder. These methods comprise contacting such an agent with an PRO polypeptide or fragment thereof and assaying (i) for the presence of a complex between the agent and the PRO polypeptide or fragment, or (ii) for the presence of a complex between the PRO polypeptide or fragment and the cell, by methods well known in the art. In such competitive binding assays, the PRO polypeptide or fragment is typically labeled. After suitable incubation, free PRO polypeptide or fragment is separated from that present in bound form, and the amount of free or uncomplexed label is a measure of the ability of the particular agent to bind to PRO polypeptide or to interfere with the PRO polypeptide/cell complex.

Another technique for drug screening provides high throughput screening for compounds having suitable binding affinity to a polypeptide and is described in detail in WO 84/03564, published on September 13, 1984. Briefly stated, large numbers of different small peptide test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. As applied to a PRO polypeptide, the peptide test compounds are reacted with PRO polypeptide and washed. Bound PRO polypeptide is detected by methods well known in the art. Purified PRO polypeptide can also be coated directly onto plates for use in the aforementioned drug screening techniques. In addition, non-neutralizing antibodies can be used to capture the peptide and immobilize it on the solid support.

This invention also contemplates the use of competitive drug screening assays in which neutralizing antibodies capable of binding PRO polypeptide specifically compete with a test compound for binding to PRO polypeptide or fragments thereof. In this manner, the antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with PRO polypeptide.

EXAMPLE 13: Rational Drug Design

The goal of rational drug design is to produce structural analogs of biologically active polypeptide of interest (*i.e.*, a PRO polypeptide) or of small molecules with which they interact, *e.g.*, agonists, antagonists, or inhibitors. Any of these examples can be used to fashion drugs which are more active or stable forms of the PRO polypeptide or which enhance or interfere with the function of the PRO polypeptide *in vivo* (*c.f.*, Hodgson, Bio/Technology, 9: 19-21 (1991)).

In one approach, the three-dimensional structure of the PRO polypeptide, or of an PRO

polypeptide-inhibitor complex, is determined by x-ray crystallography, by computer modeling or, most typically, by a combination of the two approaches. Both the shape and charges of the PRO polypeptide must be ascertained to elucidate the structure and to determine active site(s) of the molecule. Less often, useful information regarding the structure of the PRO polypeptide may be gained by modeling based on the structure of homologous proteins. In both cases, relevant structural information is used to design analogous PRO polypeptide-like molecules or to identify efficient inhibitors. Useful examples of rational drug design may include molecules which have improved activity or stability as shown by Braxton and Wells, *Biochemistry*, 31:7796-7801 (1992) or which act as inhibitors, agonists, or antagonists of native peptides as shown by Athauda *et al.*, *J. Biochem.*, 113:742-746 (1993).

It is also possible to isolate a target-specific antibody, selected by functional assay, as described above, and then to solve its crystal structure. This approach, in principle, yields a pharmacore upon which subsequent drug design can be based. It is possible to bypass protein crystallography altogether by generating anti-idiotypic antibodies (anti-ids) to a functional, pharmacologically active antibody. As a mirror image of a mirror image, the binding site of the anti-ids would be expected to be an analog of the original receptor. The anti-id could then be used to identify and isolate peptides from banks of chemically or biologically produced peptides. The isolated peptides would then act as the pharmacore.

By virtue of the present invention, sufficient amounts of the PRO polypeptide may be made available to perform such analytical studies as X-ray crystallography. In addition, knowledge of the PRO polypeptide amino acid sequence provided herein will provide guidance to those employing computer modeling techniques in place of or in addition to x-ray crystallography.

EXAMPLE 14: Identification of PRO Polypeptides That Stimulate TNF- α Release In Human Blood (Assay 128)

This assay shows that certain PRO polypeptides of the present invention act to stimulate the release of TNF- α in human blood. PRO polypeptides testing positive in this assay are useful for, among other things, research purposes where stimulation of the release of TNF- α would be desired and for the therapeutic treatment of conditions wherein enhanced TNF- α release would be beneficial. Specifically, 200 μ l of human blood supplemented with 50mM Hepes buffer (pH 7.2) is aliquoted per well in a 96 well test plate. To each well is then added 300 μ l of either the test PRO polypeptide in 50 mM Hepes buffer (at various concentrations) or 50 mM Hepes buffer alone (negative control) and the plates are incubated at 37°C for 6 hours. The samples are then centrifuged and 50 μ l of plasma is collected from each well and tested for the presence of TNF- α by ELISA assay. A positive in the assay is a higher amount of TNF- α in the PRO polypeptide treated samples as compared to the negative control samples.

The following PRO polypeptides tested positive in this assay:

PRO1079, PRO827, PRO791, PRO1131, PRO1316, PRO1183, PRO1343, PRO1760, PRO1567, and PRO4333.

EXAMPLE 15: Promotion of Chondrocyte Redifferentiation (Assay 129)

This assay is designed to determine whether PRO polypeptides of the present invention show the ability to induce the proliferation and/or redifferentiation of chondrocytes in culture. PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of various bone and/or cartilage

disorders such as, for example, sports injuries and arthritis.

Porcine chondrocytes are isolated by overnight collagenase digestion of articular cartilage of the metacarpophalangeal joint of 4-6 month old female pigs. The isolated cells are then seeded at 25,000 cells/cm² in Ham F-12 containing 10% FBS and 4 µg/ml gentamycin. The culture media is changed every third day. On day 12, the cells are seeded in 96 well plates at 5,000 cells/well in 100µl of the same media without serum and 100 µl of either serum-free medium (negative control), staurosporin (final concentration of 5 nM; positive control) or the test PRO polypeptide are added to give a final volume of 200 µl/well. After 5 days at 37°C, 22 µl of media containing 100µg/ml Hoechst 33342 and 50 µg/ml 5-CFDA is added to each well and incubated for an additional 10 minutes at 37°C. A picture of the green fluorescence is taken for each well and the differentiation state of the chondrocytes is calculated by morphometric analysis. A positive result in the assay is obtained when the >50% of the PRO polypeptide treated cells are differentiated (compared to the background obtained by the negative control).

PRO6029 polypeptide tested positive in this assay.

EXAMPLE 16: Microarray Analysis to Detect Overexpression of PRO Polypeptides in Cancerous Tumors

Nucleic acid microarrays, often containing thousands of gene sequences, are useful for identifying differentially expressed genes in diseased tissues as compared to their normal counterparts. Using nucleic acid microarrays, test and control mRNA samples from test and control tissue samples are reverse transcribed and labeled to generate cDNA probes. The cDNA probes are then hybridized to an array of nucleic acids immobilized on a solid support. The array is configured such that the sequence and position of each member of the array is known. For example, a selection of genes known to be expressed in certain disease states may be arrayed on a solid support. Hybridization of a labeled probe with a particular array member indicates that the sample from which the probe was derived expresses that gene. If the hybridization signal of a probe from a test (disease tissue) sample is greater than hybridization signal of a probe from a control (normal tissue) sample, the gene or genes overexpressed in the disease tissue are identified. The implication of this result is that an overexpressed protein in a diseased tissue is useful not only as a diagnostic marker for the presence of the disease condition, but also as a therapeutic target for treatment of the disease condition.

The methodology of hybridization of nucleic acids and microarray technology is well known in the art. In the present example, the specific preparation of nucleic acids for hybridization and probes, slides, and hybridization conditions are all detailed in U.S. Provisional Patent Application Serial No. 60/193,767, filed on March 31, 2000 and which is herein incorporated by reference.

In the present example, cancerous tumors derived from various human tissues were studied for PRO polypeptide-encoding gene expression relative to non-cancerous human tissue in an attempt to identify those PRO polypeptides which are overexpressed in cancerous tumors. Two sets of experimental data were generated. In one set, cancerous human colon tumor tissue and matched non-cancerous human colon tumor tissue from the same patient ("matched colon control") were obtained and analyzed for PRO polypeptide expression using the above described microarray technology. In the second set of data, cancerous human tumor tissue from any of a variety of different human tumors was obtained and compared to a "universal" epithelial control sample which was

prepared by pooling non-cancerous human tissues of epithelial origin, including liver, kidney, and lung. mRNA isolated from the pooled tissues represents a mixture of expressed gene products from these different tissues. Microarray hybridization experiments using the pooled control samples generated a linear plot in a 2-color analysis. The slope of the line generated in a 2-color analysis was then used to normalize the ratios of (test:control detection) within each experiment. The normalized ratios from various experiments were then compared and used to identify clustering of gene expression. Thus, the pooled "universal control" sample not only allowed effective relative gene expression determinations in a simple 2-sample comparison, it also allowed multi-sample comparisons across several experiments.

In the present experiments, nucleic acid probes derived from the herein described PRO polypeptide-encoding nucleic acid sequences were used in the creation of the microarray and RNA from the tumor tissues listed above were used for the hybridization thereto. A value based upon the normalized ratio:experimental ratio was designated as a "cutoff ratio". Only values that were above this cutoff ratio were determined to be significant. Table 8 below shows the results of these experiments, demonstrating that various PRO polypeptides of the present invention are significantly overexpressed in various human tumor tissues as compared to a non-cancerous human tissue control. As described above, these data demonstrate that the PRO polypeptides of the present invention are useful not only as diagnostic markers for the presence of one or more cancerous tumors, but also serve as therapeutic targets for the treatment of those tumors.

Table 8

<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
PRO276	lung tumor	universal normal control
PRO284	colon tumor	universal normal control
PRO284	lung tumor	universal normal control
PRO284	breast tumor	universal normal control
PRO193	colon tumor	universal normal control
PRO193	lung tumor	universal normal control
PRO193	breast tumor	universal normal control
PRO193	prostate tumor	universal normal control
PRO190	colon tumor	universal normal control
PRO190	lung tumor	universal normal control
PRO190	breast tumor	universal normal control
PRO180	colon tumor	universal normal control
PRO180	lung tumor	universal normal control
PRO180	breast tumor	universal normal control
PRO194	colon tumor	universal normal control
PRO194	lung tumor	universal normal control
PRO194	breast tumor	universal normal control
PRO194	cervical tumor	universal normal control
PRO218	colon tumor	universal normal control
PRO218	lung tumor	universal normal control
PRO260	colon tumor	universal normal control
PRO260	lung tumor	universal normal control
PRO260	breast tumor	universal normal control
PRO260	rectal tumor	universal normal control
PRO233	colon tumor	universal normal control
PRO233	lung tumor	universal normal control
PRO233	breast tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO234	colon tumor	universal normal control
	PRO234	lung tumor	universal normal control
	PRO234	breast tumor	universal normal control
5	PRO234	liver tumor	universal normal control
	PRO236	colon tumor	universal normal control
	PRO236	lung tumor	universal normal control
	PRO236	breast tumor	universal normal control
	PRO244	colon tumor	universal normal control
10	PRO244	lung tumor	universal normal control
	PRO262	colon tumor	universal normal control
	PRO262	lung tumor	universal normal control
	PRO262	breast tumor	universal normal control
	PRO271	colon tumor	universal normal control
15	PRO271	lung tumor	universal normal control
	PRO268	colon tumor	universal normal control
	PRO268	lung tumor	universal normal control
	PRO268	breast tumor	universal normal control
	PRO270	colon tumor	universal normal control
20	PRO270	lung tumor	universal normal control
	PRO270	breast tumor	universal normal control
	PRO270	liver tumor	universal normal control
	PRO355	lung tumor	universal normal control
	PRO355	breast tumor	universal normal control
25	PRO355	prostate tumor	universal normal control
	PRO298	colon tumor	universal normal control
	PRO298	lung tumor	universal normal control
	PRO298	breast tumor	universal normal control
	PRO299	colon tumor	universal normal control
30	PRO299	lung tumor	universal normal control
	PRO299	breast tumor	universal normal control
	PRO296	colon tumor	universal normal control
	PRO296	breast tumor	universal normal control
	PRO329	colon tumor	universal normal control
35	PRO329	lung tumor	universal normal control
	PRO329	breast tumor	universal normal control
	PRO330	colon tumor	universal normal control
	PRO330	lung tumor	universal normal control
	PRO294	lung tumor	universal normal control
40	PRO294	breast tumor	universal normal control
	PRO300	colon tumor	universal normal control
	PRO300	lung tumor	universal normal control
	PRO300	breast tumor	universal normal control
	PRO307	lung tumor	universal normal control
45	PRO334	colon tumor	universal normal control
	PRO334	lung tumor	universal normal control
	PRO334	breast tumor	universal normal control
	PRO334	prostate tumor	universal normal control
	PRO352	colon tumor	universal normal control
50	PRO352	lung tumor	universal normal control
	PRO352	breast tumor	universal normal control
	PRO352	liver tumor	universal normal control
	PRO710	breast tumor	universal normal control
	PRO873	colon tumor	universal normal control
55	PRO873	lung tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO873	breast tumor	universal normal control
	PRO873	prostate tumor	universal normal control
	PRO354	colon tumor	universal normal control
5	PRO354	lung tumor	universal normal control
	PRO354	breast tumor	universal normal control
	PRO1151	lung tumor	universal normal control
	PRO1151	breast tumor	universal normal control
	PRO382	colon tumor	universal normal control
10	PRO382	lung tumor	universal normal control
	PRO382	breast tumor	universal normal control
	PRO1864	lung tumor	universal normal control
	PRO1864	breast tumor	universal normal control
	PRO1864	liver tumor	universal normal control
15	PRO386	colon tumor	universal normal control
	PRO386	lung tumor	universal normal control
	PRO386	prostate tumor	universal normal control
	PRO541	colon tumor	universal normal control
	PRO541	lung tumor	universal normal control
20	PRO541	breast tumor	universal normal control
	PRO852	breast tumor	universal normal control
	PRO700	colon tumor	universal normal control
	PRO700	lung tumor	universal normal control
	PRO700	breast tumor	universal normal control
25	PRO700	rectal tumor	universal normal control
	PRO708	colon tumor	universal normal control
	PRO708	lung tumor	universal normal control
	PRO708	breast tumor	universal normal control
	PRO707	colon tumor	universal normal control
30	PRO707	lung tumor	universal normal control
	PRO864	colon tumor	universal normal control
	PRO864	lung tumor	universal normal control
	PRO864	breast tumor	universal normal control
	PRO706	colon tumor	universal normal control
35	PRO706	lung tumor	universal normal control
	PRO706	breast tumor	universal normal control
	PRO706	liver tumor	universal normal control
	PRO732	lung tumor	universal normal control
	PRO732	breast tumor	universal normal control
40	PRO732	cervical tumor	universal normal control
	PRO537	colon tumor	universal normal control
	PRO537	lung tumor	universal normal control
	PRO537	breast tumor	universal normal control
	PRO545	lung tumor	universal normal control
45	PRO545	breast tumor	universal normal control
	PRO718	lung tumor	universal normal control
	PRO718	breast tumor	universal normal control
	PRO872	lung tumor	universal normal control
	PRO872	breast tumor	universal normal control
50	PRO872	liver tumor	universal normal control
	PRO704	colon tumor	universal normal control
	PRO704	lung tumor	universal normal control
	PRO704	breast tumor	universal normal control
	PRO705	lung tumor	universal normal control
55	PRO705	breast tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO871	lung tumor	universal normal control
	PRO871	breast tumor	universal normal control
	PRO871	liver tumor	universal normal control
5	PRO702	lung tumor	universal normal control
	PRO944	colon tumor	universal normal control
	PRO944	lung tumor	universal normal control
	PRO944	rectal tumor	universal normal control
	PRO739	lung tumor	universal normal control
10	PRO739	breast tumor	universal normal control
	PRO739	prostate tumor	universal normal control
	PRO941	colon tumor	universal normal control
	PRO941	lung tumor	universal normal control
	PRO941	breast tumor	universal normal control
15	PRO941	rectal tumor	universal normal control
	PRO1082	lung tumor	universal normal control
	PRO1082	breast tumor	universal normal control
	PRO1133	colon tumor	universal normal control
	PRO1133	lung tumor	universal normal control
20	PRO983	colon tumor	universal normal control
	PRO983	lung tumor	universal normal control
	PRO983	breast tumor	universal normal control
	PRO784	colon tumor	universal normal control
	PRO784	lung tumor	universal normal control
25	PRO784	breast tumor	universal normal control
	PRO784	prostate tumor	universal normal control
	PRO783	colon tumor	universal normal control
	PRO783	lung tumor	universal normal control
	PRO783	breast tumor	universal normal control
30	PRO783	liver tumor	universal normal control
	PRO940	colon tumor	universal normal control
	PRO940	lung tumor	universal normal control
	PRO940	breast tumor	universal normal control
	PRO768	colon tumor	universal normal control
35	PRO768	lung tumor	universal normal control
	PRO768	breast tumor	universal normal control
	PRO1079	colon tumor	universal normal control
	PRO1079	lung tumor	universal normal control
	PRO1079	breast tumor	universal normal control
40	PRO1079	rectal tumor	universal normal control
	PRO1078	colon tumor	universal normal control
	PRO1078	lung tumor	universal normal control
	PRO1018	colon tumor	universal normal control
	PRO1018	lung tumor	universal normal control
45	PRO1018	breast tumor	universal normal control
	PRO793	colon tumor	universal normal control
	PRO793	lung tumor	universal normal control
	PRO793	breast tumor	universal normal control
	PRO793	rectal tumor	universal normal control
50	PRO1773	colon tumor	universal normal control
	PRO1773	lung tumor	universal normal control
	PRO1773	prostate tumor	universal normal control
	PRO1014	lung tumor	universal normal control
	PRO1014	breast tumor	universal normal control
55	PRO1013	colon tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO1013	lung tumor	universal normal control
	PRO1013	breast tumor	universal normal control
	PRO1013	liver tumor	universal normal control
5	PRO937	colon tumor	universal normal control
	PRO937	lung tumor	universal normal control
	PRO937	breast tumor	universal normal control
	PRO937	cervical tumor	universal normal control
	PRO937	rectal tumor	universal normal control
10	PRO1477	lung tumor	universal normal control
	PRO1477	breast tumor	universal normal control
	PRO1477	rectal tumor	universal normal control
	PRO842	colon tumor	universal normal control
	PRO842	lung tumor	universal normal control
15	PRO842	breast tumor	universal normal control
	PRO839	colon tumor	universal normal control
	PRO1180	colon tumor	universal normal control
	PRO1180	lung tumor	universal normal control
	PRO1180	liver tumor	universal normal control
20	PRO1134	lung tumor	universal normal control
	PRO1134	breast tumor	universal normal control
	PRO1134	prostate tumor	universal normal control
	PRO1115	colon tumor	universal normal control
	PRO1115	lung tumor	universal normal control
25	PRO1115	breast tumor	universal normal control
	PRO1277	colon tumor	universal normal control
	PRO1277	lung tumor	universal normal control
	PRO1135	lung tumor	universal normal control
	PRO1135	breast tumor	universal normal control
30	PRO1135	cervical tumor	universal normal control
	PRO827	colon tumor	universal normal control
	PRO827	lung tumor	universal normal control
	PRO827	prostate tumor	universal normal control
	PRO827	cervical tumor	universal normal control
35	PRO1057	lung tumor	universal normal control
	PRO1057	breast tumor	universal normal control
	PRO1113	colon tumor	universal normal control
	PRO1113	lung tumor	universal normal control
	PRO1006	colon tumor	universal normal control
40	PRO1006	lung tumor	universal normal control
	PRO1006	breast tumor	universal normal control
	PRO1006	rectal tumor	universal normal control
	PRO1074	lung tumor	universal normal control
	PRO1074	rectal tumor	universal normal control
45	PRO1073	lung tumor	universal normal control
	PRO1073	breast tumor	universal normal control
	PRO1136	colon tumor	universal normal control
	PRO1136	lung tumor	universal normal control
	PRO1136	breast tumor	universal normal control
50	PRO1004	lung tumor	universal normal control
	PRO1344	colon tumor	universal normal control
	PRO1344	lung tumor	universal normal control
	PRO1344	breast tumor	universal normal control
	PRO1344	rectal tumor	universal normal control
55	PRO1110	colon tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO1110	lung tumor	universal normal control
	PRO1110	breast tumor	universal normal control
	PRO1378	colon tumor	universal normal control
5	PRO1378	lung tumor	universal normal control
	PRO1378	prostate tumor	universal normal control
	PRO1378	cervical tumor	universal normal control
	PRO1481	colon tumor	universal normal control
	PRO1481	lung tumor	universal normal control
10	PRO1109	lung tumor	universal normal control
	PRO1109	breast tumor	universal normal control
	PRO1383	colon tumor	universal normal control
	PRO1383	lung tumor	universal normal control
	PRO1383	breast tumor	universal normal control
15	PRO1072	lung tumor	universal normal control
	PRO1189	colon tumor	universal normal control
	PRO1189	lung tumor	universal normal control
	PRO1189	breast tumor	universal normal control
	PRO1189	prostate tumor	universal normal control
20	PRO1003	colon tumor	universal normal control
	PRO1003	lung tumor	universal normal control
	PRO1003	breast tumor	universal normal control
	PRO1003	liver tumor	universal normal control
	PRO1003	rectal tumor	universal normal control
25	PRO1108	colon tumor	universal normal control
	PRO1108	lung tumor	universal normal control
	PRO1108	breast tumor	universal normal control
	PRO1137	colon tumor	universal normal control
	PRO1137	lung tumor	universal normal control
30	PRO1137	breast tumor	universal normal control
	PRO1138	colon tumor	universal normal control
	PRO1138	lung tumor	universal normal control
	PRO1138	breast tumor	universal normal control
	PRO1415	colon tumor	universal normal control
35	PRO1415	lung tumor	universal normal control
	PRO1415	prostate tumor	universal normal control
	PRO1054	lung tumor	universal normal control
	PRO1054	breast tumor	universal normal control
	PRO994	colon tumor	universal normal control
40	PRO994	lung tumor	universal normal control
	PRO994	rectal tumor	universal normal control
	PRO1069	lung tumor	universal normal control
	PRO1069	breast tumor	universal normal control
	PRO1411	colon tumor	universal normal control
45	PRO1411	lung tumor	universal normal control
	PRO1129	lung tumor	universal normal control
	PRO1129	rectal tumor	universal normal control
	PRO1359	colon tumor	universal normal control
	PRO1359	lung tumor	universal normal control
50	PRO1359	breast tumor	universal normal control
	PRO1359	prostate tumor	universal normal control
	PRO1139	lung tumor	universal normal control
	PRO1065	lung tumor	universal normal control
	PRO1028	colon tumor	universal normal control
55	PRO1028	lung tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO1028	breast tumor	universal normal control
	PRO1028	cervical tumor	universal normal control
	PRO1027	colon tumor	universal normal control
5	PRO1027	lung tumor	universal normal control
	PRO1027	breast tumor	universal normal control
	PRO1140	colon tumor	universal normal control
	PRO1140	breast tumor	universal normal control
	PRO1291	colon tumor	universal normal control
10	PRO1291	breast tumor	universal normal control
	PRO1105	colon tumor	universal normal control
	PRO1105	lung tumor	universal normal control
	PRO1026	lung tumor	universal normal control
	PRO1026	prostate tumor	universal normal control
15	PRO1104	colon tumor	universal normal control
	PRO1104	lung tumor	universal normal control
	PRO1104	breast tumor	universal normal control
	PRO1100	colon tumor	universal normal control
	PRO1100	lung tumor	universal normal control
20	PRO1100	breast tumor	universal normal control
	PRO1100	rectal tumor	universal normal control
	PRO1141	lung tumor	universal normal control
	PRO1772	colon tumor	universal normal control
	PRO1772	lung tumor	universal normal control
25	PRO1772	breast tumor	universal normal control
	PRO1772	cervical tumor	universal normal control
	PRO1064	colon tumor	universal normal control
	PRO1064	lung tumor	universal normal control
	PRO1379	colon tumor	universal normal control
30	PRO1379	lung tumor	universal normal control
	PRO1379	cervical tumor	universal normal control
	PRO3573	lung tumor	universal normal control
	PRO3573	breast tumor	universal normal control
	PRO3566	colon tumor	universal normal control
35	PRO3566	lung tumor	universal normal control
	PRO1156	lung tumor	universal normal control
	PRO1156	breast tumor	universal normal control
	PRO1156	prostate tumor	universal normal control
	PRO1098	colon tumor	universal normal control
40	PRO1098	lung tumor	universal normal control
	PRO1098	rectal tumor	universal normal control
	PRO1128	colon tumor	universal normal control
	PRO1128	lung tumor	universal normal control
	PRO1128	breast tumor	universal normal control
45	PRO1248	lung tumor	universal normal control
	PRO1248	breast tumor	universal normal control
	PRO1127	colon tumor	universal normal control
	PRO1127	lung tumor	universal normal control
	PRO1127	breast tumor	universal normal control
50	PRO1316	colon tumor	universal normal control
	PRO1316	lung tumor	universal normal control
	PRO1316	breast tumor	universal normal control
	PRO1197	colon tumor	universal normal control
	PRO1197	lung tumor	universal normal control
55	PRO1197	breast tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO1125	lung tumor	universal normal control
	PRO1158	breast tumor	universal normal control
	PRO1124	colon tumor	universal normal control
5	PRO1124	lung tumor	universal normal control
	PRO1380	colon tumor	universal normal control
	PRO1380	lung tumor	universal normal control
	PRO1380	breast tumor	universal normal control
	PRO1380	liver tumor	universal normal control
10	PRO1377	colon tumor	universal normal control
	PRO1377	lung tumor	universal normal control
	PRO1287	lung tumor	universal normal control
	PRO1287	breast tumor	universal normal control
	PRO1249	lung tumor	universal normal control
15	PRO1249	breast tumor	universal normal control
	PRO1335	colon tumor	universal normal control
	PRO1335	lung tumor	universal normal control
	PRO1335	breast tumor	universal normal control
	PRO3572	lung tumor	universal normal control
20	PRO1599	colon tumor	universal normal control
	PRO1599	lung tumor	universal normal control
	PRO1599	breast tumor	universal normal control
	PRO1374	lung tumor	universal normal control
	PRO1374	breast tumor	universal normal control
25	PRO1345	lung tumor	universal normal control
	PRO1345	breast tumor	universal normal control
	PRO1311	lung tumor	universal normal control
	PRO1311	breast tumor	universal normal control
	PRO1357	colon tumor	universal normal control
30	PRO1357	lung tumor	universal normal control
	PRO1557	colon tumor	universal normal control
	PRO1557	lung tumor	universal normal control
	PRO1557	breast tumor	universal normal control
	PRO1305	colon tumor	universal normal control
35	PRO1305	lung tumor	universal normal control
	PRO1305	breast tumor	universal normal control
	PRO1302	colon tumor	universal normal control
	PRO1302	lung tumor	universal normal control
	PRO1302	breast tumor	universal normal control
40	PRO1302	rectal tumor	universal normal control
	PRO1266	colon tumor	universal normal control
	PRO1336	colon tumor	universal normal control
	PRO1336	lung tumor	universal normal control
	PRO1336	breast tumor	universal normal control
45	PRO1278	colon tumor	universal normal control
	PRO1278	lung tumor	universal normal control
	PRO1270	breast tumor	universal normal control
	PRO1298	colon tumor	universal normal control
	PRO1298	lung tumor	universal normal control
50	PRO1301	lung tumor	universal normal control
	PRO1301	breast tumor	universal normal control
	PRO1268	colon tumor	universal normal control
	PRO1268	breast tumor	universal normal control
	PRO1327	lung tumor	universal normal control
55	PRO1327	breast tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO1328	colon tumor	universal normal control
	PRO1328	lung tumor	universal normal control
	PRO1328	breast tumor	universal normal control
5	PRO1329	colon tumor	universal normal control
	PRO1329	lung tumor	universal normal control
	PRO1329	breast tumor	universal normal control
	PRO1339	colon tumor	universal normal control
	PRO1339	lung tumor	universal normal control
10	PRO1342	colon tumor	universal normal control
	PRO1342	lung tumor	universal normal control
	PRO1342	breast tumor	universal normal control
	PRO1342	rectal tumor	universal normal control
	PRO1487	colon tumor	universal normal control
15	PRO1487	breast tumor	universal normal control
	PRO3579	lung tumor	universal normal control
	PRO3579	breast tumor	universal normal control
	PRO1472	colon tumor	universal normal control
	PRO1472	lung tumor	universal normal control
20	PRO1385	lung tumor	universal normal control
	PRO1385	breast tumor	universal normal control
	PRO1461	colon tumor	universal normal control
	PRO1461	lung tumor	universal normal control
	PRO1461	breast tumor	universal normal control
25	PRO1429	colon tumor	universal normal control
	PRO1429	lung tumor	universal normal control
	PRO1429	breast tumor	universal normal control
	PRO1568	lung tumor	universal normal control
	PRO1568	breast tumor	universal normal control
30	PRO1569	colon tumor	universal normal control
	PRO1569	lung tumor	universal normal control
	PRO1569	breast tumor	universal normal control
	PRO1753	colon tumor	universal normal control
	PRO1753	lung tumor	universal normal control
35	PRO1570	colon tumor	universal normal control
	PRO1570	lung tumor	universal normal control
	PRO1570	breast tumor	universal normal control
	PRO1570	prostate tumor	universal normal control
	PRO1570	rectal tumor	universal normal control
40	PRO1559	colon tumor	universal normal control
	PRO1559	lung tumor	universal normal control
	PRO1559	breast tumor	universal normal control
	PRO1486	lung tumor	universal normal control
	PRO1486	breast tumor	universal normal control
45	PRO1433	colon tumor	universal normal control
	PRO1433	lung tumor	universal normal control
	PRO1433	breast tumor	universal normal control
	PRO1433	rectal tumor	universal normal control
	PRO1490	lung tumor	universal normal control
50	PRO1490	breast tumor	universal normal control
	PRO1482	lung tumor	universal normal control
	PRO1482	breast tumor	universal normal control
	PRO1409	colon tumor	universal normal control
	PRO1409	lung tumor	universal normal control
55	PRO1409	breast tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO1446	colon tumor	universal normal control
	PRO1446	lung tumor	universal normal control
	PRO1446	breast tumor	universal normal control
5	PRO1446	prostate tumor	universal normal control
	PRO1604	colon tumor	universal normal control
	PRO1604	lung tumor	universal normal control
	PRO1604	breast tumor	universal normal control
	PRO1491	colon tumor	universal normal control
10	PRO1491	lung tumor	universal normal control
	PRO1491	breast tumor	universal normal control
	PRO1431	colon tumor	universal normal control
	PRO1431	lung tumor	universal normal control
	PRO1563	colon tumor	universal normal control
15	PRO1563	lung tumor	universal normal control
	PRO1563	breast tumor	universal normal control
	PRO1571	colon tumor	universal normal control
	PRO1571	lung tumor	universal normal control
	PRO1571	breast tumor	universal normal control
20	PRO1572	lung tumor	universal normal control
	PRO1572	prostate tumor	universal normal control
	PRO1573	lung tumor	universal normal control
	PRO1573	breast tumor	universal normal control
	PRO1508	lung tumor	universal normal control
25	PRO1508	breast tumor	universal normal control
	PRO1485	colon tumor	universal normal control
	PRO1485	lung tumor	universal normal control
	PRO1564	colon tumor	universal normal control
	PRO1564	lung tumor	universal normal control
30	PRO1564	breast tumor	universal normal control
	PRO1550	colon tumor	universal normal control
	PRO1550	lung tumor	universal normal control
	PRO1550	breast tumor	universal normal control
	PRO1757	lung tumor	universal normal control
35	PRO1757	breast tumor	universal normal control
	PRO1757	prostate tumor	universal normal control
	PRO1758	lung tumor	universal normal control
	PRO1781	colon tumor	universal normal control
	PRO1781	lung tumor	universal normal control
40	PRO1781	breast tumor	universal normal control
	PRO1606	lung tumor	universal normal control
	PRO1606	breast tumor	universal normal control
	PRO1784	colon tumor	universal normal control
	PRO1784	lung tumor	universal normal control
45	PRO1784	breast tumor	universal normal control
	PRO1774	colon tumor	universal normal control
	PRO1774	lung tumor	universal normal control
	PRO1774	breast tumor	universal normal control
	PRO1605	colon tumor	universal normal control
50	PRO1605	lung tumor	universal normal control
	PRO1605	prostate tumor	universal normal control
	PRO1928	colon tumor	universal normal control
	PRO1928	lung tumor	universal normal control
	PRO1928	cervical tumor	universal normal control
55	PRO1865	lung tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO1865	liver tumor	universal normal control
	PRO1925	lung tumor	universal normal control
	PRO1926	liver tumor	universal normal control
5	PRO2630	colon tumor	universal normal control
	PRO2630	lung tumor	universal normal control
	PRO2630	breast tumor	universal normal control
	PRO2630	liver tumor	universal normal control
	PRO3443	colon tumor	universal normal control
10	PRO3443	lung tumor	universal normal control
	PRO3443	breast tumor	universal normal control
	PRO3301	colon tumor	universal normal control
	PRO3301	lung tumor	universal normal control
	PRO3301	breast tumor	universal normal control
15	PRO3301	rectal tumor	universal normal control
	PRO3442	colon tumor	universal normal control
	PRO3442	lung tumor	universal normal control
	PRO3442	rectal tumor	universal normal control
	PRO4978	colon tumor	universal normal control
20	PRO4978	lung tumor	universal normal control
	PRO4978	breast tumor	universal normal control
	PRO4978	rectal tumor	universal normal control
	PRO5801	colon tumor	universal normal control
	PRO5801	breast tumor	universal normal control
25	PRO19630	colon tumor	universal normal control
	PRO203	colon tumor	universal normal control
	PRO204	colon tumor	universal normal control
	PRO204	lung tumor	universal normal control
	PRO204	breast tumor	universal normal control
30	PRO204	prostate tumor	universal normal control
	PRO210	colon tumor	universal normal control
	PRO210	lung tumor	universal normal control
	PRO223	lung tumor	universal normal control
	PRO223	breast tumor	universal normal control
35	PRO247	colon tumor	universal normal control
	PRO247	lung tumor	universal normal control
	PRO247	breast	universal normal control
	PRO358	lung tumor	universal normal control
	PRO358	breast tumor	universal normal control
40	PRO358	prostate tumor	universal normal control
	PRO724	lung tumor	universal normal control
	PRO868	colon tumor	universal normal control
	PRO868	lung tumor	universal normal control
	PRO868	prostate tumor	universal normal control
45	PRO868	rectal tumor	universal normal control
	PRO740	colon tumor	universal normal control
	PRO1478	colon tumor	universal normal control
	PRO1478	lung tumor	universal normal control
	PRO162	colon tumor	universal normal control
50	PRO162	lung tumor	universal normal control
	PRO162	breast tumor	universal normal control
	PRO828	colon tumor	universal normal control
	PRO828	lung tumor	universal normal control
	PRO828	breast tumor	universal normal control
55	PRO828	cervical tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO828	liver tumor	universal normal control
	PRO819	lung tumor	universal normal control
	PRO819	breast tumor	universal normal control
5	PRO819	rectal tumor	universal normal control
	PRO813	colon tumor	universal normal control
	PRO813	lung tumor	universal normal control
	PRO813	breast tumor	universal normal control
	PRO813	prostate tumor	universal normal control
10	PRO1194	colon tumor	universal normal control
	PRO1194	lung tumor	universal normal control
	PRO1194	breast tumor	universal normal control
	PRO887	colon tumor	universal normal control
	PRO887	lung tumor	universal normal control
15	PRO887	rectal tumor	universal normal control
	PRO1071	colon tumor	universal normal control
	PRO1071	lung tumor	universal normal control
	PRO1071	breast tumor	universal normal control
	PRO1029	colon tumor	universal normal control
20	PRO1029	lung tumor	universal normal control
	PRO1029	breast tumor	universal normal control
	PRO1190	lung tumor	universal normal control
	PRO1190	breast tumor	universal normal control
	PRO4334	lung tumor	universal normal control
25	PRO1155	colon tumor	universal normal control
	PRO1155	lung tumor	universal normal control
	PRO1157	breast tumor	universal normal control
	PRO1157	cervical tumor	universal normal control
	PRO1122	lung tumor	universal normal control
30	PRO1122	breast tumor	universal normal control
	PRO1183	colon tumor	universal normal control
	PRO1183	lung tumor	universal normal control
	PRO1183	breast tumor	universal normal control
	PRO1337	colon tumor	universal normal control
35	PRO1337	lung tumor	universal normal control
	PRO1337	breast tumor	universal normal control
	PRO1480	colon tumor	universal normal control
	PRO1480	lung tumor	universal normal control
	PRO1480	breast tumor	universal normal control
40	PRO19645	colon tumor	universal normal control
	PRO9782	colon tumor	universal normal control
	PRO1419	colon tumor	universal normal control
	PRO1575	colon tumor	universal normal control
	PRO1575	lung tumor	universal normal control
45	PRO1567	colon tumor	universal normal control
	PRO1567	lung tumor	universal normal control
	PRO1567	breast tumor	universal normal control
	PRO1891	colon tumor	universal normal control
	PRO1889	colon tumor	universal normal control
50	PRO1889	lung tumor	universal normal control
	PRO1785	lung tumor	universal normal control
	PRO1785	prostate tumor	universal normal control
	PRO6003	colon tumor	universal normal control
	PRO4333	colon tumor	universal normal control
55	PRO4356	colon tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO4352	colon tumor	universal normal control
	PRO4354	colon tumor	universal normal control
	PRO4354	lung tumor	universal normal control
5	PRO4354	prostate tumor	universal normal control
	PRO4369	colon tumor	universal normal control
	PRO6030	colon tumor	universal normal control
	PRO4433	colon tumor	universal normal control
	PRO4424	colon tumor	universal normal control
10	PRO4424	breast tumor	universal normal control
	PRO6017	colon tumor	universal normal control
	PRO19563	colon tumor	universal normal control
	PRO6015	colon tumor	universal normal control
	PRO5779	colon tumor	universal normal control
15	PRO5776	colon tumor	universal normal control
	PRO4430	lung tumor	universal normal control
	PRO4421	colon tumor	universal normal control
	PRO4499	colon tumor	universal normal control
	PRO4423	colon tumor	universal normal control
20	PRO5998	colon tumor	universal normal control
	PRO5998	lung tumor	universal normal control
	PRO4501	colon tumor	universal normal control
	PRO6240	colon tumor	universal normal control
	PRO6245	colon tumor	universal normal control
25	PRO6175	colon tumor	universal normal control
	PRO9742	colon tumor	universal normal control
	PRO7179	colon tumor	universal normal control
	PRO6239	colon tumor	universal normal control
	PRO6493	colon tumor	universal normal control
30	PRO9741	colon tumor	universal normal control
	PRO9822	colon tumor	universal normal control
	PRO6244	colon tumor	universal normal control
	PRO9740	colon tumor	universal normal control
	PRO9739	colon tumor	universal normal control
35	PRO7177	colon tumor	universal normal control
	PRO7178	colon tumor	universal normal control
	PRO6246	colon tumor	universal normal control
	PRO6241	colon tumor	universal normal control
	PRO9835	colon tumor	universal normal control
40	PRO9857	colon tumor	universal normal control
	PRO7436	colon tumor	universal normal control
	PRO9856	colon tumor	universal normal control
	PRO19605	colon tumor	universal normal control
	PRO9859	colon tumor	universal normal control
45	PRO12970	colon tumor	universal normal control
	PRO19626	colon tumor	universal normal control
	PRO9883	colon tumor	universal normal control
	PRO19670	colon tumor	universal normal control
	PRO19624	colon tumor	universal normal control
50	PRO19680	colon tumor	universal normal control
	PRO19675	colon tumor	universal normal control
	PRO9834	colon tumor	universal normal control
	PRO9744	colon tumor	universal normal control
	PRO19644	colon tumor	universal normal control
55	PRO19625	colon tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO19597	colon tumor	universal normal control
	PRO16090	colon tumor	universal normal control
	PRO19576	colon tumor	universal normal control
5	PRO19646	colon tumor	universal normal control
	PRO19814	colon tumor	universal normal control
	PRO19669	colon tumor	universal normal control
	PRO19818	colon tumor	universal normal control
	PRO20088	colon tumor	universal normal control
10	PRO16089	colon tumor	universal normal control
	PRO20025	colon tumor	universal normal control
	PRO20040	colon tumor	universal normal control
	PRO1760	adrenal tumor	universal normal control
	PRO1760	breast tumor	universal normal control
15	PRO1760	cervical tumor	universal normal control
	PRO1760	colon tumor	universal normal control
	PRO1760	liver tumor	universal normal control
	PRO1760	lung tumor	universal normal control
	PRO1760	prostate tumor	universal normal control
20	PRO1760	rectal tumor	universal normal control
	PRO6029	adrenal tumor	universal normal control
	PRO6029	colon tumor	universal normal control
	PRO6029	prostate tumor	universal normal control
	PRO1801	colon tumor	universal normal control
25	PRO1801	lung tumor	universal normal control

WHAT IS CLAIMED IS:

1. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence that encodes an amino acid sequence selected from the group consisting of the amino acid sequence shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16),
5 Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54),
10 Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92),
15 Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure
20 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure
30 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), Figure 244 (SEQ ID NO:244), Figure 246 (SEQ ID NO:246), Figure 248 (SEQ ID NO:248), Figure 250 (SEQ ID NO:250), Figure 252 (SEQ ID NO:252), Figure 254 (SEQ ID NO:254)

5
10
15
20
25
30
35

NO:520), Figure 522 (SEQ ID NO:522), Figure 524 (SEQ ID NO:524), Figure 526 (SEQ ID NO:526), Figure 528 (SEQ ID NO:528), Figure 530 (SEQ ID NO:530), Figure 532 (SEQ ID NO:532), Figure 534 (SEQ ID NO:534), Figure 536 (SEQ ID NO:536), Figure 538 (SEQ ID NO:538), Figure 540 (SEQ ID NO:540), Figure 542 (SEQ ID NO:542), Figure 544 (SEQ ID NO:544), Figure 546 (SEQ ID NO:546), Figure 548 (SEQ ID NO:548), Figure 550 (SEQ ID NO:550), Figure 552 (SEQ ID NO:552), Figure 554 (SEQ ID NO:554), Figure 556 (SEQ ID NO:556), Figure 558 (SEQ ID NO:558), Figure 560 (SEQ ID NO:560), Figure 562 (SEQ ID NO:562), Figure 564 (SEQ ID NO:564), Figure 566 (SEQ ID NO:566), Figure 568 (SEQ ID NO:568), Figure 570 (SEQ ID NO:570), Figure 572 (SEQ ID NO:572), Figure 574 (SEQ ID NO:574), Figure 576 (SEQ ID NO:576), Figure 578 (SEQ ID NO:578), Figure 580 (SEQ ID NO:580), Figure 582 (SEQ ID NO:582), Figure 584 (SEQ ID NO:584), Figure 586 (SEQ ID NO:586), Figure 588 (SEQ ID NO:588), Figure 590 (SEQ ID NO:590), Figure 592 (SEQ ID NO:592), Figure 594 (SEQ ID NO:594), Figure 596 (SEQ ID NO:596), Figure 598 (SEQ ID NO:598), Figure 600 (SEQ ID NO:600), Figure 602 (SEQ ID NO:602), Figure 604 (SEQ ID NO:604), Figure 606 (SEQ ID NO:606), Figure 608 (SEQ ID NO:608), and Figure 610 (SEQ ID NO:610).

2. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of the nucleotide sequence shown in Figure 1 (SEQ ID NO:1), Figure 3 (SEQ ID NO:3), Figure 5 (SEQ ID NO:5), Figure 7 (SEQ ID NO:7), Figure 9 (SEQ ID NO:9), Figure 11 (SEQ ID NO:11), Figure 13 (SEQ ID NO:13), Figure 15 (SEQ ID NO:15), Figure 17 (SEQ ID NO:17), Figure 19 (SEQ ID NO:19), Figure 21 (SEQ ID NO:21), Figure 23 (SEQ ID NO:23), Figure 25 (SEQ ID NO:25), Figure 27 (SEQ ID NO:27), Figure 29 (SEQ ID NO:29), Figure 31 (SEQ ID NO:31), Figure 33 (SEQ ID NO:33), Figure 35 (SEQ ID NO:35), Figure 37 (SEQ ID NO:37), Figure 39 (SEQ ID NO:39), Figure 41 (SEQ ID NO:41), Figure 43 (SEQ ID NO:43), Figure 45 (SEQ ID NO:45), Figure 47 (SEQ ID NO:47), Figure 49 (SEQ ID NO:49), Figure 51 (SEQ ID NO:51), Figure 53 (SEQ ID NO:53), Figure 55 (SEQ ID NO:55), Figure 57 (SEQ ID NO:57), Figure 59 (SEQ ID NO:59), Figure 61 (SEQ ID NO:61), Figure 63 (SEQ ID NO:63), Figure 65 (SEQ ID NO:65), Figure 67 (SEQ ID NO:67), Figure 69 (SEQ ID NO:69), Figure 71 (SEQ ID NO:71), Figure 73 (SEQ ID NO:73), Figures 75A-75B (SEQ ID NO:75), Figure 77 (SEQ ID NO:77), Figure 79 (SEQ ID NO:79), Figure 81 (SEQ ID NO:81), Figure 83 (SEQ ID NO:83), Figure 85 (SEQ ID NO:85), Figure 87 (SEQ ID NO:87), Figure 89 (SEQ ID NO:89), Figure 91 (SEQ ID NO:91), Figure 93 (SEQ ID NO:93), Figure 95 (SEQ ID NO:95), Figure 97 (SEQ ID NO:97), Figure 99 (SEQ ID NO:99), Figure 101 (SEQ ID NO:101), Figure 103 (SEQ ID NO:103), Figure 105 (SEQ ID NO:105), Figure 107 (SEQ ID NO:107), Figure 109 (SEQ ID NO:109), Figure 111 (SEQ ID NO:111), Figure 113 (SEQ ID NO:113), Figure 115 (SEQ ID NO:115), Figure 117 (SEQ ID NO:117), Figure 119 (SEQ ID NO:119), Figure 121 (SEQ ID NO:121), Figure 123 (SEQ ID NO:123), Figure 125 (SEQ ID NO:125), Figure 127 (SEQ ID NO:127), Figure 129 (SEQ ID NO:129), Figure 131 (SEQ ID NO:131), Figure 133 (SEQ ID NO:133), Figure 135 (SEQ ID NO:135), Figure 137 (SEQ ID NO:137), Figure 139 (SEQ ID NO:139), Figure 141 (SEQ ID NO:141), Figure 143 (SEQ ID NO:143), Figure 145 (SEQ ID NO:145), Figure 147 (SEQ ID NO:147), Figure 149 (SEQ ID NO:149), Figure 151 (SEQ ID NO:151), Figure 153 (SEQ ID NO:153), Figure 155 (SEQ ID NO:155), Figure 157 (SEQ ID NO:157), Figure 159 (SEQ ID NO:159), Figure 161 (SEQ ID NO:161), Figure 163 (SEQ ID NO:163), Figure 165 (SEQ ID

NO:165), Figure 167 (SEQ ID NO:167), Figure 169 (SEQ ID NO:169), Figure 171 (SEQ ID NO:171), Figure 173 (SEQ ID NO:173), Figure 175 (SEQ ID NO:175), Figure 177 (SEQ ID NO:177), Figure 179 (SEQ ID NO:179), Figure 181 (SEQ ID NO:181), Figure 183 (SEQ ID NO:183), Figure 185 (SEQ ID NO:185), Figure 187 (SEQ ID NO:187), Figure 189 (SEQ ID NO:189), Figure 191 (SEQ ID NO:191), Figure 193 (SEQ ID NO:193), Figure 195 (SEQ ID NO:195), Figure 197 (SEQ ID NO:197), Figure 199 (SEQ ID NO:199), Figure 201 (SEQ ID NO:201), Figure 203 (SEQ ID NO:203), Figure 205 (SEQ ID NO:205), Figure 207 (SEQ ID NO:207), Figure 209 (SEQ ID NO:209), Figure 211 (SEQ ID NO:211), Figure 213 (SEQ ID NO:213), Figure 215 (SEQ ID NO:215), Figure 217 (SEQ ID NO:217), Figure 219 (SEQ ID NO:219), Figure 221 (SEQ ID NO:221), Figure 223 (SEQ ID NO:223), Figure 225 (SEQ ID NO:225), Figure 227 (SEQ ID NO:227), Figure 229 (SEQ ID NO:229), Figure 231 (SEQ ID NO:231), Figure 233 (SEQ ID NO:233), Figure 235 (SEQ ID NO:235), Figure 237 (SEQ ID NO:237), Figure 239 (SEQ ID NO:239), Figure 241 (SEQ ID NO:241), Figure 243 (SEQ ID NO:243), Figure 245 (SEQ ID NO:245), Figure 247 (SEQ ID NO:247), Figure 249 (SEQ ID NO:249), Figure 251 (SEQ ID NO:251), Figure 253 (SEQ ID NO:253), Figure 255 (SEQ ID NO:255), Figure 257 (SEQ ID NO:257), Figure 259 (SEQ ID NO:259), Figure 261 (SEQ ID NO:261), Figure 263 (SEQ ID NO:263), Figure 265 (SEQ ID NO:265), Figure 267 (SEQ ID NO:267), Figure 269 (SEQ ID NO:269), Figure 271 (SEQ ID NO:271), Figure 273 (SEQ ID NO:273), Figure 275 (SEQ ID NO:275), Figure 277 (SEQ ID NO:277), Figure 279 (SEQ ID NO:279), Figure 281 (SEQ ID NO:281), Figure 283 (SEQ ID NO:283), Figure 285 (SEQ ID NO:285), Figure 287 (SEQ ID NO:287), Figures 289A-289B (SEQ ID NO:289), Figure 291 (SEQ ID NO:291), Figure 293 (SEQ ID NO:293), Figure 295 (SEQ ID NO:295), Figure 297 (SEQ ID NO:297), Figure 299 (SEQ ID NO:299), Figure 301 (SEQ ID NO:301), Figure 303 (SEQ ID NO:303), Figure 305 (SEQ ID NO:305), Figure 307 (SEQ ID NO:307), Figure 309 (SEQ ID NO:309), Figures 311A-311B (SEQ ID NO:311), Figure 313 (SEQ ID NO:313), Figure 315 (SEQ ID NO:315), Figure 317 (SEQ ID NO:317), Figure 319 (SEQ ID NO:319), Figure 321 (SEQ ID NO:321), Figure 323 (SEQ ID NO:323), Figure 325 (SEQ ID NO:325), Figure 327 (SEQ ID NO:327), Figure 329 (SEQ ID NO:329), Figure 331 (SEQ ID NO:331), Figure 333 (SEQ ID NO:333), Figure 335 (SEQ ID NO:335), Figure 337 (SEQ ID NO:337), Figure 339 (SEQ ID NO:339), Figure 341 (SEQ ID NO:341), Figure 343 (SEQ ID NO:343), Figure 345 (SEQ ID NO:345), Figure 347 (SEQ ID NO:347), Figure 349 (SEQ ID NO:349), Figures 351A-351B (SEQ ID NO:351), Figure 353 (SEQ ID NO:353), Figure 355 (SEQ ID NO:355), Figure 357 (SEQ ID NO:357), Figure 359 (SEQ ID NO:359), Figure 361 (SEQ ID NO:361), Figure 363 (SEQ ID NO:363), Figure 365 (SEQ ID NO:365), Figure 367 (SEQ ID NO:367), Figure 369 (SEQ ID NO:369), Figure 371 (SEQ ID NO:371), Figure 373 (SEQ ID NO:373), Figure 375 (SEQ ID NO:375), Figure 377 (SEQ ID NO:377), Figure 379 (SEQ ID NO:379), Figure 381 (SEQ ID NO:381), Figure 383 (SEQ ID NO:383), Figure 385 (SEQ ID NO:385), Figure 387 (SEQ ID NO:387), Figure 389 (SEQ ID NO:389), Figure 391 (SEQ ID NO:391), Figure 393 (SEQ ID NO:393), Figure 395 (SEQ ID NO:395), Figure 397 (SEQ ID NO:397), Figure 399 (SEQ ID NO:399), Figure 401 (SEQ ID NO:401), Figure 403 (SEQ ID NO:403), Figure 405 (SEQ ID NO:405), Figure 407 (SEQ ID NO:407), Figure 409 (SEQ ID NO:409), Figure 411 (SEQ ID NO:411), Figure 413 (SEQ ID NO:413), Figure 415 (SEQ ID NO:415), Figure 417 (SEQ ID NO:417), Figure 419 (SEQ ID NO:419), Figure 421 (SEQ ID NO:421), Figure 423 (SEQ ID NO:423), Figure 425 (SEQ ID NO:425), Figure 427 (SEQ ID NO:427), Figure 429 (SEQ ID NO:429), Figure 431 (SEQ ID

NO:431), Figure 433 (SEQ ID NO:433), Figure 435 (SEQ ID NO:435), Figure 437 (SEQ ID NO:437), Figure 439 (SEQ ID NO:439), Figure 441 (SEQ ID NO:441), Figure 443 (SEQ ID NO:443), Figure 445 (SEQ ID NO:445), Figure 447 (SEQ ID NO:447), Figure 449 (SEQ ID NO:449), Figure 451 (SEQ ID NO:451), Figure 453 (SEQ ID NO:453), Figure 455 (SEQ ID NO:455), Figure 457 (SEQ ID NO:457), Figure 459 (SEQ ID NO:459), Figure 461 (SEQ ID NO:461), Figure 463 (SEQ ID NO:463), Figure 465 (SEQ ID NO:465), Figure 467 (SEQ ID NO:467), Figure 469 (SEQ ID NO:469), Figure 471 (SEQ ID NO:471), Figure 473 (SEQ ID NO:473), Figure 475 (SEQ ID NO:475), Figure 477 (SEQ ID NO:477), Figure 479 (SEQ ID NO:479), Figure 481 (SEQ ID NO:481), Figure 483 (SEQ ID NO:483), Figure 485 (SEQ ID NO:485), Figure 487 (SEQ ID NO:487), Figure 489 (SEQ ID NO:489), Figure 491 (SEQ ID NO:491), Figure 493 (SEQ ID NO:493), Figure 495 (SEQ ID NO:495), Figure 497 (SEQ ID NO:497), Figure 499 (SEQ ID NO:499), Figure 501 (SEQ ID NO:501), Figure 503 (SEQ ID NO:503), Figure 505 (SEQ ID NO:505), Figure 507 (SEQ ID NO:507), Figure 509 (SEQ ID NO:509), Figure 511 (SEQ ID NO:511), Figure 513 (SEQ ID NO:513), Figure 515 (SEQ ID NO:515), Figure 517 (SEQ ID NO:517), Figure 519 (SEQ ID NO:519), Figure 521 (SEQ ID NO:521), Figure 523 (SEQ ID NO:523), Figures 525A-525B (SEQ ID NO:525), Figure 527 (SEQ ID NO:527), Figure 529 (SEQ ID NO:529), Figure 531 (SEQ ID NO:531), Figure 533 (SEQ ID NO:533), Figure 535 (SEQ ID NO:535), Figure 537 (SEQ ID NO:537), Figure 539 (SEQ ID NO:539), Figure 541 (SEQ ID NO:541), Figure 543 (SEQ ID NO:543), Figure 545 (SEQ ID NO:545), Figure 547 (SEQ ID NO:547), Figure 549 (SEQ ID NO:549), Figure 551 (SEQ ID NO:551), Figure 553 (SEQ ID NO:553), Figure 555 (SEQ ID NO:555), Figure 557 (SEQ ID NO:557), Figure 559 (SEQ ID NO:559), Figure 561 (SEQ ID NO:561), Figure 563 (SEQ ID NO:563), Figure 565 (SEQ ID NO:565), Figure 567 (SEQ ID NO:567), Figure 569 (SEQ ID NO:569), Figure 571 (SEQ ID NO:571), Figure 573 (SEQ ID NO:573), Figure 575 (SEQ ID NO:575), Figure 577 (SEQ ID NO:577), Figure 579 (SEQ ID NO:579), Figure 581 (SEQ ID NO:581), Figure 583 (SEQ ID NO:583), Figure 585 (SEQ ID NO:585), Figure 587 (SEQ ID NO:587), Figure 589 (SEQ ID NO:589), Figure 591 (SEQ ID NO:591), Figure 593 (SEQ ID NO:593), Figure 595 (SEQ ID NO:595), Figure 597 (SEQ ID NO:597), Figure 599 (SEQ ID NO:599), Figure 601 (SEQ ID NO:601), Figure 603 (SEQ ID NO:603), Figure 605 (SEQ ID NO:605), Figure 607 (SEQ ID NO:607), and Figure 609 (SEQ ID NO:609).

3. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of the full-length coding sequence of the nucleotide sequence shown in Figure 1 (SEQ ID NO:1), Figure 3 (SEQ ID NO:3), Figure 5 (SEQ ID NO:5), Figure 7 (SEQ ID NO:7), Figure 9 (SEQ ID NO:9), Figure 11 (SEQ ID NO:11), Figure 13 (SEQ ID NO:13), Figure 15 (SEQ ID NO:15), Figure 17 (SEQ ID NO:17), Figure 19 (SEQ ID NO:19), Figure 21 (SEQ ID NO:21), Figure 23 (SEQ ID NO:23), Figure 25 (SEQ ID NO:25), Figure 27 (SEQ ID NO:27), Figure 29 (SEQ ID NO:29), Figure 31 (SEQ ID NO:31), Figure 33 (SEQ ID NO:33), Figure 35 (SEQ ID NO:35), Figure 37 (SEQ ID NO:37), Figure 39 (SEQ ID NO:39), Figure 41 (SEQ ID NO:41), Figure 43 (SEQ ID NO:43), Figure 45 (SEQ ID NO:45), Figure 47 (SEQ ID NO:47), Figure 49 (SEQ ID NO:49), Figure 51 (SEQ ID NO:51), Figure 53 (SEQ ID NO:53), Figure 55 (SEQ ID NO:55), Figure 57 (SEQ ID NO:57), Figure 59 (SEQ ID NO:59), Figure 61 (SEQ ID NO:61), Figure 63 (SEQ ID NO:63), Figure 65 (SEQ ID NO:65), Figure 67 (SEQ ID NO:67), Figure 69 (SEQ ID NO:69), Figure

71 (SEQ ID NO:71), Figure 73 (SEQ ID NO:73), Figures 75A-75B (SEQ ID NO:75), Figure 77 (SEQ ID NO:77), Figure 79 (SEQ ID NO:79), Figure 81 (SEQ ID NO:81), Figure 83 (SEQ ID NO:83), Figure 85 (SEQ ID NO:85), Figure 87 (SEQ ID NO:87), Figure 89 (SEQ ID NO:89), Figure 91 (SEQ ID NO:91), Figure 93 (SEQ ID NO:93), Figure 95 (SEQ ID NO:95), Figure 97 (SEQ ID NO:97), Figure 99 (SEQ ID NO:99), Figure 101 (SEQ ID NO:101), Figure 103 (SEQ ID NO:103), Figure 105 (SEQ ID NO:105), Figure 107 (SEQ ID NO:107), Figure 109 (SEQ ID NO:109), Figure 111 (SEQ ID NO:111), Figure 113 (SEQ ID NO:113), Figure 115 (SEQ ID NO:115), Figure 117 (SEQ ID NO:117), Figure 119 (SEQ ID NO:119), Figure 121 (SEQ ID NO:121), Figure 123 (SEQ ID NO:123), Figure 125 (SEQ ID NO:125), Figure 127 (SEQ ID NO:127), Figure 129 (SEQ ID NO:129), Figure 131 (SEQ ID NO:131), Figure 133 (SEQ ID NO:133), Figure 135 (SEQ ID NO:135), Figure 137 (SEQ ID NO:137), Figure 139 (SEQ ID NO:139), Figure 141 (SEQ ID NO:141), Figure 143 (SEQ ID NO:143), Figure 145 (SEQ ID NO:145), Figure 147 (SEQ ID NO:147), Figure 149 (SEQ ID NO:149), Figure 151 (SEQ ID NO:151), Figure 153 (SEQ ID NO:153), Figure 155 (SEQ ID NO:155), Figure 157 (SEQ ID NO:157), Figure 159 (SEQ ID NO:159), Figure 161 (SEQ ID NO:161), Figure 163 (SEQ ID NO:163), Figure 165 (SEQ ID NO:165), Figure 167 (SEQ ID NO:167), Figure 169 (SEQ ID NO:169), Figure 171 (SEQ ID NO:171), Figure 173 (SEQ ID NO:173), Figure 175 (SEQ ID NO:175), Figure 177 (SEQ ID NO:177), Figure 179 (SEQ ID NO:179), Figure 181 (SEQ ID NO:181), Figure 183 (SEQ ID NO:183), Figure 185 (SEQ ID NO:185), Figure 187 (SEQ ID NO:187), Figure 189 (SEQ ID NO:189), Figure 191 (SEQ ID NO:191), Figure 193 (SEQ ID NO:193), Figure 195 (SEQ ID NO:195), Figure 197 (SEQ ID NO:197), Figure 199 (SEQ ID NO:199), Figure 201 (SEQ ID NO:201), Figure 203 (SEQ ID NO:203), Figure 205 (SEQ ID NO:205), Figure 207 (SEQ ID NO:207), Figure 209 (SEQ ID NO:209), Figure 211 (SEQ ID NO:211), Figure 213 (SEQ ID NO:213), Figure 215 (SEQ ID NO:215), Figure 217 (SEQ ID NO:217), Figure 219 (SEQ ID NO:219), Figure 221 (SEQ ID NO:221), Figure 223 (SEQ ID NO:223), Figure 225 (SEQ ID NO:225), Figure 227 (SEQ ID NO:227), Figure 229 (SEQ ID NO:229), Figure 231 (SEQ ID NO:231), Figure 233 (SEQ ID NO:233), Figure 235 (SEQ ID NO:235), Figure 237 (SEQ ID NO:237), Figure 239 (SEQ ID NO:239), Figure 241 (SEQ ID NO:241), Figure 243 (SEQ ID NO:243), Figure 245 (SEQ ID NO:245), Figure 247 (SEQ ID NO:247), Figure 249 (SEQ ID NO:249), Figure 251 (SEQ ID NO:251), Figure 253 (SEQ ID NO:253), Figure 255 (SEQ ID NO:255), Figure 257 (SEQ ID NO:257), Figure 259 (SEQ ID NO:259), Figure 261 (SEQ ID NO:261), Figure 263 (SEQ ID NO:263), Figure 265 (SEQ ID NO:265), Figure 267 (SEQ ID NO:267), Figure 269 (SEQ ID NO:269), Figure 271 (SEQ ID NO:271), Figure 273 (SEQ ID NO:273), Figure 275 (SEQ ID NO:275), Figure 277 (SEQ ID NO:277), Figure 279 (SEQ ID NO:279), Figure 281 (SEQ ID NO:281), Figure 283 (SEQ ID NO:283), Figure 285 (SEQ ID NO:285), Figure 287 (SEQ ID NO:287), Figures 289A-289B (SEQ ID NO:289), Figure 291 (SEQ ID NO:291), Figure 293 (SEQ ID NO:293), Figure 295 (SEQ ID NO:295), Figure 297 (SEQ ID NO:297), Figure 299 (SEQ ID NO:299), Figure 301 (SEQ ID NO:301), Figure 303 (SEQ ID NO:303), Figure 305 (SEQ ID NO:305), Figure 307 (SEQ ID NO:307), Figure 309 (SEQ ID NO:309), Figures 311A-311B (SEQ ID NO:311), Figure 313 (SEQ ID NO:313), Figure 315 (SEQ ID NO:315), Figure 317 (SEQ ID NO:317), Figure 319 (SEQ ID NO:319), Figure 321 (SEQ ID NO:321), Figure 323 (SEQ ID NO:323), Figure 325 (SEQ ID NO:325), Figure 327 (SEQ ID NO:327), Figure 329 (SEQ ID NO:329), Figure 331 (SEQ ID NO:331), Figure 333 (SEQ ID NO:333), Figure 335 (SEQ ID NO:335), Figure 337 (SEQ ID NO:337), Figure

339 (SEQ ID NO:339), Figure 341 (SEQ ID NO:341), Figure 343 (SEQ ID NO:343), Figure 345 (SEQ ID NO:345), Figure 347 (SEQ ID NO:347), Figure 349 (SEQ ID NO:349), Figures 351A-351B (SEQ ID NO:351), Figure 353 (SEQ ID NO:353), Figure 355 (SEQ ID NO:355), Figure 357 (SEQ ID NO:357), Figure 359 (SEQ ID NO:359), Figure 361 (SEQ ID NO:361), Figure 363 (SEQ ID NO:363), Figure 365 (SEQ ID NO:365), Figure 367 (SEQ ID NO:367), Figure 369 (SEQ ID NO:369), Figure 371 (SEQ ID NO:371), Figure 373 (SEQ ID NO:373), Figure 375 (SEQ ID NO:375), Figure 377 (SEQ ID NO:377), Figure 379 (SEQ ID NO:379), Figure 381 (SEQ ID NO:381), Figure 383 (SEQ ID NO:383), Figure 385 (SEQ ID NO:385), Figure 387 (SEQ ID NO:387), Figure 389 (SEQ ID NO:389), Figure 391 (SEQ ID NO:391), Figure 393 (SEQ ID NO:393), Figure 395 (SEQ ID NO:395), Figure 397 (SEQ ID NO:397), Figure 399 (SEQ ID NO:399), Figure 401 (SEQ ID NO:401), Figure 403 (SEQ ID NO:403), Figure 405 (SEQ ID NO:405), Figure 407 (SEQ ID NO:407), Figure 409 (SEQ ID NO:409), Figure 411 (SEQ ID NO:411), Figure 413 (SEQ ID NO:413), Figure 415 (SEQ ID NO:415), Figure 417 (SEQ ID NO:417), Figure 419 (SEQ ID NO:419), Figure 421 (SEQ ID NO:421), Figure 423 (SEQ ID NO:423), Figure 425 (SEQ ID NO:425), Figure 427 (SEQ ID NO:427), Figure 429 (SEQ ID NO:429), Figure 431 (SEQ ID NO:431), Figure 433 (SEQ ID NO:433), Figure 435 (SEQ ID NO:435), Figure 437 (SEQ ID NO:437), Figure 439 (SEQ ID NO:439), Figure 441 (SEQ ID NO:441), Figure 443 (SEQ ID NO:443), Figure 445 (SEQ ID NO:445), Figure 447 (SEQ ID NO:447), Figure 449 (SEQ ID NO:449), Figure 451 (SEQ ID NO:451), Figure 453 (SEQ ID NO:453), Figure 455 (SEQ ID NO:455), Figure 457 (SEQ ID NO:457), Figure 459 (SEQ ID NO:459), Figure 461 (SEQ ID NO:461), Figure 463 (SEQ ID NO:463), Figure 465 (SEQ ID NO:465), Figure 467 (SEQ ID NO:467), Figure 469 (SEQ ID NO:469), Figure 471 (SEQ ID NO:471), Figure 473 (SEQ ID NO:473), Figure 475 (SEQ ID NO:475), Figure 477 (SEQ ID NO:477), Figure 479 (SEQ ID NO:479), Figure 481 (SEQ ID NO:481), Figure 483 (SEQ ID NO:483), Figure 485 (SEQ ID NO:485), Figure 487 (SEQ ID NO:487), Figure 489 (SEQ ID NO:489), Figure 491 (SEQ ID NO:491), Figure 493 (SEQ ID NO:493), Figure 495 (SEQ ID NO:495), Figure 497 (SEQ ID NO:497), Figure 499 (SEQ ID NO:499), Figure 501 (SEQ ID NO:501), Figure 503 (SEQ ID NO:503), Figure 505 (SEQ ID NO:505), Figure 507 (SEQ ID NO:507), Figure 509 (SEQ ID NO:509), Figure 511 (SEQ ID NO:511), Figure 513 (SEQ ID NO:513), Figure 515 (SEQ ID NO:515), Figure 517 (SEQ ID NO:517), Figure 519 (SEQ ID NO:519), Figure 521 (SEQ ID NO:521), Figure 523 (SEQ ID NO:523), Figures 525A-525B (SEQ ID NO:525), Figure 527 (SEQ ID NO:527), Figure 529 (SEQ ID NO:529), Figure 531 (SEQ ID NO:531), Figure 533 (SEQ ID NO:533), Figure 535 (SEQ ID NO:535), Figure 537 (SEQ ID NO:537), Figure 539 (SEQ ID NO:539), Figure 541 (SEQ ID NO:541), Figure 543 (SEQ ID NO:543), Figure 545 (SEQ ID NO:545), Figure 547 (SEQ ID NO:547), Figure 549 (SEQ ID NO:549), Figure 551 (SEQ ID NO:551), Figure 553 (SEQ ID NO:553), Figure 555 (SEQ ID NO:555), Figure 557 (SEQ ID NO:557), Figure 559 (SEQ ID NO:559), Figure 561 (SEQ ID NO:561), Figure 563 (SEQ ID NO:563), Figure 565 (SEQ ID NO:565), Figure 567 (SEQ ID NO:567), Figure 569 (SEQ ID NO:569), Figure 571 (SEQ ID NO:571), Figure 573 (SEQ ID NO:573), Figure 575 (SEQ ID NO:575), Figure 577 (SEQ ID NO:577), Figure 579 (SEQ ID NO:579), Figure 581 (SEQ ID NO:581), Figure 583 (SEQ ID NO:583), Figure 585 (SEQ ID NO:585), Figure 587 (SEQ ID NO:587), Figure 589 (SEQ ID NO:589), Figure 591 (SEQ ID NO:591), Figure 593 (SEQ ID NO:593), Figure 595 (SEQ ID NO:595), Figure 597 (SEQ ID NO:597), Figure 599 (SEQ ID NO:599), Figure 601 (SEQ ID NO:601), Figure 603 (SEQ ID NO:603), Figure

605 (SEQ ID NO:605), Figure 607 (SEQ ID NO:607), and Figure 609 (SEQ ID NO:609).

4. Isolated nucleic acid having at least 80% nucleic acid sequence identity to the full-length coding sequence of the DNA deposited under any ATCC accession number shown in Table 7.

5. A vector comprising the nucleic acid of Claim 1.

6. A host cell comprising the vector of Claim 5.

7. The host cell of Claim 6, wherein said cell is a CHO cell.

10

8. The host cell of Claim 6, wherein said cell is an *E. coli*.

9. The host cell of Claim 6, wherein said cell is a yeast cell.

15

10. A process for producing a PRO polypeptide comprising culturing the host cell of Claim 6 under conditions suitable for expression of said PRO polypeptide and recovering said PRO polypeptide from the cell culture.

20

11. An isolated polypeptide having at least 80% amino acid sequence identity to an amino acid sequence selected from the group consisting of the amino acid sequence shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID

35

5
10
15
20
25
30
35

NO:396), Figure 398 (SEQ ID NO:398), Figure 400 (SEQ ID NO:400), Figure 402 (SEQ ID NO:402), Figure 404 (SEQ ID NO:404), Figure 406 (SEQ ID NO:406), Figure 408 (SEQ ID NO:408), Figure 410 (SEQ ID NO:410), Figure 412 (SEQ ID NO:412), Figure 414 (SEQ ID NO:414), Figure 416 (SEQ ID NO:416), Figure 418 (SEQ ID NO:418), Figure 420 (SEQ ID NO:420), Figure 422 (SEQ ID NO:422), Figure 424 (SEQ ID NO:424), Figure 426 (SEQ ID NO:426), Figure 428 (SEQ ID NO:428), Figure 430 (SEQ ID NO:430), Figure 432 (SEQ ID NO:432), Figure 434 (SEQ ID NO:434), Figure 436 (SEQ ID NO:436), Figure 438 (SEQ ID NO:438), Figure 440 (SEQ ID NO:440), Figure 442 (SEQ ID NO:442), Figure 444 (SEQ ID NO:444), Figure 446 (SEQ ID NO:446), Figure 448 (SEQ ID NO:448), Figure 450 (SEQ ID NO:450), Figure 452 (SEQ ID NO:452), Figure 454 (SEQ ID NO:454), Figure 456 (SEQ ID NO:456), Figure 458 (SEQ ID NO:458), Figure 460 (SEQ ID NO:460), Figure 462 (SEQ ID NO:462), Figure 464 (SEQ ID NO:464), Figure 466 (SEQ ID NO:466), Figure 468 (SEQ ID NO:468), Figure 470 (SEQ ID NO:470), Figure 472 (SEQ ID NO:472), Figure 474 (SEQ ID NO:474), Figure 476 (SEQ ID NO:476), Figure 478 (SEQ ID NO:478), Figure 480 (SEQ ID NO:480), Figure 482 (SEQ ID NO:482), Figure 484 (SEQ ID NO:484), Figure 486 (SEQ ID NO:486), Figure 488 (SEQ ID NO:488), Figure 490 (SEQ ID NO:490), Figure 492 (SEQ ID NO:492), Figure 494 (SEQ ID NO:494), Figure 496 (SEQ ID NO:496), Figure 498 (SEQ ID NO:498), Figure 500 (SEQ ID NO:500), Figure 502 (SEQ ID NO:502), Figure 504 (SEQ ID NO:504), Figure 506 (SEQ ID NO:506), Figure 508 (SEQ ID NO:508), Figure 510 (SEQ ID NO:510), Figure 512 (SEQ ID NO:512), Figure 514 (SEQ ID NO:514), Figure 516 (SEQ ID NO:516), Figure 518 (SEQ ID NO:518), Figure 520 (SEQ ID NO:520), Figure 522 (SEQ ID NO:522), Figure 524 (SEQ ID NO:524), Figure 526 (SEQ ID NO:526), Figure 528 (SEQ ID NO:528), Figure 530 (SEQ ID NO:530), Figure 532 (SEQ ID NO:532), Figure 534 (SEQ ID NO:534), Figure 536 (SEQ ID NO:536), Figure 538 (SEQ ID NO:538), Figure 540 (SEQ ID NO:540), Figure 542 (SEQ ID NO:542), Figure 544 (SEQ ID NO:544), Figure 546 (SEQ ID NO:546), Figure 548 (SEQ ID NO:548), Figure 550 (SEQ ID NO:550), Figure 552 (SEQ ID NO:552), Figure 554 (SEQ ID NO:554), Figure 556 (SEQ ID NO:556), Figure 558 (SEQ ID NO:558), Figure 560 (SEQ ID NO:560), Figure 562 (SEQ ID NO:562), Figure 564 (SEQ ID NO:564), Figure 566 (SEQ ID NO:566), Figure 568 (SEQ ID NO:568), Figure 570 (SEQ ID NO:570), Figure 572 (SEQ ID NO:572), Figure 574 (SEQ ID NO:574), Figure 576 (SEQ ID NO:576), Figure 578 (SEQ ID NO:578), Figure 580 (SEQ ID NO:580), Figure 582 (SEQ ID NO:582), Figure 584 (SEQ ID NO:584), Figure 586 (SEQ ID NO:586), Figure 588 (SEQ ID NO:588), Figure 590 (SEQ ID NO:590), Figure 592 (SEQ ID NO:592), Figure 594 (SEQ ID NO:594), Figure 596 (SEQ ID NO:596), Figure 598 (SEQ ID NO:598), Figure 600 (SEQ ID NO:600), Figure 602 (SEQ ID NO:602), Figure 604 (SEQ ID NO:604), Figure 606 (SEQ ID NO:606), Figure 608 (SEQ ID NO:608), and Figure 610 (SEQ ID NO:610).

12. An isolated polypeptide having at least 80% amino acid sequence identity to an amino acid sequence encoded by the full-length coding sequence of the DNA deposited under any ATCC accession number shown in Table 7.

13. A chimeric molecule comprising a polypeptide according to Claim 11 fused to a heterologous amino acid sequence.

14. The chimeric molecule of Claim 13, wherein said heterologous amino acid sequence is an epitope tag sequence.

15. The chimeric molecule of Claim 13, wherein said heterologous amino acid sequence is a Fc region of an immunoglobulin.

5

16. An antibody which specifically binds to a polypeptide according to Claim 11.

17. The antibody of Claim 16, wherein said antibody is a monoclonal antibody, a humanized antibody or a single-chain antibody.

10

18. Isolated nucleic acid having at least 80% nucleic acid sequence identity to:

(a) a nucleotide sequence encoding the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure

35

188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), Figure 244 (SEQ ID NO:244), Figure 246 (SEQ ID NO:246), Figure 248 (SEQ ID NO:248), Figure 250 (SEQ ID NO:250), Figure 252 (SEQ ID NO:252), Figure 254 (SEQ ID NO:254), Figure 256 (SEQ ID NO:256), Figure 258 (SEQ ID NO:258), Figure 260 (SEQ ID NO:260), Figure 262 (SEQ ID NO:262), Figure 264 (SEQ ID NO:264), Figure 266 (SEQ ID NO:266), Figure 268 (SEQ ID NO:268), Figure 270 (SEQ ID NO:270), Figure 272 (SEQ ID NO:272), Figure 274 (SEQ ID NO:274), Figure 276 (SEQ ID NO:276), Figure 278 (SEQ ID NO:278), Figure 280 (SEQ ID NO:280), Figure 282 (SEQ ID NO:282), Figure 284 (SEQ ID NO:284), Figure 286 (SEQ ID NO:286), Figure 288 (SEQ ID NO:288), Figure 290 (SEQ ID NO:290), Figure 292 (SEQ ID NO:292), Figure 294 (SEQ ID NO:294), Figure 296 (SEQ ID NO:296), Figure 298 (SEQ ID NO:298), Figure 300 (SEQ ID NO:300), Figure 302 (SEQ ID NO:302), Figure 304 (SEQ ID NO:304), Figure 306 (SEQ ID NO:306), Figure 308 (SEQ ID NO:308), Figure 310 (SEQ ID NO:310), Figure 312 (SEQ ID NO:312), Figure 314 (SEQ ID NO:314), Figure 316 (SEQ ID NO:316), Figure 318 (SEQ ID NO:318), Figure 320 (SEQ ID NO:320), Figure 322 (SEQ ID NO:322), Figure 324 (SEQ ID NO:324), Figure 326 (SEQ ID NO:326), Figure 328 (SEQ ID NO:328), Figure 330 (SEQ ID NO:330), Figure 332 (SEQ ID NO:332), Figure 334 (SEQ ID NO:334), Figure 336 (SEQ ID NO:336), Figure 338 (SEQ ID NO:338), Figure 340 (SEQ ID NO:340), Figure 342 (SEQ ID NO:342), Figure 344 (SEQ ID NO:344), Figure 346 (SEQ ID NO:346), Figure 348 (SEQ ID NO:348), Figure 350 (SEQ ID NO:350), Figure 352 (SEQ ID NO:352), Figure 354 (SEQ ID NO:354), Figure 356 (SEQ ID NO:356), Figure 358 (SEQ ID NO:358), Figure 360 (SEQ ID NO:360), Figure 362 (SEQ ID NO:362), Figure 364 (SEQ ID NO:364), Figure 366 (SEQ ID NO:366), Figure 368 (SEQ ID NO:368), Figure 370 (SEQ ID NO:370), Figure 372 (SEQ ID NO:372), Figure 374 (SEQ ID NO:374), Figure 376 (SEQ ID NO:376), Figure 378 (SEQ ID NO:378), Figure 380 (SEQ ID NO:380), Figure 382 (SEQ ID NO:382), Figure 384 (SEQ ID NO:384), Figure 386 (SEQ ID NO:386), Figure 388 (SEQ ID NO:388), Figure 390 (SEQ ID NO:390), Figure 392 (SEQ ID NO:392), Figure 394 (SEQ ID NO:394), Figure 396 (SEQ ID NO:396), Figure 398 (SEQ ID NO:398), Figure 400 (SEQ ID NO:400), Figure 402 (SEQ ID NO:402), Figure 404 (SEQ ID NO:404), Figure 406 (SEQ ID NO:406), Figure 408 (SEQ ID NO:408), Figure 410 (SEQ ID NO:410), Figure 412 (SEQ ID NO:412), Figure 414 (SEQ ID NO:414), Figure 416 (SEQ ID NO:416), Figure 418 (SEQ ID NO:418), Figure 420 (SEQ ID NO:420), Figure 422 (SEQ ID NO:422), Figure 424 (SEQ ID NO:424), Figure 426 (SEQ ID NO:426), Figure 428 (SEQ ID NO:428), Figure 430 (SEQ ID NO:430), Figure 432 (SEQ ID NO:432), Figure 434 (SEQ ID NO:434), Figure 436 (SEQ ID NO:436), Figure 438 (SEQ ID NO:438), Figure 440 (SEQ ID NO:440), Figure 442 (SEQ ID NO:442), Figure 444 (SEQ ID NO:444), Figure 446 (SEQ ID NO:446), Figure 448 (SEQ ID NO:448), Figure 450 (SEQ ID NO:450), Figure 452 (SEQ ID NO:452), Figure

454 (SEQ ID NO:454), Figure 456 (SEQ ID NO:456), Figure 458 (SEQ ID NO:458), Figure 460 (SEQ ID NO:460), Figure 462 (SEQ ID NO:462), Figure 464 (SEQ ID NO:464), Figure 466 (SEQ ID NO:466), Figure 468 (SEQ ID NO:468), Figure 470 (SEQ ID NO:470), Figure 472 (SEQ ID NO:472), Figure 474 (SEQ ID NO:474), Figure 476 (SEQ ID NO:476), Figure 478 (SEQ ID NO:478), Figure 480 (SEQ ID NO:480), Figure 482 (SEQ ID NO:482), Figure 484 (SEQ ID NO:484), Figure 486 (SEQ ID NO:486), Figure 488 (SEQ ID NO:488), Figure 490 (SEQ ID NO:490), Figure 492 (SEQ ID NO:492), Figure 494 (SEQ ID NO:494), Figure 496 (SEQ ID NO:496), Figure 498 (SEQ ID NO:498), Figure 500 (SEQ ID NO:500), Figure 502 (SEQ ID NO:502), Figure 504 (SEQ ID NO:504), Figure 506 (SEQ ID NO:506), Figure 508 (SEQ ID NO:508), Figure 510 (SEQ ID NO:510), Figure 512 (SEQ ID NO:512), Figure 514 (SEQ ID NO:514), Figure 516 (SEQ ID NO:516), Figure 518 (SEQ ID NO:518), Figure 520 (SEQ ID NO:520), Figure 522 (SEQ ID NO:522), Figure 524 (SEQ ID NO:524), Figure 526 (SEQ ID NO:526), Figure 528 (SEQ ID NO:528), Figure 530 (SEQ ID NO:530), Figure 532 (SEQ ID NO:532), Figure 534 (SEQ ID NO:534), Figure 536 (SEQ ID NO:536), Figure 538 (SEQ ID NO:538), Figure 540 (SEQ ID NO:540), Figure 542 (SEQ ID NO:542), Figure 544 (SEQ ID NO:544), Figure 546 (SEQ ID NO:546), Figure 548 (SEQ ID NO:548), Figure 550 (SEQ ID NO:550), Figure 552 (SEQ ID NO:552), Figure 554 (SEQ ID NO:554), Figure 556 (SEQ ID NO:556), Figure 558 (SEQ ID NO:558), Figure 560 (SEQ ID NO:560), Figure 562 (SEQ ID NO:562), Figure 564 (SEQ ID NO:564), Figure 566 (SEQ ID NO:566), Figure 568 (SEQ ID NO:568), Figure 570 (SEQ ID NO:570), Figure 572 (SEQ ID NO:572), Figure 574 (SEQ ID NO:574), Figure 576 (SEQ ID NO:576), Figure 578 (SEQ ID NO:578), Figure 580 (SEQ ID NO:580), Figure 582 (SEQ ID NO:582), Figure 584 (SEQ ID NO:584), Figure 586 (SEQ ID NO:586), Figure 588 (SEQ ID NO:588), Figure 590 (SEQ ID NO:590), Figure 592 (SEQ ID NO:592), Figure 594 (SEQ ID NO:594), Figure 596 (SEQ ID NO:596), Figure 598 (SEQ ID NO:598), Figure 600 (SEQ ID NO:600), Figure 602 (SEQ ID NO:602), Figure 604 (SEQ ID NO:604), Figure 606 (SEQ ID NO:606), Figure 608 (SEQ ID NO:608), or Figure 610 (SEQ ID NO:610), lacking its associated signal peptide;

(b) a nucleotide sequence encoding an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ

5

10

15

20

25

30

35

- NO:374), Figure 376 (SEQ ID NO:376), Figure 378 (SEQ ID NO:378), Figure 380 (SEQ ID NO:380), Figure 382 (SEQ ID NO:382), Figure 384 (SEQ ID NO:384), Figure 386 (SEQ ID NO:386), Figure 388 (SEQ ID NO:388), Figure 390 (SEQ ID NO:390), Figure 392 (SEQ ID NO:392), Figure 394 (SEQ ID NO:394), Figure 396 (SEQ ID NO:396), Figure 398 (SEQ ID NO:398), Figure 400 (SEQ ID NO:400), Figure 402 (SEQ ID NO:402), Figure 404 (SEQ ID NO:404), Figure 406 (SEQ ID NO:406), Figure 408 (SEQ ID NO:408), Figure 410 (SEQ ID NO:410), Figure 412 (SEQ ID NO:412), Figure 414 (SEQ ID NO:414), Figure 416 (SEQ ID NO:416), Figure 418 (SEQ ID NO:418), Figure 420 (SEQ ID NO:420), Figure 422 (SEQ ID NO:422), Figure 424 (SEQ ID NO:424), Figure 426 (SEQ ID NO:426), Figure 428 (SEQ ID NO:428), Figure 430 (SEQ ID NO:430), Figure 432 (SEQ ID NO:432), Figure 434 (SEQ ID NO:434), Figure 436 (SEQ ID NO:436), Figure 438 (SEQ ID NO:438), Figure 440 (SEQ ID NO:440), Figure 442 (SEQ ID NO:442), Figure 444 (SEQ ID NO:444), Figure 446 (SEQ ID NO:446), Figure 448 (SEQ ID NO:448), Figure 450 (SEQ ID NO:450), Figure 452 (SEQ ID NO:452), Figure 454 (SEQ ID NO:454), Figure 456 (SEQ ID NO:456), Figure 458 (SEQ ID NO:458), Figure 460 (SEQ ID NO:460), Figure 462 (SEQ ID NO:462), Figure 464 (SEQ ID NO:464), Figure 466 (SEQ ID NO:466), Figure 468 (SEQ ID NO:468), Figure 470 (SEQ ID NO:470), Figure 472 (SEQ ID NO:472), Figure 474 (SEQ ID NO:474), Figure 476 (SEQ ID NO:476), Figure 478 (SEQ ID NO:478), Figure 480 (SEQ ID NO:480), Figure 482 (SEQ ID NO:482), Figure 484 (SEQ ID NO:484), Figure 486 (SEQ ID NO:486), Figure 488 (SEQ ID NO:488), Figure 490 (SEQ ID NO:490), Figure 492 (SEQ ID NO:492), Figure 494 (SEQ ID NO:494), Figure 496 (SEQ ID NO:496), Figure 498 (SEQ ID NO:498), Figure 500 (SEQ ID NO:500), Figure 502 (SEQ ID NO:502), Figure 504 (SEQ ID NO:504), Figure 506 (SEQ ID NO:506), Figure 508 (SEQ ID NO:508), Figure 510 (SEQ ID NO:510), Figure 512 (SEQ ID NO:512), Figure 514 (SEQ ID NO:514), Figure 516 (SEQ ID NO:516), Figure 518 (SEQ ID NO:518), Figure 520 (SEQ ID NO:520), Figure 522 (SEQ ID NO:522), Figure 524 (SEQ ID NO:524), Figure 526 (SEQ ID NO:526), Figure 528 (SEQ ID NO:528), Figure 530 (SEQ ID NO:530), Figure 532 (SEQ ID NO:532), Figure 534 (SEQ ID NO:534), Figure 536 (SEQ ID NO:536), Figure 538 (SEQ ID NO:538), Figure 540 (SEQ ID NO:540), Figure 542 (SEQ ID NO:542), Figure 544 (SEQ ID NO:544), Figure 546 (SEQ ID NO:546), Figure 548 (SEQ ID NO:548), Figure 550 (SEQ ID NO:550), Figure 552 (SEQ ID NO:552), Figure 554 (SEQ ID NO:554), Figure 556 (SEQ ID NO:556), Figure 558 (SEQ ID NO:558), Figure 560 (SEQ ID NO:560), Figure 562 (SEQ ID NO:562), Figure 564 (SEQ ID NO:564), Figure 566 (SEQ ID NO:566), Figure 568 (SEQ ID NO:568), Figure 570 (SEQ ID NO:570), Figure 572 (SEQ ID NO:572), Figure 574 (SEQ ID NO:574), Figure 576 (SEQ ID NO:576), Figure 578 (SEQ ID NO:578), Figure 580 (SEQ ID NO:580), Figure 582 (SEQ ID NO:582), Figure 584 (SEQ ID NO:584), Figure 586 (SEQ ID NO:586), Figure 588 (SEQ ID NO:588), Figure 590 (SEQ ID NO:590), Figure 592 (SEQ ID NO:592), Figure 594 (SEQ ID NO:594), Figure 596 (SEQ ID NO:596), Figure 598 (SEQ ID NO:598), Figure 600 (SEQ ID NO:600), Figure 602 (SEQ ID NO:602), Figure 604 (SEQ ID NO:604), Figure 606 (SEQ ID NO:606), Figure 608 (SEQ ID NO:608), or Figure 610 (SEQ ID NO:610), with its associated signal peptide; or
- (c) a nucleotide sequence encoding an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18

(SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), Figure 244 (SEQ ID NO:244), Figure 246 (SEQ ID NO:246), Figure 248 (SEQ ID NO:248), Figure 250 (SEQ ID NO:250), Figure 252 (SEQ ID NO:252), Figure 254 (SEQ ID NO:254), Figure 256 (SEQ ID NO:256), Figure 258 (SEQ ID NO:258), Figure 260 (SEQ ID NO:260), Figure 262 (SEQ ID NO:262), Figure 264 (SEQ ID NO:264), Figure 266 (SEQ ID NO:266), Figure 268 (SEQ ID NO:268), Figure 270 (SEQ ID NO:270), Figure 272 (SEQ ID NO:272), Figure 274 (SEQ ID NO:274), Figure 276 (SEQ ID NO:276), Figure 278 (SEQ ID NO:278), Figure 280 (SEQ ID NO:280), Figure 282 (SEQ ID NO:282), Figure 284 (SEQ ID NO:284), Figure 286 (SEQ ID NO:286), Figure 288 (SEQ ID NO:288), Figure 290 (SEQ ID

NO:290), Figure 292 (SEQ ID NO:292), Figure 294 (SEQ ID NO:294), Figure 296 (SEQ ID NO:296), Figure 298 (SEQ ID NO:298), Figure 300 (SEQ ID NO:300), Figure 302 (SEQ ID NO:302), Figure 304 (SEQ ID NO:304), Figure 306 (SEQ ID NO:306), Figure 308 (SEQ ID NO:308), Figure 310 (SEQ ID NO:310), Figure 312 (SEQ ID NO:312), Figure 314 (SEQ ID NO:314), Figure 316 (SEQ ID NO:316), Figure 318 (SEQ ID NO:318), Figure 320 (SEQ ID NO:320), Figure 322 (SEQ ID NO:322), Figure 324 (SEQ ID NO:324), Figure 326 (SEQ ID NO:326), Figure 328 (SEQ ID NO:328), Figure 330 (SEQ ID NO:330), Figure 332 (SEQ ID NO:332), Figure 334 (SEQ ID NO:334), Figure 336 (SEQ ID NO:336), Figure 338 (SEQ ID NO:338), Figure 340 (SEQ ID NO:340), Figure 342 (SEQ ID NO:342), Figure 344 (SEQ ID NO:344), Figure 346 (SEQ ID NO:346), Figure 348 (SEQ ID NO:348), Figure 350 (SEQ ID NO:350), Figure 352 (SEQ ID NO:352), Figure 354 (SEQ ID NO:354), Figure 356 (SEQ ID NO:356), Figure 358 (SEQ ID NO:358), Figure 360 (SEQ ID NO:360), Figure 362 (SEQ ID NO:362), Figure 364 (SEQ ID NO:364), Figure 366 (SEQ ID NO:366), Figure 368 (SEQ ID NO:368), Figure 370 (SEQ ID NO:370), Figure 372 (SEQ ID NO:372), Figure 374 (SEQ ID NO:374), Figure 376 (SEQ ID NO:376), Figure 378 (SEQ ID NO:378), Figure 380 (SEQ ID NO:380), Figure 382 (SEQ ID NO:382), Figure 384 (SEQ ID NO:384), Figure 386 (SEQ ID NO:386), Figure 388 (SEQ ID NO:388), Figure 390 (SEQ ID NO:390), Figure 392 (SEQ ID NO:392), Figure 394 (SEQ ID NO:394), Figure 396 (SEQ ID NO:396), Figure 398 (SEQ ID NO:398), Figure 400 (SEQ ID NO:400), Figure 402 (SEQ ID NO:402), Figure 404 (SEQ ID NO:404), Figure 406 (SEQ ID NO:406), Figure 408 (SEQ ID NO:408), Figure 410 (SEQ ID NO:410), Figure 412 (SEQ ID NO:412), Figure 414 (SEQ ID NO:414), Figure 416 (SEQ ID NO:416), Figure 418 (SEQ ID NO:418), Figure 420 (SEQ ID NO:420), Figure 422 (SEQ ID NO:422), Figure 424 (SEQ ID NO:424), Figure 426 (SEQ ID NO:426), Figure 428 (SEQ ID NO:428), Figure 430 (SEQ ID NO:430), Figure 432 (SEQ ID NO:432), Figure 434 (SEQ ID NO:434), Figure 436 (SEQ ID NO:436), Figure 438 (SEQ ID NO:438), Figure 440 (SEQ ID NO:440), Figure 442 (SEQ ID NO:442), Figure 444 (SEQ ID NO:444), Figure 446 (SEQ ID NO:446), Figure 448 (SEQ ID NO:448), Figure 450 (SEQ ID NO:450), Figure 452 (SEQ ID NO:452), Figure 454 (SEQ ID NO:454), Figure 456 (SEQ ID NO:456), Figure 458 (SEQ ID NO:458), Figure 460 (SEQ ID NO:460), Figure 462 (SEQ ID NO:462), Figure 464 (SEQ ID NO:464), Figure 466 (SEQ ID NO:466), Figure 468 (SEQ ID NO:468), Figure 470 (SEQ ID NO:470), Figure 472 (SEQ ID NO:472), Figure 474 (SEQ ID NO:474), Figure 476 (SEQ ID NO:476), Figure 478 (SEQ ID NO:478), Figure 480 (SEQ ID NO:480), Figure 482 (SEQ ID NO:482), Figure 484 (SEQ ID NO:484), Figure 486 (SEQ ID NO:486), Figure 488 (SEQ ID NO:488), Figure 490 (SEQ ID NO:490), Figure 492 (SEQ ID NO:492), Figure 494 (SEQ ID NO:494), Figure 496 (SEQ ID NO:496), Figure 498 (SEQ ID NO:498), Figure 500 (SEQ ID NO:500), Figure 502 (SEQ ID NO:502), Figure 504 (SEQ ID NO:504), Figure 506 (SEQ ID NO:506), Figure 508 (SEQ ID NO:508), Figure 510 (SEQ ID NO:510), Figure 512 (SEQ ID NO:512), Figure 514 (SEQ ID NO:514), Figure 516 (SEQ ID NO:516), Figure 518 (SEQ ID NO:518), Figure 520 (SEQ ID NO:520), Figure 522 (SEQ ID NO:522), Figure 524 (SEQ ID NO:524), Figure 526 (SEQ ID NO:526), Figure 528 (SEQ ID NO:528), Figure 530 (SEQ ID NO:530), Figure 532 (SEQ ID NO:532), Figure 534 (SEQ ID NO:534), Figure 536 (SEQ ID NO:536), Figure 538 (SEQ ID NO:538), Figure 540 (SEQ ID NO:540), Figure 542 (SEQ ID NO:542), Figure 544 (SEQ ID NO:544), Figure 546 (SEQ ID NO:546), Figure 548 (SEQ ID NO:548), Figure 550 (SEQ ID NO:550), Figure 552 (SEQ ID NO:552), Figure 554 (SEQ ID NO:554), Figure 556 (SEQ ID

NO:556), Figure 558 (SEQ ID NO:558), Figure 560 (SEQ ID NO:560), Figure 562 (SEQ ID NO:562), Figure 564 (SEQ ID NO:564), Figure 566 (SEQ ID NO:566), Figure 568 (SEQ ID NO:568), Figure 570 (SEQ ID NO:570), Figure 572 (SEQ ID NO:572), Figure 574 (SEQ ID NO:574), Figure 576 (SEQ ID NO:576), Figure 578 (SEQ ID NO:578), Figure 580 (SEQ ID NO:580), Figure 582 (SEQ ID NO:582), Figure 584 (SEQ ID NO:584), Figure 586 (SEQ ID NO:586), Figure 588 (SEQ ID NO:588), Figure 590 (SEQ ID NO:590), Figure 592 (SEQ ID NO:592), Figure 594 (SEQ ID NO:594), Figure 596 (SEQ ID NO:596), Figure 598 (SEQ ID NO:598), Figure 600 (SEQ ID NO:600), Figure 602 (SEQ ID NO:602), Figure 604 (SEQ ID NO:604), Figure 606 (SEQ ID NO:606), Figure 608 (SEQ ID NO:608), or Figure 610 (SEQ ID NO:610), lacking its associated signal peptide.

- 10 19. An isolated polypeptide having at least 80% amino acid sequence identity to:
- (a) an amino acid sequence of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194),

NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), Figure 244 (SEQ ID NO:244), Figure 246 (SEQ ID NO:246), Figure 248 (SEQ ID NO:248), Figure 250 (SEQ ID NO:250), Figure 252 (SEQ ID NO:252), Figure 254 (SEQ ID NO:254), Figure 256 (SEQ ID NO:256), Figure 258 (SEQ ID NO:258), Figure 260 (SEQ ID NO:260), Figure 262 (SEQ ID NO:262), Figure 264 (SEQ ID NO:264), Figure 266 (SEQ ID NO:266), Figure 268 (SEQ ID NO:268), Figure 270 (SEQ ID NO:270), Figure 272 (SEQ ID NO:272), Figure 274 (SEQ ID NO:274), Figure 276 (SEQ ID NO:276), Figure 278 (SEQ ID NO:278), Figure 280 (SEQ ID NO:280), Figure 282 (SEQ ID NO:282), Figure 284 (SEQ ID NO:284), Figure 286 (SEQ ID NO:286), Figure 288 (SEQ ID NO:288), Figure 290 (SEQ ID NO:290), Figure 292 (SEQ ID NO:292), Figure 294 (SEQ ID NO:294), Figure 296 (SEQ ID NO:296), Figure 298 (SEQ ID NO:298), Figure 300 (SEQ ID NO:300), Figure 302 (SEQ ID NO:302), Figure 304 (SEQ ID NO:304), Figure 306 (SEQ ID NO:306), Figure 308 (SEQ ID NO:308), Figure 310 (SEQ ID NO:310), Figure 312 (SEQ ID NO:312), Figure 314 (SEQ ID NO:314), Figure 316 (SEQ ID NO:316), Figure 318 (SEQ ID NO:318), Figure 320 (SEQ ID NO:320), Figure 322 (SEQ ID NO:322), Figure 324 (SEQ ID NO:324), Figure 326 (SEQ ID NO:326), Figure 328 (SEQ ID NO:328), Figure 330 (SEQ ID NO:330), Figure 332 (SEQ ID NO:332), Figure 334 (SEQ ID NO:334), Figure 336 (SEQ ID NO:336), Figure 338 (SEQ ID NO:338), Figure 340 (SEQ ID NO:340), Figure 342 (SEQ ID NO:342), Figure 344 (SEQ ID NO:344), Figure 346 (SEQ ID NO:346), Figure 348 (SEQ ID NO:348), Figure 350 (SEQ ID NO:350), Figure 352 (SEQ ID NO:352), Figure 354 (SEQ ID NO:354), Figure 356 (SEQ ID NO:356), Figure 358 (SEQ ID NO:358), Figure 360 (SEQ ID NO:360), Figure 362 (SEQ ID NO:362), Figure 364 (SEQ ID NO:364), Figure 366 (SEQ ID NO:366), Figure 368 (SEQ ID NO:368), Figure 370 (SEQ ID NO:370), Figure 372 (SEQ ID NO:372), Figure 374 (SEQ ID NO:374), Figure 376 (SEQ ID NO:376), Figure 378 (SEQ ID NO:378), Figure 380 (SEQ ID NO:380), Figure 382 (SEQ ID NO:382), Figure 384 (SEQ ID NO:384), Figure 386 (SEQ ID NO:386), Figure 388 (SEQ ID NO:388), Figure 390 (SEQ ID NO:390), Figure 392 (SEQ ID NO:392), Figure 394 (SEQ ID NO:394), Figure 396 (SEQ ID NO:396), Figure 398 (SEQ ID NO:398), Figure 400 (SEQ ID NO:400), Figure 402 (SEQ ID NO:402), Figure 404 (SEQ ID NO:404), Figure 406 (SEQ ID NO:406), Figure 408 (SEQ ID NO:408), Figure 410 (SEQ ID NO:410), Figure 412 (SEQ ID NO:412), Figure 414 (SEQ ID NO:414), Figure 416 (SEQ ID NO:416), Figure 418 (SEQ ID NO:418), Figure 420 (SEQ ID NO:420), Figure 422 (SEQ ID NO:422), Figure 424 (SEQ ID NO:424), Figure 426 (SEQ ID NO:426), Figure 428 (SEQ ID NO:428), Figure 430 (SEQ ID NO:430), Figure 432 (SEQ ID NO:432), Figure 434 (SEQ ID NO:434), Figure 436 (SEQ ID NO:436), Figure 438 (SEQ ID NO:438), Figure 440 (SEQ ID NO:440), Figure 442 (SEQ ID NO:442), Figure 444 (SEQ ID NO:444), Figure 446 (SEQ ID NO:446), Figure 448 (SEQ ID NO:448), Figure 450 (SEQ ID NO:450), Figure 452 (SEQ ID NO:452), Figure 454 (SEQ ID NO:454), Figure 456 (SEQ ID NO:456), Figure 458 (SEQ ID NO:458), Figure 460 (SEQ ID

NO:460), Figure 462 (SEQ ID NO:462), Figure 464 (SEQ ID NO:464), Figure 466 (SEQ ID NO:466), Figure 468 (SEQ ID NO:468), Figure 470 (SEQ ID NO:470), Figure 472 (SEQ ID NO:472), Figure 474 (SEQ ID NO:474), Figure 476 (SEQ ID NO:476), Figure 478 (SEQ ID NO:478), Figure 480 (SEQ ID NO:480), Figure 482 (SEQ ID NO:482), Figure 484 (SEQ ID NO:484), Figure 486 (SEQ ID NO:486), Figure 488 (SEQ ID NO:488), Figure 490 (SEQ ID NO:490), Figure 492 (SEQ ID NO:492), Figure 494 (SEQ ID NO:494), Figure 496 (SEQ ID NO:496), Figure 498 (SEQ ID NO:498), Figure 500 (SEQ ID NO:500), Figure 502 (SEQ ID NO:502), Figure 504 (SEQ ID NO:504), Figure 506 (SEQ ID NO:506), Figure 508 (SEQ ID NO:508), Figure 510 (SEQ ID NO:510), Figure 512 (SEQ ID NO:512), Figure 514 (SEQ ID NO:514), Figure 516 (SEQ ID NO:516), Figure 518 (SEQ ID NO:518), Figure 520 (SEQ ID NO:520), Figure 522 (SEQ ID NO:522), Figure 524 (SEQ ID NO:524), Figure 526 (SEQ ID NO:526), Figure 528 (SEQ ID NO:528), Figure 530 (SEQ ID NO:530), Figure 532 (SEQ ID NO:532), Figure 534 (SEQ ID NO:534), Figure 536 (SEQ ID NO:536), Figure 538 (SEQ ID NO:538), Figure 540 (SEQ ID NO:540), Figure 542 (SEQ ID NO:542), Figure 544 (SEQ ID NO:544), Figure 546 (SEQ ID NO:546), Figure 548 (SEQ ID NO:548), Figure 550 (SEQ ID NO:550), Figure 552 (SEQ ID NO:552), Figure 554 (SEQ ID NO:554), Figure 556 (SEQ ID NO:556), Figure 558 (SEQ ID NO:558), Figure 560 (SEQ ID NO:560), Figure 562 (SEQ ID NO:562), Figure 564 (SEQ ID NO:564), Figure 566 (SEQ ID NO:566), Figure 568 (SEQ ID NO:568), Figure 570 (SEQ ID NO:570), Figure 572 (SEQ ID NO:572), Figure 574 (SEQ ID NO:574), Figure 576 (SEQ ID NO:576), Figure 578 (SEQ ID NO:578), Figure 580 (SEQ ID NO:580), Figure 582 (SEQ ID NO:582), Figure 584 (SEQ ID NO:584), Figure 586 (SEQ ID NO:586), Figure 588 (SEQ ID NO:588), Figure 590 (SEQ ID NO:590), Figure 592 (SEQ ID NO:592), Figure 594 (SEQ ID NO:594), Figure 596 (SEQ ID NO:596), Figure 598 (SEQ ID NO:598), Figure 600 (SEQ ID NO:600), Figure 602 (SEQ ID NO:602), Figure 604 (SEQ ID NO:604), Figure 606 (SEQ ID NO:606), Figure 608 (SEQ ID NO:608), or Figure 610 (SEQ ID NO:610), lacking its associated signal peptide;

(b) an amino acid sequence of an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ

5
10
15
20
25
30
35

NO:382), Figure 384 (SEQ ID NO:384), Figure 386 (SEQ ID NO:386), Figure 388 (SEQ ID NO:388), Figure 390 (SEQ ID NO:390), Figure 392 (SEQ ID NO:392), Figure 394 (SEQ ID NO:394), Figure 396 (SEQ ID NO:396), Figure 398 (SEQ ID NO:398), Figure 400 (SEQ ID NO:400), Figure 402 (SEQ ID NO:402), Figure 404 (SEQ ID NO:404), Figure 406 (SEQ ID NO:406), Figure 408 (SEQ ID NO:408), Figure 410 (SEQ ID NO:410), Figure 412 (SEQ ID NO:412), Figure 414 (SEQ ID NO:414), Figure 416 (SEQ ID NO:416), Figure 418 (SEQ ID NO:418), Figure 420 (SEQ ID NO:420), Figure 422 (SEQ ID NO:422), Figure 424 (SEQ ID NO:424), Figure 426 (SEQ ID NO:426), Figure 428 (SEQ ID NO:428), Figure 430 (SEQ ID NO:430), Figure 432 (SEQ ID NO:432), Figure 434 (SEQ ID NO:434), Figure 436 (SEQ ID NO:436), Figure 438 (SEQ ID NO:438), Figure 440 (SEQ ID NO:440), Figure 442 (SEQ ID NO:442), Figure 444 (SEQ ID NO:444), Figure 446 (SEQ ID NO:446), Figure 448 (SEQ ID NO:448), Figure 450 (SEQ ID NO:450), Figure 452 (SEQ ID NO:452), Figure 454 (SEQ ID NO:454), Figure 456 (SEQ ID NO:456), Figure 458 (SEQ ID NO:458), Figure 460 (SEQ ID NO:460), Figure 462 (SEQ ID NO:462), Figure 464 (SEQ ID NO:464), Figure 466 (SEQ ID NO:466), Figure 468 (SEQ ID NO:468), Figure 470 (SEQ ID NO:470), Figure 472 (SEQ ID NO:472), Figure 474 (SEQ ID NO:474), Figure 476 (SEQ ID NO:476), Figure 478 (SEQ ID NO:478), Figure 480 (SEQ ID NO:480), Figure 482 (SEQ ID NO:482), Figure 484 (SEQ ID NO:484), Figure 486 (SEQ ID NO:486), Figure 488 (SEQ ID NO:488), Figure 490 (SEQ ID NO:490), Figure 492 (SEQ ID NO:492), Figure 494 (SEQ ID NO:494), Figure 496 (SEQ ID NO:496), Figure 498 (SEQ ID NO:498), Figure 500 (SEQ ID NO:500), Figure 502 (SEQ ID NO:502), Figure 504 (SEQ ID NO:504), Figure 506 (SEQ ID NO:506), Figure 508 (SEQ ID NO:508), Figure 510 (SEQ ID NO:510), Figure 512 (SEQ ID NO:512), Figure 514 (SEQ ID NO:514), Figure 516 (SEQ ID NO:516), Figure 518 (SEQ ID NO:518), Figure 520 (SEQ ID NO:520), Figure 522 (SEQ ID NO:522), Figure 524 (SEQ ID NO:524), Figure 526 (SEQ ID NO:526), Figure 528 (SEQ ID NO:528), Figure 530 (SEQ ID NO:530), Figure 532 (SEQ ID NO:532), Figure 534 (SEQ ID NO:534), Figure 536 (SEQ ID NO:536), Figure 538 (SEQ ID NO:538), Figure 540 (SEQ ID NO:540), Figure 542 (SEQ ID NO:542), Figure 544 (SEQ ID NO:544), Figure 546 (SEQ ID NO:546), Figure 548 (SEQ ID NO:548), Figure 550 (SEQ ID NO:550), Figure 552 (SEQ ID NO:552), Figure 554 (SEQ ID NO:554), Figure 556 (SEQ ID NO:556), Figure 558 (SEQ ID NO:558), Figure 560 (SEQ ID NO:560), Figure 562 (SEQ ID NO:562), Figure 564 (SEQ ID NO:564), Figure 566 (SEQ ID NO:566), Figure 568 (SEQ ID NO:568), Figure 570 (SEQ ID NO:570), Figure 572 (SEQ ID NO:572), Figure 574 (SEQ ID NO:574), Figure 576 (SEQ ID NO:576), Figure 578 (SEQ ID NO:578), Figure 580 (SEQ ID NO:580), Figure 582 (SEQ ID NO:582), Figure 584 (SEQ ID NO:584), Figure 586 (SEQ ID NO:586), Figure 588 (SEQ ID NO:588), Figure 590 (SEQ ID NO:590), Figure 592 (SEQ ID NO:592), Figure 594 (SEQ ID NO:594), Figure 596 (SEQ ID NO:596), Figure 598 (SEQ ID NO:598), Figure 600 (SEQ ID NO:600), Figure 602 (SEQ ID NO:602), Figure 604 (SEQ ID NO:604), Figure 606 (SEQ ID NO:606), Figure 608 (SEQ ID NO:608), or Figure 610 (SEQ ID NO:610), with its associated signal peptide; or

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure

34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40),
Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID
NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ
ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64
(SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure
5 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78),
Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID
NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ
ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102
(SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108),
10 Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ
ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure
124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID
NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure
138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID
15 NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure
152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID
NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure
166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID
NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure
20 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID
NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure
194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID
NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure
208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID
25 NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure
222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID
NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure
236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID
NO:242), Figure 244 (SEQ ID NO:244), Figure 246 (SEQ ID NO:246), Figure 248 (SEQ ID NO:248), Figure
30 250 (SEQ ID NO:250), Figure 252 (SEQ ID NO:252), Figure 254 (SEQ ID NO:254), Figure 256 (SEQ ID
NO:256), Figure 258 (SEQ ID NO:258), Figure 260 (SEQ ID NO:260), Figure 262 (SEQ ID NO:262), Figure
264 (SEQ ID NO:264), Figure 266 (SEQ ID NO:266), Figure 268 (SEQ ID NO:268), Figure 270 (SEQ ID
NO:270), Figure 272 (SEQ ID NO:272), Figure 274 (SEQ ID NO:274), Figure 276 (SEQ ID NO:276), Figure
278 (SEQ ID NO:278), Figure 280 (SEQ ID NO:280), Figure 282 (SEQ ID NO:282), Figure 284 (SEQ ID
35 NO:284), Figure 286 (SEQ ID NO:286), Figure 288 (SEQ ID NO:288), Figure 290 (SEQ ID NO:290), Figure
292 (SEQ ID NO:292), Figure 294 (SEQ ID NO:294), Figure 296 (SEQ ID NO:296), Figure 298 (SEQ ID
NO:298), Figure 300 (SEQ ID NO:300), Figure 302 (SEQ ID NO:302), Figure 304 (SEQ ID NO:304), Figure

5
10
15
20
25
30
35

572 (SEQ ID NO:572), Figure 574 (SEQ ID NO:574), Figure 576 (SEQ ID NO:576), Figure 578 (SEQ ID NO:578), Figure 580 (SEQ ID NO:580), Figure 582 (SEQ ID NO:582), Figure 584 (SEQ ID NO:584), Figure 586 (SEQ ID NO:586), Figure 588 (SEQ ID NO:588), Figure 590 (SEQ ID NO:590), Figure 592 (SEQ ID NO:592), Figure 594 (SEQ ID NO:594), Figure 596 (SEQ ID NO:596), Figure 598 (SEQ ID NO:598), Figure 600 (SEQ ID NO:600), Figure 602 (SEQ ID NO:602), Figure 604 (SEQ ID NO:604), Figure 606 (SEQ ID NO:606), Figure 608 (SEQ ID NO:608), or Figure 610 (SEQ ID NO:610), lacking its associated signal peptide.

20. A method for stimulating the release of TNF- α from human blood, said method comprising contacting said blood with a PRO1079, PRO827, PRO791, PRO1131, PRO1316, PRO1183, PRO1343, PRO1760, PRO1567 or PRO4333 polypeptide, wherein the release of TNF- α from said blood is stimulated.

10

21. A method for stimulating the proliferation or differentiation of chondrocyte cells, said method comprising contacting said cells with a PRO6029 polypeptide, wherein the proliferation or differentiation of said cells is stimulated.

15

22. A method for detecting the presence of tumor in an mammal, said method comprising comparing the level of expression of any PRO polypeptide shown in Table 8 in (a) a test sample of cells taken from said mammal and (b) a control sample of normal cells of the same cell type, wherein a higher level of expression of said PRO polypeptide in the test sample as compared to the control sample is indicative of the presence of tumor in said mammal.

20

23. The method of Claim 22, wherein said tumor is adrenal tumor, lung tumor, colon tumor, breast tumor, prostate tumor, rectal tumor, cervical tumor or liver tumor.

24. An oligonucleotide probe derived from any of the nucleotide sequences shown in the accompanying figures.

25

1/615

FIGURE 1

GAAGGCTGCCTCGCTGGTCCGAATTCGGTGGCGCCACGTCCGCCCGTCTCCGCCTTCTGCATCGCGGCTTCGGCG
GCTTCCACCTAGACACCTAACAGTCGCGGAGCCGGCCGCGTCTGAGGGGGTTCGGCACGGGGAGTCGGGCGGTCT
TGTGCATCTTGGCTACCTGTGGGTCCAAGATGTCGGACATCGGAGACTGGTTCAGGAGCATCCCGGCGATCACGC
GCTATTGGTTCGCGCCACCGTCGCCGTGCCCTTGGTCCGCAAACTCGGCCCTCATCAGCCCGGCTACCTCTTCC
TCTGGCCCCGAAGCCTTCCTTTATCGCTTTCAGATTTGGAGGCCAATCACTGCCACCTTTTATTTCCCTGTGGGT
CAGGAACCTGGATTTCTTTATTTGGTCAATTTATTTCTTATATCAGTATTCTACGCGACTTGAACAGGAGCTT
TTGATGGGAGGCCAGCAGACTATTTATTCATGCTCCTCTTTAACTGGATTTGCATCGTGATTACTGGCTTAGCAA
TGGATATGCAGTTGCTGATGATTCCTCTGATCATGTCACTACTTTATGTCTGGGCCAGCTGAACAGAGACATGA
TTGTATCATTTTGGTTTGGACACGATTAAAGGCCTGCTATTTACCCTGGGTATCCTTGGATTCAACTATATCA
TCGGAGGCTCGGTAATCAATGAGCTTATTGAAATCTGGTTGGACATCTTTATTTTTTCTAATGTTTCAGATACC
CAATGGACTTGGGAGGAAGAAATTTCTATCCACACCTCAGTTTTTGTACCGCTGGCTGCCAGTAGGAGAGGAG
GAGTATCAGGATTTGGTGTGCCCCCTGCTAGCATGAGGCGAGCTGCTGATCAGAATGGCGGAGGCCGGAGACACA
ACTGGGGCCAGGGCTTTCGACTTGGAGACCAGTGAAGGGCGGCCCTCGGGCAGCCGCTCCTCTCAAGCCACATTT
CCTCCCAGTGCTGGGTGCCTTAACAACTGCGTTCTGGCTAACACTGTTGGACCTGACCCACACTGAATGTAGTC
TTTCAGTACGAGACAAAGTTTCTTAAATCCCGAAGAAAAATATAAGTGTTCCACAAGTTTTCACGATTCTCATTCA
AGTCTTACTGCTGTGAAGAACAATACCAACTGTGCAAACTGACTACATTTTTTGGTGCTTCTCT
TCTCCCTTTTCCGTATGAATAATGGGTTTAGCGGGTCCCTAATCTGCTGGCATTGAGCTGGGGCTGGGTACCAA
ACCTTCCCAAAGGACCTTATCTCTTCTTGCACACATGCCTCTCTCCACTTTTCCCAACCCCAACATTTGCA
ACTAGAAAAAGTTGCCCATAAATTTGCTCTGCCCTTGACAGGTTCTGTTATTTATTGACTTTTGCCAAGGCTGGT
CACAAACATCATATTCACGTTATTTTCCCTTTTGGTGGCAGAACTGTTACCAATAGGGGGAGAAAGACAGCCACG
GATGAAGCGTTTCTCAGCTTTTGAATTTGCTTCGACTGACATCCGTTGTTAACCCTTTGCCACTCTTCAGATATT
TTTTATAAAAAAGTACCACTGAGTTCATGAGGGCCACAGATTGGTTATTAATGAGATACGAGGTTGGTGCTGG
GTGTTTGTTCCTGAGCTAAGTGATCAAGACTGTAGTGAGTTGCAGCTAACATGGGTTAGGTTTAAACCATGGG
GGATGCACCCCTTTGCGTTTCATATGTAGCCCTACTGGCTTTGTGTAGCTGGAGTAGTTGGGTTGCTTTGTGTTA
GGAGGATCCAGATCATGTTGGCTACAGGGAGATGCTCTCTTTGAGAGGTCCTGGGCATTGATTCCCATTTCAATC
TCATTCTGGATATGTGTTTCATTGAGTAAAGGAGGAGAGCCCTCATACGCTATTTAAATGTCACCTTTTTTGCTA
TCCCCGTTTTTTGGTCATGTTTCAATTAATGTGAGGAAGGCGAGCTCCTCTCTGCACGTAGATCATTTTTTA
AAGCTAATGTAAGCACATCTAAGGGAATAACATGATTTAAGGTTGAAATGGCTTTAGAATCATTTGGGTTTGAGG
GTGTGTTATTTTGTGATCATGAATGTACAAGCTCTGTGAATCAGACCAGCTTAAATACCCACACCTTTTTTTCGTA
GGTGGGCTTTTCTATCAGAGCTTGGCTCATAACCAATAAAGTTTTTTGAAGGCCATGGCTTTTACACAGTTA
TTTTATTTTATGACGTTATCTGAAAGCAGACTGTTAGGAGCAGTATTGAGTGGCTGTACACTTTGAGGCAACTA
AAAAGGCTTCAAACGTTTTGATCAGTTTCTTTTCAGGAACATTGTGCTCTAACAGTATGACTATTCTTTCCCC
ACTCTTAAACAGTGTGATGTGTGTTATCCTAGGAAATGAGAGTTGGCAAACAACCTCTCATTTTGAATAGAGTTT
GTGTGTAATTTCTCCATATTTAATTTATATGATAAAATAGGTGGGGAGAGTCTGAACCTTAAGTGTATGTTTTGT
TGTTTCATCTGTGGCCACAATAAAGTTTACTTGTAAATTTTAGAGGCCATTACTCCAATTATGTTGCACGTACAC
TCATTGTACAGGCGTGGAGACTCATTGTATGTATAAGAATATTTCTGACAGTGAGTGACCCGGAGTCTCTGGTGT
ACCTCTTACCAGTCAGCTGCCTGCGAGCAGTCATTTTTTCTAAAGGTTTACAAGTATTTAGAACTTTTCAGTT
CAGGGCAAAATGTTTCATGAAGTTATTCCTCTTAAACATGGTTAGGAAGCTGATGACGTTATTGATTTTGTCTGGA
TTATGTTTCTGGAATAATTTTACCAAAACAAGCTATTTGAGTTTGTGACTTGACAAGGCAAAACATGACAGTGGAT
TCTCTTTACAAATGGAAAAAAAATCCTTATTTGTATAAAGGACTTCCCTTTTTGTAAACTAATCCTTTTTAT
TGGTAAAAATGTAAATTAATGTGCAACTTG

2/615

FIGURE 2

MSDIGDWERSIPATRYWFAATVAVPLVGKLGGLISPAYLFLWPEAFLYRFQIWRPITATFFYPVGP GTGFLYLVN
LYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLLMIPLIMSVLYVWAQLNRDMIVSFWFGTRF
KACYLPWVILGFNYIIGGSVINELIGNLVGHLYFFLMFRYPMDLGGRNFLSTPQFLYRWLPSRRGGVSGFGVPPA
SMRRAADQNGGGGRHNWGQGFR LGDQ

Transmembrane domain:

amino acids 98-116, 152-172

N-myristoylation site.

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

Glycosaminoglycan attachment site.

amino acids 218-222

3/615

FIGURE 3

GAGCGAGGCCGGGGACTGAAGGTGTGGGTGTGCGAGCCCTCTGGCAGAGGGTTAACCTGGGTCAAATGCACGGATT
CTCACCTCGTACAGTTACGCTCTCCCGCGGCACGTCCGCGAGGACTTGAAGTCCTGAGCGCTCAAGTTTGTCCGT
AGGTCGAGAGAAGGCCATGGAGGTGCCGCCACCGGCACCGCGAGCTTTCTCTGTAGAGCATTGTGCCTATTTCC
CCGAGTCTTTGCTGCCGAAGCTGTGACTGCCGATTCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGT
CCCAGAGCCCTATTACCCGGAATCTGGATGGGACCGCCTCCGGGAGCTGTTGGCAAAGATGAACAGCAGAGAAT
TTCAAAGGACCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGAATACC
AGCTTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATCATAACCGGTTTGATGCTGT
GCAATCTGCACATCGTGCTGCCACACGAGGCTTCATTGTTATGGCTGGCGCTGGGCTTGGAGAAGTGCAGTGTT
TGTGACTATATTCAACACAGTGAACACTAGTCTGAATGTATACCGAAATAAAGATGCCTTAAGCCATTTTGTAAAT
TGCAGGAGCTGTACGGGAAGTCTTTTAGGATAAACGTAGGCCTGCCGTGGCCTGGTGGCTGGTGGCATAATTGG
AGCCTTGCTGGGCACTCCTGTAGGAGGCCTGCTGATGGCATTTCAGAAGTACGCTGGTGAGACTGTTTCAGGAAAG
AAAACAGAAGGATCGAAAGGCACTCCATGAGCTAAAAGTGGAAAGTGGAAAGGCAGACTACAAGTTACTGAGCA
CCTCCCTGAGAAAATTGAAAGTAGTTTACGGGAAGATGAACCTGAGAATGATGCTAAGAAAATTGAAGCACTGCT
AAACCTTCCTAGAAACCCTTCAGTAATAGATAAACAAGACAAGGACTGAAAGTGCCTGAACTTGAAACTCACTG
GAGAGCTGAAGGGAGCTGCCATGTCCGATGAATGCCAACAGACAGGCCACTCTTTGGTCAGCCTGCTGACAAATT
TAAGTCTGGTACCTGTGGTGGCAGTGGCTTGTCTTTTTCTTTCTTTTAACTAAGAATGGGGCTGTT
GTACTCTCACTTTACTTATCCTTAAATTTAAATACATACTTATGTTTGTATTAACTATCAATATATGCATACAT
GGATATATCCACCCACCTAGATTTTAAAGCAGTAAATAAAACATTTTCGCAAAAGATTAAAGTTGAATTTTACAGTTT

4/615

FIGURE 4

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23318
><subunit 1 of 1, 285 aa, 1 stop
><MW: 32190, pI: 9.03, NX(S/T): 2
MEVPPPPAPRSFLCRALCLFPRVFAAEAVTADSEVLEERQKRLPYVPEPYYPESGWDRLRELFQKDEQQRISKDLA
NICKTAATAGIIGWVYGGIPAFIHAKQQYIEQSQAETIYHNRFDAVQSAHRAATRGFIRYGWRWGWRRTAVFVTIFN
TVNTSLNVYRNKDLSHFVIAGAVTGSLFRINVGLRGLVAGGIIGALLGTPVGGLLMAFQKYAGETVQERKQKDR
KALHELKLEEWKGRILQVTEHLPEKIESSLREDEPENDAKKIEALLNLPRNPSVIDKQDKD

Important Features:**Signal Peptide:**

amino acids 1-24

Transmembrane domains:

amino acids 76-96 and 171-195

N-glycosylation site:

amino acids 153-156

5/615

FIGURE 5

CGGACGCGTGGGCGCGGGACGCCGCGAGGGTTGTGGCGCAGCAGTCTCCTTCCTGCGCGCGCGCCTGAAGTCGGC
GTGGGCGTTTTGAGGAAGCTGGGATACAGCATTTAATGAAAAATTTATGCTTAAGAAGTAAAAATGGCAGGCTTCC
TAGATAATTTTCGTTGGCCAGAATGTGAATGTATTGACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTGCG
CAGGTATATTGTTTTTACAGGCTGGTGGATAATGATTGATGCAGCTGTGGTGTATCCTAAGCCAGAACAGTTGA
ACCATGCCTTTCACACATGTGGTGTATTTCCACATTGGCTTCTTCATGATAAATGCTGTATCCAATGCTCAGG
TGAGAGGTGATAGCTATGAAAGCGGCTGTTTAGGAAGAACAGGTGCTCGAGTTTGGCTTTTCATTGGTTTCATGT
TGATGTTTGGGTCACCTTATTGCTTCCATGTGGATTCTTTTGGTGCATATGTTACCCAAAATACTGATGTTTATC
CGGGACTAGCTGTGTTTTTCAAATGCACTTATATTTTTTAGCACTCTGATCTACAAATTTGGAAGAACCGAAG
AGCTATGGACCTGAGATCACTTCTTAAGTCACATTTTCTTTTGTATATTCTGTTGTAGATAGGTTTTTTATC
TCTCAGTACACATTGCCAAATGGAGTAGATTGTACATTAATGTTTTGTTTCTTTACATTTTTATGTTCTGAGTT
TTGAAATAGTTTTATGAAATTTCTTATTTTTTCAATGCATAGACTGTTAATATGTATATAATAAGACTATATG
AATTGGATAATGAGTATCAGTTTTTTATTCCTGAGATTTAGAACTTGATCTACTCCCTGAGCCAGGTTACATCA
TCTTGTCATTTTAGAAGTAACCACTCTTGTCTCTCTGGCTGGGCACGGTGGCTCATGCCTGTAATCCCAGCACTT
TGGGAGGCCGAGGCGGGCCGATTGCTTGAGGTCAAGTGTGTTGAGACCAGCCTGGCCAACATGGCGAAACCCCATC
TACTAAAAATACAAAATTAGCCAGGCATGGTGGTGGGTGCCTGTAATCCCAGCTACCTGGGAGGCTGAGGCAGG
AGAATCGCTTGAACCCGGGGGGCAGAGGTTGCAGTGAGCTGAGTTTGCGCCACTGCACTCTAGCCTGGGGGAGAA
AGTGAAACTCCCTCTCAAAAAAAGACCACTCTCAGTATCTCTGATTTCTGAAGATGTACAAAAAATATAGCTT
CATATATCTGGAATGAGCACTGAGCCATAAAAGGTTTTTCAGCAAGTTGTAACCTATTTTGGCCTAAAAATGAGGT
TTTTTTGGTAAAGAAAAAATATTTGTTCTTATGTATTGAAGAAGTGTACTTTTATATAATGATTTTTTAAATGCC
CAAAGGACTAGTTTGAAAGCTTCTTTTAAAAAGAATTCCTCTAATATGACTTTTATGTGAGAA

6/615

FIGURE 6

MAGFLDNFRWPECECIDWSERRNAVASVVAGILFFTGWIMIDAADVYPKPEQLNHAFHTCGVFSTLAFFMINAV
SNAQVRGDSYESGCLGRTGARVWLFIFGMLMFGSLIASMWILFGAYVTQNTDVYPGLAVFFQNALIFFSTLIYKF
GRTEELWT

Important features:

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 23-42 (type II), 60-80, 97-117, 128-148

7/615

FIGURE 7

GCCTGGTTTTTGTCTGCAATAGGCGGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTGTAGCTTCTCCACG
TATGGACCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAGGATGTGCGTTCTTC
CACTAGAAGCTCTTCTGAGGGAGGTAATTAACAAACAGTGGAAATGGAAAAACAGTGCTGTAGTCATCCTGTAATA
TGCTCCTTGTCAACAATGTATACATTCTGCTAGGTGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTA
GTGAAGTATTCTGCCAATGAAGAAAACAAGTATGATTATCTTCCAACACTGTGAATGTGTGCTCAGAACTGGTG
AAGCTAGTTTTCTGTGTGCTTGTGTCAATTCTGTGTTATAAAGAAAGATCATCAAAGTAGAAATTTGAAATATGCT
TCCTGGAAGGAATTCCTGATTTTCATGAAGTGGTCCATTCTGCTTTCTTTATTTCTGGATAACTTGATTGTC
TTCTATGCTCTGCTATCTTCAACCAGCCATGGCTGTTATCTTCTCAAATTTTAGCATTATAACACAGCTCTT
CTATTCAGGATAGTGCTGAAGAGGCGTCTAACTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATT
GTGGCCTTGACTGCCGGGACTAAAACCTTTACAGCACAACCTTGGCAGGACGTGGATTTCATCACGATGCCCTTTTC
AGCCCTTCCAATTCCTGCCTTCTTTTCAGAAAGTGAGTGTCCCAGAAAAGACAATTGTACAGCAAAGGAATGGACT
TTTCCTGAAGCTAAATGGAACACCACAGCCAGAGTTTTTCAGTCACATCCGTCTTGGCATGGGCCATGTTCTTATT
ATAGTCCAGTGTTTTATTTCTTCAATGGCTAATATCTATAATGAAAAGATACTGAAGGAGGGGAACAGCTCACT
GAAAGCATCTTCATACAGAACAGCAAACCTCTATTTCTTTGGCATTCTGTTTAAATGGGCTGACTCTGGGCCTTCAG
AGGAGTAACCGTGATCAGATTAAGAAGTGTGGATTTTTTATGGCCACAGTGCATTTTCAGTAGCCCTTATTTTT
GTAACCTGCATTCCAGGGCCTTTCAGTGGCTTTCATTCTGAAGTTCCTGGATAACATGTTCCATGCTTGTATGGCC
CAGGTTACCAGTGTCTATATCACAACAGTGTCTGTCTGGTCTTTGACTTCAGGCCCTCCCTGGAATTTTTCTTG
GAAGCCCCATCAGTCTTCTCTCTATATTTATTTATAATGCCAGCAAGCCTCAAGTTCGGGAATACGCACCTAGG
CAAGAAAGGATCCGAGATCTAAGTGGCAATCTTTGGGAGCGTTCAGTGGGGATGGAGAAGAACTAGAAAGACTT
ACCAAACCAAGAGTGATGAGTCAGATGAAGATACTTTCTAACTGGTACCCACATAGTTTGCAGCTCTCTTGAAC
CTTATTTTTCACATTTTCAGTGTGTTGTAATATTTATCTTTTCACTTTGATAAACCAGAAATGTTTCTAAATCCTAA
TATTCCTTTCATATATCTAGTACTCCCTAAATGGTTCCATCCAAGGCTTAGAGTACCCAAAGGCTAAGAAATTC
TAAAGAACTGATACAGGAGTAACAATATGAAGAATTCATTAATATCTCAGTACTTGATAAATCAGAAAGTTATAT
GTGCAGATTATTTTCCCTTGGCCTTCAAGCTTCCAAAAAAGTGTGAATAATCATGTTAGCTATAGCTTGTATATAC
ACATAGAGATCAATTTGCCAAATATTCACAATCATGTAGTTCTAGTTTACATGCCAAAGTCTTCCCTTTTTAACA
TTATAAAAGCTAGGTTGTCTCTTGAATTTTGAGGCCCTAGAGATAGTCATTTTGCAAGTAAGAGCAACGGGACC
CTTCTTAAAAACGTTGGTTGAAGGACCTAAATACCTGGCCATACCATAGATTTGGGATGATGTAGTCTGTGCTAA
ATATTTTGCTGAAGAAGCAGTTTCTCAGACACAACATCTCAGAATTTTAATTTTAGAAATTCATGGGAAATTGG
ATTTTGTGAATAATCTTTTGTATGTTTTAAACATTGGTTCCCTAGTCACCATAGTTTACCACTTGTATTTTAAGTCA
TTTAAACAAGCCACGGTGGGGCTTTTTCTCCTCAGTTTGAGGAGAAAAATCTTGATGTCATTACTCCTGAATTA
TTACATTTTGGAGAATAAGAGGGCATTATTTTATTAGTTACTAATTCAAGCTGTGACTATTGTATATCTTTCC
AAGAGTTGAAATGCTGGCTTCAGAATCATACCAGATTGTGAGTGAAGCTGATGCCCTAGGAACTTTAAAGGGATC
CTTTCAAAGGATCACTTAGCAAACACATGTTGACTTTTAACTGATGTATGAATATTAATACTCTAAAAATAGAA
AGACCAGTAATATATAAGTCACTTTACAGTGTACTTCACTTAAAAGTGCATGGTATTTTTTCATGGTATTTTG
CATGCAGCCAGTTAACTCTCGTAGATAGAGAAGTCAGGTGATAGATGATATTAATAATAGCAAAACAAAGTGAC
TTGCTCAGGGTCATGCAGCTGGGTGATGATAGAAGAGTGGGCTTAACTGGCAGGCCTGTATGTTTACAGACTAC
CATACTGTAAATATGAGCTTTATGGTGTCAATTCAGAAACTTATACATTTCTGCTCTCCTTTCTCCTAAGTTTC
ATGCAGATGAATATAAGGTAATATACTATTATATAATTCATTTGTGATATCCACAATAATATGACTGGCAAGAAT
TGGTGGAAATTTGTAATTAAATAATTATTAAACCT

8/615

FIGURE 8

MEKQCCSHPVICSLSTMYTFLLGAIFIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVKLVFCVLVSFCVIK
KDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLPAMAVIFS NFSIITTALLFRIVLKRRLNWIQ
WASLLTLFLSIVALTAGTKTLQHNLGRGFHHDAFFSPSNSCLLFRSECPRKDNCTAKEWTFPEAKWNTTARVFS
HIRLGMGHVLIIVQCFISSMANIYNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRSNRDQIKNCGFFY
GHSAFSVALIFVTAFQGLSVAFILKFLDNMFHVLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFIYNA
SKPQVPEYAPRQERIRDLSGNLWERSSSGDGEELERLTKPKSDEDEDTF

Transmembrane domains:

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293, 298-318,
328-368

N-glycosylation sites.

amino acids 128-132, 204-208, 218-222, 374-378

Glycosaminoglycan attachment site.

amino acids 402-406

N-myristoylation sites.

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

9/615

FIGURE 9

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGTATGAGCAGGTCTG
AAGACTAACATTTTTGTGAAGTTGTAAAACAGAAAACCTGTTAGAAATGTGGTGGTTTCAGCAAGGCCTCAGTTTC
CTTCCTTCAGCCCTTGTAAATTTGGACATCTGCTGCTTTCATATTTTCATACATTACTGCAGTAACACTCCACCAT
ATAGACCCGGCTTTACCTTATATCAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTA
AATATTGCGGCAGTTTTATGCATTGCTACCATTTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAAGAG
AACGTTATCATCAAATTAACAAGGCTGGCCTTGTACTTGAATACTGAGTTGTTTAGGACTTCTATTGTGGCA
AACTTCCAGAAAACAACCCTTTTGCTGCACATGTAAGTGGAGCTGTGCTTACCTTTGGTATGGGCTCATTATAT
ATGTTTGTTCAGACCATCCTTTCCTACCAAATGCAGCCCAAATCCATGGCAAACAAGTCTTCTGGATCAGACTG
TTGTTGGTTATCTGGTGTGGAGTAAGTGCACCTTAGCATGCTGACTTGCTCATCAGTTTGCACAGTGGCAATTTT
GGGACTGATTTAGAACAGAACTCCATTGGAACCCCGAGGACAAAGGTTATGTGCTTCACATGATCACTACTGCA
GCAGAAATGGTCTATGTCATTTTCCTTCTTTGGTTTTTTCCTGACTTACATTTCGTGATTTTCAGAAAATTTCTTTA
CGGGTGGAAGCCAATTTACATGGATTAAACCCTCTATGACACTGCACCTTGCCCTATTAACAATGAACGAACACGG
CTACTTTCCAGAGATATTTGATGAAAGGATAAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGG
TTCACAGAAGTTGCTTATTCTTCTCTGAAATTTCAACCACCTAATCAAGGCTGACAGTAACACTGATGAATGCT
GATAATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTCTAAAGGATATCATCAAGAAGACTATTAAAAACA
CCTATGCCTATACTTTTTTATCTCAGAAAATAAAGTCAAAAGACTATG

10/615

FIGURE 10

MWWFQQGLSFLPSALVIWTSAAFIIFS YITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAVLCIATIIYVRY
KQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSGAVLTFGMGSLYMFVQTILSYQMOPKI
HGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSGNFGTDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFFLT
YIRDFQKISLRVEANLHGLTLYDTAPCPINNERTRLLSRDI

11/615

FIGURE 11

CCCACGCGTCCGCCCCGCGCTGCGTCCCGGAGTGCAAGTGAGCTTCTCGGCTGCCCCGCGGGCCGGGGTGCGGAG
CCGACATGCGCCCCGCTTCTCGGCTCCTTCTGGTCTTCGCCGGCTGCACCTTCGCCTTGCTACTTGCTGTCGACGC
GACTGCCCCGCGGGCGGAGACTGGGCTCCACCGAGGAGGCTGGAGGCAGGTCGCTGTGGTTCCCTCCGACCTGG
CAGAGCTGCGGGAGCTCTCTGAGGTCTTCGAGAGTACCGGAAGGAGCACCAGGCCTACGTGTTCTGCTCTTCT
GCGGCGCCTACCTCTACAAAACAGGGCTTTGCCATCCCCGGCTCCAGCTTCTGAATGTTTTAGCTGGTGCCTTGT
TTGGGCCATGGCTGGGGCTTCTGCTGTCTGTGTGTTGACCTCGGTGGGTGCCACATGCTGCTACCTGCTCTCCA
GTATTTTTGGCAAACAGTTGGTGGTGTCTACTTTCTGATAAAGTGGCCCTGCTGCAGAGAAAGGTGGAGGAGA
ACAGAAACAGCTTGTTTTTTTTCTTATTGTTTTTGAGACTTTTCCCCATGACACCAAACCTGGTCTTGAACCTCT
CGGCCCCAATTCTGAACATTCCCATCGTGCAGTTCTTCTCTCAGTTCTTATCGGTTTGATCCCATATAATTTCA
TCTGTGTGCAGACAGGGTCCATCCTGTCAACCCTAACCTCTCTGGATGCTCTTTCTCCTGGGACACTGTCTTTA
AGCTGTTGGCCATTGCCATGGTGGCATTAAATTCCTGGAACCCCTATTAAAAAATTTAGTCAGAAACATCTGCAAT
TGAATGAAACAAGTACTGCTAATCATATACACAGTAGAAAAGACACATGATCTGGATTTTCTGTTTGCCACATCC
CTGGACTCAGTTGCTTATTTGTGTAATGGATGTGGTCTCTAAAGCCCCTCATTGTTTTTGATTGCCTTCTATAG
GTGATGTGGACACTGTGCATCAATGTGCAGTGTCTTTTCAGAAAGGACACTCTGCTCTTGAAGGTGTATTACATC
AGGTTTTCAAACCAGCCCTGGTGTAGCAGACACTGCAACAGATGCCTCCTAGAAAAATGCTGTTTGTGGCCGGGCG
CGGTGGCTCACGCCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCCGGTGATTACAAAGGTCAGGAGTTCAAGACC
AGCCTGGCCAAGATGGTGAATCCTGTCTCTAATAAAAAATACAAAAATTAGCCAGGCGTGGTGGCAGGCACCTGT
AATCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATTGCTTGAACCAAGGTGGCAGAGGTTGCAGTAAGCCAAGAT
CACACCACTGCACCTCCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

12/615

FIGURE 12

MRPLLGLLLVFAGCTFALYLLSTRLPGRRLGSTEEAGGRSLWFPSDLAELRELVREYRKEHQAYVFLFCG
AYLYKQGFAIPGSSFLNVLGALFGPWLGLLCCVLTSGATCCYLLSSIFGKQLVVSYPDKVALLQRKVEENR
NSLFFFLFLRLFPMPNWFNLNLSAPILNIPVQFFSVLIGLIPYNFICVQTGSILSTLTSLDALFSWDTVFKL
LAIAMVALIPGTLIKFSQKHLQLNETSTANHIHSRKDT

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domains:

amino acids 101-123, 189-211

N-glycosylation sites.

amino acids 172-176, 250-254

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 240-244, 261-265

N-myristoylation site.

amino acids 13-19, 104-110, 115-121, 204-210

Amidation site.

amino acids 27-31

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 4-15

Protein splicing proteins.

amino acids 25-31

Sugar transport proteins.

amino acids 162-172

13/615

FIGURE 13

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGAGTCCCGGCTGCAGCACCTGGGAGAAGGCAGACCGTGTGAG
GGGGCCCTGTGGCCCCAGCGTGCTGTGGCCTCGGGGAGTGGGAAGTGGAGGCAGGAGCCCTTCCTTACACTTCGCCA
TGAGTTTCTCATCGACTCCAGCATCATGATTACCTCCCAGATACTATTTTTTGGATTTGGGTGGCTTTTCTTCA
TGCGCCAAATTGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAGGTGATCTTCTCCGTGACGTTTGCATTTT
CTTGACCATGTTTGTAGCTCATCATCTTTGAAATCTTAGGAGTATTGAATAGCAGCTCCCGTTATTTTCACTGGA
AAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTTTTCATGGTGCCTTTTTACATTGGCTATTTTATTGTGAGCA
ATATCCGACTACTGCATAAACAACGACTGCTTTTTTCTGTCTCTTATGGCTGACCTTTATGTATTTCTTCTGGA
AACTAGGAGATCCCTTTCCCATCTCAGCCCAAACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTTG
GTGTGATTGGAGTGACTCTCATGGCTCTTCTTTCTGGATTTGGTGTGTCAACTGCCCATACACTTACATGTCTT
ACTTCCCTCAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATATGATCA
TAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAAGTGCATAACAAACCATCAG
GTTTCTGGGGAATGATAAAAAGTGTACCCTTCAGCATCAGGAAGTGAAAATCTTACTCTTATTCAACAGGAAG
TGGATGCTTTGGAAGAATTAAGCAGGCAGCTTTTTCTGGAACAGCTGATCTATATGCTACCAAGGAGAGAATAG
AATACTCCAAACCTTCAAGGGGAAATATTTTAAATTTCTTGGTTACTTTTTCTCTATTTACTGTGTTTGGAAAA
TTTTCATGGCTACCATCAATATTGTTTTTGATCGAGTTGGGAAAACGGATCCTGTCAAGAGGCATTGAGATCA
CTGTGAATTATCTGGGAATCCAATTTGATGTGAAGTTTTGGTCCCAACACATTTCTTCTTGTGGAATAA
TCATCGTCACATCCATCAGAGGATTGCTGATCACTCTTACCAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCCT
CCAATGTCATTGTCTCTGCTATTAGCACAGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGA
GTATGCCCTTAGAATACCGCACCATAATCACTGAAGTCCTTGGAGAAGTGCAGTTCAACTTCTATCACCCTTGGT
TTGATGTGATCTTCTCTGGTCAGCGCTCTCTCTAGCATACTCTTCTCTATTTGGCTCACAAACAGGCACCAGAGA
AGCAAAATGGCACCTTGAACCTTAAGCCTACTACAGACTGTTAGAGGCCAGTGGTTTCAAAATTTAGATATAAGAGG
GGGGAATAATGGAACCGGCGCTGACATTTTATAAACAAACAAAATGCTATGGTAGCATTTTTTACCTTCATAGC
ATACTCCTTCCCCGTGAGGTGATACTATGACCATGAGTAGCATCAGCCAGAACATGAGAGGGAGAACTAACTCAA
GACAATACTCAGCAGAGAGCATCCCGTGTGGATATGAGGCTGGTGTAGAGGCGGAGAGGAGCCAAGAACTAAAG
GTGAAAAATACACTGGAACCTCTGGGGCAAGACATGTCTATGGTAGCTGAGCCAAACACGTAGGATTTCCGTTTTA
AGGTTACATGGAAGGTTATAGCTTTGCCTTGAGATTGACTCATTTAAATCAGAGACTGTAACAAAAA
AAAAAAGGGCGGCGGACTCTAGAGTCGACCTGCAGAAGCTTGGCCGCATGGCCCACTTGTATTG
CAGCTTATAATG

14/615

FIGURE 14

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEILGVLNSSSRYPFW
KMNLGVILLILVFMVPFYIGYFIVSNIRLLHKQRLLFSCLLWLTFFMYFFWKLGDPPILSPKHGILSIEQLISRV
GVIGVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDILALERLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPS
GFWGMIKSVTTSASGSENLTLIQQEVDLEELSRQLFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWK
IFMATINIVFDRVGKTDVPTRGIEITVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAISSSKS
SNVIVLLLAQIMGMFYVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSALESSILFLYLAHKQAPE
KQMAP

Important features:**Signal peptide:**

amino acids 1-23

Potential transmembrane domains:

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398, 425-444

N-glycosylation sites.

amino acids 67-70, 180-183 and 243-246

Eukaryotic cobalamin-binding proteins

amino acids 151-160

FIGURE 15

GACGGAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCGGGACATGCGGGCC
CAGGAGCTCCCCAGGCTCGCGTTTCCCGTTCTGCTGTTGCTGTTGCTGCTGCTGCCGCCGCCGCCGTGCCCTGCC
CACAGCGCCACGCGCTTCGACCCCACTGGGAGTCCCTGGACGCCCGCCAGCTGCCCGCTGGTTTGCACAGGCC
AAGTTTCGGCATCTTCATCCACTGGGAGTGTTTTCCGTGCCAGCTTCGGTAGCGATGGTTCTGGTGGTATTGG
CAAAAGGAAAAGATACCGAAGTATGTGGAATTTATGAAAGATAATTACCTCCTAGTTTCAAATATGAAGATTTT
GGACCACTATTTACAGCAAAATTTTTTAATGCCAACCAGTGGGCAGATATTTTTTCAGGCCTCTGGTGCCAAATA
ATTGTCTTAACTTCCAAACATCATGAAGGCTTACCTTTGTGGGGGTCAGAAATTATCGTGGAACTGGAATGCCATA
GATGAGGGGCCCAAGAGGACATTTGTCAAGGAATCTTGGATAGCCATTAGGAACAGAACTGACCTGCGTTTGGGA
CTGTACTATTCCTTTTTGAATGGTTTCACTCCGCTCTCTCTGTGAGGATGAATCCAGTTTCATTCCATAAGCGGCAA
TTTCCAGTTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACATATCAGCCTGAGGTTCTGTGGTGGAT
GGTGACGGAGGAGCACCGGATCAATACTGGAACAGCACAGGCTTCTTGGCCTGGTTATATAATGAAAGCCCAGTT
CGGGGCACAGTAGTCAGGCAATGCTTGTGGGGAGCTGGTAGCATCTGTAAGCATGGTGGCTTCTATACCTGCGAGT
GATCGTTATAACCCAGGACATCTTTGGCCATAAATGGGAAAACATGCATGACAATAGACAACTGTCTGGGGC
TATAGGAGGGAAGCTGGAATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTGTAGAGACAGTTTCA
TGTGGAGGAAATCTTTTGATGAATATTTGGGCCCACACTAGATGGCACCATTCTGTAGTTTGTGAGGAGCGACTG
AGCAAGTGGGGTCTGGCTAAAAGTCAATGGAGAAGCTATTTATGAAACCTATACCTGGCGATCCCAAGATGAC
ACTGTCACCCCAGATGTGTGGTACACATCCCAAGCTAAAGCAAAATAGTCTATGCCATTTTTCTTAAATGGCCC
ACATCAGGACAGTGTCTTGGCCATCCCAAGCTAATCTGGGGGCAACAGAGGTGAAACTACTGGCCATGGA
CAGCCACTTAACTGGATTTCTTTGGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTTCATCAGATG
CCGTGTAAATGGGGCTGGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTGATGCTGCAAGTT
ATGTCTAAGGCTAGGAACATCAGGTGTCTATAATTGTAGCAGCATGGAGAAAGCAATGTAACTGGATAAGAAA
TTATTTGGCAGTTGAGCCCTTTCCCTTTTCCCACATAATTTTTCTTAAATATACCATTTAACCTTTAACTCT
CCAGTGCACTTTGCCATTAAGAGTCTCTTACATGATTTGTTTCCATGTGTGACTCAGAGGTGAGAATTTTTTCA
CATTATAGTAGCAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTTTATGTTGAAGCCATATCCCCCATGAT
TATATAGTTATGCATCACTTAATATGGGGATATTTTCTGGGAAATGCATTGCTAGTCAATTTTTTTTTTGTGCCAA
CATCATAGAGTGTATTTACAAAATCTTAGATGGCATAGCCTACTACACACCTAATGTGTATGGTATGACTGTTG
CTCCTAGGCTACAGACATATACAGATGTTACTGAATACTGTAGGCATAGTAACAGTGGTATTGTATGATCGAA
ACATATGGAACATAGAGAAGGTACAGTAAAAATACTGTAAAATAAATGGTGCACCTGTATAGGGCACTTACCAC
GAATGGAGCTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCCTAGGACATTATTGAA
CACTGCCAGACGTTATAAAATACTGTATGCTTAGGCTACACTACATTTATAAAAAAAGTTTTTCTTCTTCAATT
ATAAATTAACATAAGTGTACTGTAACTTTACAAACGTTTTAATTTTTAAACCTTTTTGGCTCTTTGTGAATAAC
CTTAGCTTTAAACATAAACTCATTGTGCAAAATGTAA

16/615

FIGURE 16

MRPQELPRLAFPLLLLLLLLLLPPPPCPAHSATRFDPWTWESLDARQLPAWFDQAKFGIFIHGVSFVPSFGSEFW
WYWQKEKIPKYVEFMKDNYPSPFKYEDFGPLFTAKFFNANQWADIFQASGAKYIVLTSKHHEGFTLWGSEYSWNW
NAIDEGPKRDIVKELEVAIRNRTDLRFGLYYSLEFWFHLFLEDESSSFHKRQFPVSKTLPELYELVNNYQPEVL
WSDGDGGAPDQYWNSTGFLAWLYNESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMITDKL
SWGYYREAGISDYLTIEELVKQLVETVSCGNNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYTWRS
QNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWISLEQNGIMVELPQITI
HQPCKKGWALALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319, 375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

17/615

FIGURE 17

CCCACGCGTCCGCTGGTGTAGATCGAGCAACCTCTAAAAGCAGTTTAGAGTGGTAAAAAAAAAAAAAAAAACACA
CCAAACGCTCGCAGCCACAAAAGGGATGAAATTTCTTCTGGACATCCTCCTGCTTCTCCCGTTACTGATCGTCTG
CTCCCTAGAGTCCTTCGTGAAGCTTTTTATTCTTAAGAGGAGAAAATCAGTCACCGGCGAAATCGTGCTGATTAC
AGGAGCTGGGCATGGAATTGGGAGACTGACTGCCTATGAATTTGCTAAACTTAAAAGCAAGCTGGTTCTCTGGGA
TATAAATAAGCATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTTACACCTTTGTGGT
AGACTGCAGCAACCGAGAAGATATTTACAGCTCTGCAAGAAGGTGAAGGCAGAAATTGGAGATGTTAGTATTTT
AGTAAATAATGCTGGTGTAGTCTATACATCAGATTTGTTTGCTACACAAGATCCTCAGATTGAAAAGACTTTTGA
AGTTAATGTACTTGCACATTTCTGGACTACAAAGGCATTTCTTCTGCAATGACGAAGAATAACCATGGCCATAT
TGTCACGTGTGGCTTCGGCAGCTGGACATGTCTCGGTCCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGCTGC
TGTTGGATTTTCATAAACTTTGACAGATGAAGTGGCTGCCTTACAAATAACTGGAGTCAAAACAACATGTCTGTG
TCCTAATTTTCGTAAACACTGGCTTCATCAAAAATCCAAGTACAAGTTTGGGACCCACTCTGGAACCTGAGGAAGT
GGTAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAGATGATTTTTATTCCATCTTCTATAGCTTTTTTAAC
AACATTGGAAAGGATCCTTCTGAGCGTTTCTGGCAGTTTAAAACGAAAAATCAGTGTTAAGTTTGATGCAGT
TATTGGATATAAAATGAAAGCGCAATAAGCACCTAGTTTTCTGAAAACAGTTTACCAGGTTTAGGTTGATGTCA
TCTAATAGTGCCAGAATTTAATGTTTGAAGTCTGTTTTCTAATTATCCCCATTTCTTCAATATCATTTTTG
AGGCTTTGGCAGTCTTCATTTACTACCACTTGTTCTTTAGCCAAAAGCTGATTACATATGATATAACAGAGAAA
TACCTTTAGAGGTGACTTTAAGGAAAATGAAGAAAAAGAACCAAAATGACTTTATTAAAATAATTTCCAAGATTA
TTTGTGGCTCACCTGAAGGCTTTGCAAAATTTGTACCATAACCGTTTATTTAACATATATTTTATTTTTGATTG
CACTTAAATTTTGTATAATTTGTGTTTCTTTTTCTGTTCTACATAAAATCAGAACTTCAAGCTCTCTAAATAAA
ATGAAGGACTATATCTAGTGGTATTTACAATGAATATCATGAAGTCTCAATGGGTAGGTTTCATCCTACCCATT
GCCACTCTGTTTCTGAGAGATACCTCACATTCCAATGCCAAACATTTCTGCACAGGGAAGCTAGAGGTGGATAC
ACGTGTTGCAAGTATAAAAGCATCACTGGGATTTAAGGAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAA
TAAATGGATCACACTTAAA
AAA

18/615

FIGURE 18

MKFLLDILLLLPLLIIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSKL
VLWDINKHGLEETAACKKGLGAKVHTFVVDCSNREDIYSSAKKVKAIEIGDVSILVNNAGVVYT
SDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPELLAYCSSK
FAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVNRLMHGILT
EQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKF'DAVIGYKMKAQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

19/615

FIGURE 19

CCCACGCGTCCGCTCCGCGCCCTCCCCCGCCTCCCGTGCGGTCCGTCGGTGGCCTAGAGAT
GCTGCTGCCGCGGTTGCAGTTGTCGCGCACGCCTCTGCCCCGCCAGCCCGCTCCACCGCCGTAG
CGCCCGAGTGTCGGGGGGCGCACCCGAGTCGGGGCCATGAGGCCGGAACCGCGCTACAGGCCG
TGCTGCTGGCCGTGCTGCTGGTGGGGCTGCGGGCCGCGACGGGTGCGCTGCTGAGTGCCTCGG
ATTTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGGAGGGACACAGAGGCCTTGTTATAAAG
TCATTTACTTCCATGATACTTCTCGAAGACTGAACTTTGAGGAAGCCAAAGAAGCCTGCAGGA
GGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAAAAGTTCA
TTGAAAACCTCTTGCCATCTGATGGTGACTTCTGGATTGGGCTCAGGAGGCGTGAGGAGAAAC
AAAGCAATAGCACAGCCTGCCAGGACCTTTATGCTTGGACTGATGGCAGCATATCACAAATTTA
GGAAGTGGTATGTGGATGAGCCGTCCTGCGGCAGCGAGGTCTGCGTGGTTCATGTACCATCAGC
CATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAATGATGACCGGTGCAACA
TGAAGAACAATTTCAATTTGCAAATATTCTGATGAGAAACCAGCAGTTCCTTCTAGAGAAGCTG
AAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAGGAAGAAGATGCCA
AAAAAACATTTAAAGAAAGTAGAGAAGCTGCCTTGAATCTGGCCTACATCCTAATCCCCAGCA
TTCCCCTTCTCCTCCTCCTTGTGGTCACCACAGTTGTATGTTGGGTTTGGATCTGTAGAAAAA
GAAAACGGGAGCAGCCAGACCCTAGCACAAAGAAGCAACACACCATCTGGCCCTCTCCTCACC
AGGGAAACAGCCCGGACCTAGAGGTCTACAATGTCATAAGAAAACAAAGCGAAGCTGACTTAG
CTGAGACCCGGCCAGACCTGAAGAATATTTCAATCCGAGTGTGTTCCGGGAGAAGCCACTCCCG
ATGACATGTCTTGTGACTATGACAACATGGCTGTGAACCCATCAGAAAGTGGGTTTGTGACTC
TGGTGAGCGTGGAGAGTGGATTTGTGACCAATGACATTTATGAGTTCTCCCCAGACCAATGG
GGAGGAGTAAGGAGTCTGGATGGGTGGAAAATGAAATATATGGTTATTAGGACATATAAAAAA
CTGAAACTGACAACAATGGAAAAGAAATGATAAGCAAAATCCTCTTATTTTCTATAAGGAAAA
TACACAGAAGGTCTATGAACAAGCTTAGATCAGGTCCTGTGGATGAGCATGTGGTCCCCACGA
CCTCCTGTTGGACCCCCACGTTTTGGCTGTATCCTTTATCCCAGCCAGTCATCCAGCTCGACC
TTATGAGAAGGTACCTTGCCCAGGTCTGGCACATAGTAGAGTCTCAATAAATGTCACTTGGTT
GGTTGTATCTAACTTTTAAGGGACAGAGCTTTACCTGGCAGTGATAAAGATGGGCTGTGGAGC
TTGGAAAACCACCTCTGTTTTCTTGCTCTATACAGCAGCACATATTATCATACAGACAGAAA
ATCCAGAATCTTTTCAAAGCCACATATGGTAGCACAGGTTGGCCTGTGCATCGGCAATTCTC
ATATCTGTTTTTTTTCAAAGAATAAAATCAAATAAAGAGCAGGAAAAAAAAA

20/615

FIGURE 20

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRLGGQPVCRRGGTQRPCYKVIYFHDTSRRLN
FEEAKEACRRDGGQLVSI ESEDEQKLIKFIENLLPSDGD F WIGLRREEKQSNSTACQDLYA
WTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDE
KPAVPSREAEGETELTTPVLPEETQEEDAKKTFKESREAA NLAYILPSIPLLLLLLVVTTV
VCWWICRKRKREQPD PSTKKQHTIWPSPHQGN SPDLEVYNVIRKQSEADLAETRPDLKNISF
RVCSGEATPDDMSCDYDNMAVNPSESGFVTLVSVESGFVTNDIYEFSPDQMGRSKESGWVENE
IYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327**N-myristoylation site.**

amino acids 18-24, 37-43, 76-82, 146-152

21/615

FIGURE 21

AGGCTCCCGCGCGCGGCTGAGTGCGGACTGGAGTGGGAACCCGGGTCCCCGCGCTTAGAGAACACGCGATGACCA
CGTGGAGCCTCCGGCGGAGGCCGCGCCGACGCTGGGACTCCTGCTGCTGGTCTGCTTGGGCTTCTGGTGCTCC
GCAGGCTGGACTGGAGCACCTGGTCCCTCTCGGGCTCCGCCATCGACAGCTGGGGCTGCAGGCCAAGGGCTGGA
ACTTCATGCTGGAGGATTCCACCTTCTGGATCTTCGGGGGCTCCATCCACTATTTCCGTGTGCCAGGGAGTACT
GGAGGGACCGCTGCTGAAGATGAAGGCCTGTGGCTTGAACACCCTCACCACCTATGTTCCGTGGAACCTGCATG
AGCCAGAAAGAGGCAAATTTGACTTCTCTGGGAACCTGGACCTGGAGGCCTTCGTCTGATGGCCGCGAGAGATCG
GGCTGTGGGTGATTCTGCGTCCAGGCCCTACATCTGCAGTGAGATGGACCTCGGGGGCTTGCCAGCTGGCTAC
TCCAAGACCCTGGCATGAGGCTGAGGACAACCTACAAGGGCTTCACCGAAGCAGTGGACCTTTATTTGACCACC
TGATGTCCAGGGTGGTGCCACTCCAGTACAAGCGTGGGGGACCTATCATTGCCGTGCAGGTGGAGATGAATATG
GTTCTATAATAAAGACCCCGCATACATGCCCTACGTCAAGAAGGCACTGGAGGACCGTGGCATTGTGGAACCTGC
TCCTGACTTCAGACAACAAGGATGGGCTGAGCAAGGGGATTGTCCAGGGAGTCTTGCCACCACCACTTGCACT
CAACACACGAGCTGCAGCTACTGACCACCTTTCTCTTCAACGTCCAGGGGACTCAGCCCAAGATGGTGATGGAGT
ACTGGACGGGGTGGTTTGAATCGTGGGAGGCCCTCACAATATCTTGGATTCTTCTGAGGTTTTGAAAACCGTGT
CTGCCATTGTGGACGCCGGCTCCTCCATCAACCTCTACATGTTCCACGGAGGCACCAACTTTGGCTTCATGAATG
GAGCCATGCACCTCCATGACTACAAGTCAGATGTCAACAGCTATGACTATGATGCTGTGCTGACAGAAGCCGGCG
ATTACACGGCCAAGTACATGAAGCTTCGAGACTTCTTCGGCTCCATCTCAGGCATCCCTCTCCCTCCCCACCTG
ACCTTCTTCCCAAGATGCCGTATGAGCCCTTAACGCCAGTCTTGTACCTGTCTCTGTGGGACGCCCTCAAGTACC
TGGGGGAGCCAAATCAAGTCTGAAAAGCCCATCAACATGGAGAACCTGCCAGTCAATGGGGGAAATGGACAGTCCT
TCGGGTACATTCTCTATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCCACGTGCATGATCGGGGGCAGG
TGTTTGTGAACACAGTATCCATAGGATTCTTGGACTACAAGACAACGAAGATTGCTGTCCCCCTGATCCAGGGTT
ACACCGTGTGAGGATCTTGGTGGAGAATCGTGGGCGAGTCAACTATGGGAGAATATTGATGACCGCGCAAAG
GCTTAATTGGAAATCTCTATCTGAATGATTACCCCTGAAAACTTCAGAATCTATAGCCTGGATATGAAGAAGA
GCTTCTTTTCAAGGTTCCGGCTGGACAAATGGNGTTCCTCTCCAGAAACACCCACATTACCTGCTTCTTCTTGG
GTAGCTTGTCCATCAGCTCCACGCCTTGTGACACCTTTCTGAAGCTGGAGGGCTGGGAGAAGGGGGTGTATTCA
TCAATGGCCAGAACCTTGGACGTTACTGGAACATTGGACCCCAAGACGCTTTACCTCCCAGGTCCCTGGTTGA
GCAGCGGAATCAACCAGGTATCGTTTTTGGAGAGACGATGGCGGGCCCTGCATTACAGTTTACGGAAACCCCC
ACCTGGGCAGGAACCACTACATTAAGTGAACGCTGGCACCCCTCCTGCTGGTGGCAGTGGGAGACTGCCGCTC
CTCTTGACCTGAAGCCTGGTGGCTGCTGCCCCACCCCTCACTGCAAAGCATCTCCTTAAGTAGCAACCTCAGGG
ACTGGGGGCTACAGTCTGCCCTGTCTCAGCTCAAACCCCTAAGCCTGCAGGGAAGGTTGGGATGGCTCTGGGCC
TGGCTTTGTTGATGATGGCTTTCCTACAGCCCTGCTCTTGTGCCGAGGCTGTGGGGCTGTCTTAGGGTGGGAGC
AGCTAATCAGATCGCCAGCCTTTGGCCCTCAGAAAAAGTGTGAAACGTGCCCTTGACCCGACGTACAGCCC
TGCGAGCATCTGCTGGACTCAGGCGTGTCTTTGCTGGTTCTTGGGAGGCTTGGCCACATCCCTCATGGCCCCAT
TTTATCCCCGAAATCCTGGGTGTGTCAACAGTGTAGAGGGTGGGGAAGGGGTGTCTCACCTGAGCTGACTTTGTT
CTTCTTCAACACCTTCTGAGCCTTCTTTGGGATTCTGGAAGGAACTCGGCGTGAGAAACATGTGACTTCCCTT
TCCCTTCCCACTCGCTGCTTCCACAGGGTGACAGGCTGGGCTGGAGAAACAGAAATCTCACCTGCGTCTTCC
CAAGTTAGCAGGTGTCTCTGGTGTTCAGTGAGGAGGACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCA
CATCCAGGGAGGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCACATCC
AGGGAGGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGA
GGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGAGGAGG
ACAGAAGGCCAGCTCAGTGGCCCCCGCTCCCCACCCCCACGCCGAACAGCAGGGGAGAGCAGCCCTCCTTC
GAAGTGTGTCCAAGTCCGCATTTGAGCCTTGTCTGGGGCCAGCCCAACACCTGGCTTGGGCTCACTGTCTGTA
GTTGCAGTAAAGCTATAACCTTGAATCACA

22/615

FIGURE 22

MTTWSLRRRPPARTLGLLLLVLGFLVLRRLDWSTLVPLRLRHRQLGLQAKGWNFMLEDSTFWI
FGGSIHYFRVPREYWRDRLLKMKACGLNTLTITYVPWNLHEPERGKFDFSGNLDLEAFVLMMAE
IGLWVILRPGPYICSEMDLGGLPSWLLQDPMRLRTTYKGFTEAVDLYFDHLSRVVPLQYKR
GGPIIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLTSDNKDGLSKGIVQGVLATINLQ
STHELQLLTTFLEFNVQGTQPKMVMEYWTGWFDWGGPHNILDSSSEVLKTVSAIVDAGSSINLY
MFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDYTAKYMKLRDFFGSISGIPLPPPPD
LLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGGNGQSFGYILYETSITSSG
ILSGHVHDRGQVFVNTVSIQFLDYKTTKIAVPLIQGYTVLRILVENRGRVNYGENIDDQRKGL
IGNLYLNDSPKFNRIYSLDMKKSFFQRFGLDKWXSLETPPTLPAFFLGSLSSISSTPCDTFLK
LEGWEKGVVFINGQNLGRYWNIGPQKTLYLPGPWLSSGINQVIVFEETMAGPALQFTETPHLG
RNQYIK

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 23

[illegible]

24/615

FIGURE 24

MNSSKSSETQCTERGCFSQMFLLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPENF
TELSYNYGSGSVKNCCPLNWEYFQSSCYFFSTDTISWALSLKNCSAMGAHLVVINSQEEQEF
LSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPPNIATLEDCAIMRDSSNPR
QNWNVDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

25/615

FIGURE 25

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACCC
TGGTGAGGGTTCTCTACTTGGCCTTCGGTGGGGGTCAAGACGCAGGCACCTACGCCAAAGGGG
AGCAAAGCCGGGCTCGGCCCCGAGGCCCCCAGGACCTCCATCTCCCAATGTTGGAGGAATCCGA
CACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCC**ATGG**GCTCCCAAGA
AGCTGTCTGCTTCGTTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCCAGGCAG
ACACTCGGTTCGTTTCGTAGTGGATAGGGGTTCATGACCGGTTTCTCCTAGACGGGGCCCCGTTCC
GCTATGTGTCTGGCAGCCTGCACTACTTTCGGGTACCGCGGGTGCTTTGGGCCGACCGGCTTT
TGAAGATGCGATGGAGCGGCCTCAACGCCATACAGTTTTATGTGCCCTGGAACCTACCACGAGC
CACAGCCTGGGGTCTATAACTTTAATGGCAGCCGGGACCTCATTGCCTTTCTGAATGAGGCAG
CTCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTTACATCTGTGCAGAGTGGGAGATGG
GGGGTCTCCCATCCTGGTTGCTTCGAAAACCTGAAATTCATCTAAGAACCTCAGATCCAGACT
TCCTTGCCGCAGTGGACTCCTGGTTCAAGGTCTTGCTGCCCAAGATATATCCATGGCTTTATC
ACAATGGGGGCAACATCATTAGCATTGAGGTGGAGAATGAATATGGTAGCTACAGAGCCTGTG
ACTTCAGCTACATGAGGCACCTGGCTGGGCTCTTCCGTGCACTGCTAGGAGAAAAGATCTTGC
TCTTCACCACAGATGGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGGGACTCTATACCACTG
TAGATTTTGGCCAGCTGACAACATGACCAAATCTTTACCCTGCTTCGGAAGTATGAACCCC
ATGGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTACTGGGGCCAGAATCACT
CCACACGGTCTGTGTGTCAGCTGTAACCAAAGGACTAGAGAACATGCTCAAGTTGGGAGCCAGTG
TGAACATGTACATGTTCCATGGAGGTACCAACTTTGGATATTGGAATGGTGCCGATAAGAAGG
GACGCTTCCTTCCGATTACTACCAGCTATGACTATGATGCACCTATATCTGAAGCAGGGGACC
CCACACCTAAGCTTTTTGCTCTTCGAGATGTCATCAGCAAGTTCCAGGAAGTTCTTTGGGAC
CTTTACCTCCCCCGAGCCCCAAGATGATGCTTGGACCTGTGACTCTGCACCTGGTTGGGCATT
TACTGGCTTTCCTAGACTTGCTTTGCCCCCGTGGGCCCATTCAATCAATCTTGCCAATGACCT
TTGAGGCTGTCAAGCAGGACCATGGCTTCATGTTGTACCGAACCTATATGACCCATACCATTT
TTGAGCCAACACCATCTGGGTGCCAAATAATGGAGTCCATGACCGTGCCTATGTGATGGTGG
ATGGGGTGTTCAGGGTGTGTGGAGCGAAATATGAGAGACAAACTATTTTGGCGGGGAAAC
TGGGGTCCAAACTGGATATCTTGGTGGAGAACATGGGGAGGCTCAGCTTTGGGTCTAACAGCA
GTGACTTCAAGGGCCTGTTGAAGCCACCAATTCCTGGGGCAAACAATCCTTACCCAGTGGATGA
TGTTCCCTCTGAAAATTGATAACCTTGTGAAGTGGTGGTTTCCCCTCCAGTTGCCAAAATGGC
CATATCCTCAAGCTCCTTCTGGCCCCACATTCTACTCCAAAACATTTCCAATTTTAGGCTCAG
TTGGGGACACATTTCTATATCTACCTGGATGGACCAAGGGCCAAGTCTGGATCAATGGGTTTA
ACTTGGGGCCGGTACTGGACAAAGCAGGGGCCACAACAGACCCTCTACGTGCCAAGATTCTTGC
TGTTTCCTAGGGGAGCCCTCAACAAAATTACATTGCTGGAAGTAGAAGATGTACCTCTCCAGC
CCCAAGTCCAATTTTTGGATAAGCCTATCCTCAATAGCACTAGTACTTTGCACAGGACACATA
TCAATTCCCTTTCAGCTGATACACTGAGTGCCTCTGAACCAATGGAGTTAAGTGGGCAC**TGAA**
AGGTAGGCCGGGCATGGTGGCTCATGCCTGTAATCCAGCACTTTGGGAGGCTGAGACGGGTG
GATTACCTGAGGTGAGGACTTCAAGACCAGCCTGGCCAACATGGTGAAACCCCGTCTCCACTA
AAAATACAAAATTAGCCGGGCGTGATGGTGGGCACCTCTAATCCAGCTACTTGGGAGGCTG
AGGGCAGGAGAATTGCTTGAATCCAGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCACTG
CACTCCAGCCTGGCTGACAGTGAGACACTCCATCTCAAAAAAAAAAAAA

26/615

FIGURE 26

MAPKKLSCLRSLLLPLSLTLTLLLPQADTRSFVVDRGHDRELLDGAPFRYVSGSLHYFRVPRVLW
ADRLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYICA
EWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENEYGS
YRACDFSVMRHLAFLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDGFPADNMTKIFTLLR
KYEPHGPLVNSEYYTGWLDYWQNHSTRSVSAVTKGLENMLKLGASVNMVMFHHGGTNFGYWNG
ADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVSKFQEVPLGPLPPPSPKMMLGPVTLH
LVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTFFWVPNNGVHDRA
YVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSFGSNSSDFKGLLKPPILGQTIL
TQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDFTLYLPGWTKGQVW
INGFNLGRYWKQGPQQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLDKPILNSTSTL
HRTHINSLSADTLSASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648**Tyrosine kinase phosphorylation site.**

amino acids 191-198

N-myristoylation site.amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 27

[illegible]

28/615

FIGURE 28

MGLLLLVPLLLLPGSYGLPFYNGFYYSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQG
ASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQDKE
HDVSLEIQDLRLLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQVCA
EQAAVVASFELFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPRHRL
HRYDVFCFATALKGRVYYLEHPEKLTLTAREACQEDDATIAKVGQLFAAWKFHGLDRCDAGW
LADGSVRYPVVHHPNCGPPEPGVRSFGFPDQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.amino acids 36-42, 184-190, 208-214, 237-243, 297-303,
307-313

29/615

FIGURE 29

GCAAGCGGCGAAATGGCGCCCTCCGGGAGTCTTGCAAGTCCCTGGCAGTCCTGGTGCTGTTG
CTTTGGGGTGCTCCCTGGACGCACGGGCGGCGGAGCAACGTTCCGCTCATCACGGACGAGAAC
TGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTTTATGCCCCGTGGTGCCCTGCTTGT
CAAAATCTTCAACCGGAATGGGAAAGTTTTGCTGAATGGGGAGAAGATCTTGAGGTTAATATT
GCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTTATCATAACTGCTCTTCCT
ACTATTTATCATTGTAAAGATGGTGAATTTAGGCGCTATCAGGGTCCAAGGACTAAGAAGGAC
TTCATAAACTTTATAAGTGATAAAGAGTGGAAGAGTATTGAGCCCGTTTCATCATGGTTTGGT
CCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTTCAGCTATCTATGTGGATCAGGACG
TGCCATAACTACTTTTATTGAAGACCTTGGATTGCCAGTGTGGGGATCATATACTGTTTTTGCT
TTAGCAACTCTGTTTTCCGGACTGTTATTAGGACTCTGTATGATATTTGTGGCAGATTGCCTT
TGTCCTTCAAAAAGGCGCAGACCACAGCCATACCCATAACCCTTCAAAAAAATTATTATCAGAA
TCTGCACAACCTTTGAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAAGATGTTTCAGAA
GAAGAAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTCCACAGAATGCCATAAGACAACGC
TCTCTGGGTCCATCATTGGCCACAGATAAATCCTAGTTAAATTTTATAGTTATCTTAATATTA
TGATTTTGTATAAAACAGAAGATTGATCATTGTTTGGTTTGAAGTGAAGTGTGACTTTTTT
GAATATTGCAGGGTTCAGTCTAGATTGTCATTAAATTGAAGAGTCTACATTCAGAACATAAAA
GCACTAGGTATACAAGTTTGAAATATGATTTAAGCACAGTATGATGGTTTAAATAGTTCTCTA
ATTTTTGAAAAATCGTGCCAAGCAATAAGATTTATGTATATTTGTTTAAATAATAACCTATTTT
AAGTCTGAGTTTTGAAAAATTTACATTTCCCAAGTATTGCATTATTGAGGTATTTAAGAAGATT
ATTTTAGAGAAAAATATTTCTCATTTGATATAATTTTCTCTGTTTCACTGTGTGAAAAAAG
AAGATATTTCCCATAAATGGGAAGTTTGCCATTGTCTCAAGAAATGTGTATTTTCAGTGACAA
TTTTCGTGGTCTTTTTTAGAGGTATATTCCAAAATTTCCCTTGTATTTTTTAGGTTATGCAACTAAT
AAAACTACCTTACATTAATTAATTACAGTTTTCTACACATGGTAATACAGGATATGCTACTG
ATTTAGGAAGTTTTTTAAGTTCATGGTATTCTCTTGATTCCAACAAAGTTTGATTTTCTCTTGT
ATTTTTCTTACTTACTATGGGTTACATTTTTTTATTTTTCAAATTGGATGATAATTTCTTGGA
ACATTTTTTATGTTTTAGTAAACAGTATTTTTTTGTTGTTTCAAAGTGAAGTTTACTGAGAGA
TCCATCAAATTGAACAATCTGTTGTAATTTAAATTTTGGCCACTTTTTTCAGATTTTACATC
ATTCTTGCTGAACCTCAACTGAAATTGTTTTTTTTTCTTTTTGGATGTGAAGGTGAACATT
CCTGATTTTTGTCTGATGTGAAAAAGCCTTGGTATTTTACATTTTGAAAATTCAAAGAAGCTT
AATATAAAAGTTTGCATTCTACTCAGGAAAAGCATCTTCTGTATATGTCTTAAATGTATTT
TTGTCCTCATATACAGAAAGTTCTTAATTGATTTTACAGTCTGTAATGCTTGATGTTTTAAA
TAATAACATTTTTATATTTTTTAAAGACAACTTCATATTATCCTGTGTTCTTTCCTGACTG
GTAATATTGTGTGGGATTTACAGGTAAAAGTCAGTAGGATGGAACATTTTAGTGTATTTTA
CTCCTTAAAGAGCTAGAATACATAGTTTTTACCTTAAAAGAAGGGGAAAATCATAAATACAA
TGAATCAACTGACCATTACGTAGTAGACAATTTCTGTAATGTCCCCTTCTTCTAGGCTCTGT
TGCTGTGTGAATCCATTAGATTTACAGTATCGTAATATACAAGTTTTCTTTAAAGCCCTCTCC
TTTAGAATTTAAATATTTGTACCATTAAAGAGTTTGGATGTGTAAGTGTGATGCCTTAGAAA
AATATCCTAAGCACAAAATAAACCTTTCTAACCACCTTCATTAAAGCTGAAAAAAAAAAAAAA
AAA

30/615

FIGURE 30

MAPSGSLAVPLAVLVLLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNLO
PEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFIN
ISDKEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFALATL
FSGLLLGLCMIFVADCLCPSKRRRPQYPYPYPSKKLLSESAQPLKKVEEQEAEDEEDVSEEEAE
SKEGTNKDFPQNAIRQPSLGPSTLTDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

31/615

FIGURE 31

AGATGGCGGTCTTGGCACCTCTAATTGCTCTCGTGATTTCGGTGCCGCGACTTTCACGATGGC
TCGCCCAACCTTACTACCTTCTGTGCGCCCTGCTCTCTGCTGCCTTCCTACTCGTGAGGAAAC
TGCCGCCGCTCTGCCACGGTCTGCCACCCAACGCGAAGACGGTAACCCGTGTGACTTTGACT
GGAGAGAAGTGGAGATCCTGATGTTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGATCCA
TCACTGTGGAGCAACATATAGGCAACATTTTCATGTTTAGTAAAGTGGCCAACACAATTCTTT
TCTTCCGCTTGGATATTTCGCATGGGCCCTACTTTACATCACACTCTGCATAGTGTTTCTGATGA
CGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAAACCATTG
ATGAGGAAGTAGAACGGGACAAGAGGGTCACCTGGATTGTGGAGTTCTTTGCCAATTGGTCTA
ATGACTGCCAATCATTTGCCCTATCTATGCTGACCTCTCCCTTAAATACAAGTGTACAGGGC
TAAATTTTGGGAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGCGGTACAAAGTGAGCA
CATCACCCCTCACCAAGCAACTCCCTACCCTGATCCTGTTCCAAGGTGGCAAGGAGGCAATGC
GGCGGCCACAGATTGACAAGAAAGGACGGGCTGTCTCATGGACCTTCTCTGAGGAGAATGTGA
TCCGAGAATTTAACTTAAATGAGCTATACCAGCGGGCCAAGAACTATCAAAGGCTGGAGACA
ATATCCCTGAGGAGCAGCCTGTGGCTTCAACCCCCACCACAGTGTGAGATGGGGAAAACAAGA
AGGATAAAATAAGATCCTCACTTTGGCAGTGCTTCCTCTCCTGTCAATTCAGGCTCTTTCCAT
AACCACAAGCCTGAGGCTGCAGCCTTTNATTNATGTTTCCCTTTGGCTGNGACTGGNTGGGG
CAGCATGCAGCTTCTGATTTTAAAGAGGCATCTAGGGAATTGTCAGGCACCCTACAGGAAGGC
CTGCCATGCTGTGGCCAAGTGTTCCTGAGCAAGAAAGAGATCTCATAGGACGGAGGGGGA
AATGGTTTCCCTCCAAGCTTGGGTGAGTGTGTTAACTGCTTATCAGCTATTCAGACATCTCCA
TGGTTTCTCCATGAACTCTGTGGTTTCATCATTCTTCTTAGTTGACCTGCACAGCTTGGTT
AGACCTAGATTTAACCCTAAGGTAAGATGCTGGGGTATAGAACGCTAAGAATTTTCCCCAAG
GACTCTTGCTTCCTTAAGCCCTTCTGGCTTCGTTTATGGTCTTCATTAAAAGTATAAGCCTAA
CTTTGTGCTAGTCCTAAGGAGAAACCTTTAACCACAAAGTTTTTATCATTGAAGACAATATT
GAACAACCCCTATTTTGTGGGGATTGAGAAGGGGTGAATAGAGGCTTGAGACTTTCCTTTGT
GTGGTAGGACTTGGAGGAGAAATCCCTGGACTTTCCTAACCCTCTGACATACTCCCCACAC
CCAGTTGATGGCTTTCGTAATAAAAAGATTGGGATTTCTTTTG

32/615

FIGURE 32

MAVLAPLIAALVYSPRLSRWLAQPYLLSALLSAAFLLVRLPPLCHGLPTQREDGNPCDFDW
REVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFLMT
CKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYNCTGL
NFGKVDVGRYTDVSTRYKVSTSP LTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSEENVI
REFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

Signal sequence:
amino acids 1-48

Transmembrane domain:
amino acids 111-125

N-glycosylation site.
amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.
amino acids 154-158, 265-269

Casein kinase II phosphorylation site.
amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.
amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.
amino acids 244-253

33/615

FIGURE 33

CGGACGCGTGGGGTGCCCGACATGGCGAGTGTAGTGCTGCCGAGCGGATCCCAGTGTGCGGCG
GCAGCGGCGGGCGGCGCGCCTCCCGGGCTCCGGCTTCTGCTGTTGCTCTTCTCCGCCGCGGCA
CTGATCCCCACAGGTGATGGGCAGAATCTGTTTACGAAAGACGTGACAGTGATCGAGGGAGAG
GTTGCGACCATCAGTTGCCAAGTCAATAAGAGTGACGACTCTGTGATTCAGCTACTGAATCCC
AACAGGCAGACCATTTATTTTCAGGGACTTCAGGCCTTTGAAGGACAGCAGGTTTCAGTTGCTG
AATTTTTCTAGCAGTGAACCTCAAAGTATCATTGACAAACGTCTCAATTTCTGATGAAGGAAGA
TACTTTTGCCAGCTCTATACCGATCCCCCACAGGAAAGTTACACCACCATCACAGTCCCTGGTC
CCACCACGTAATCTGATGATCGATATCCAGAAAGACACTGCGGTGGAAGGTGAGGAGATTGAA
GTCAACTGCACTGCTATGGCCAGCAAGCCAGCCACGACTATCAGGTGGTTCAAAGGGAACACA
GAGCTAAAAGGCAAATCGGAGGTGGAAGAGTGGTCAGACATGTACACTGTGACCAGTCAGCTG
ATGCTGAAGGTGCACAAGGAGGACGATGGGGTCCCAGTGATCTGCCAGGTGGAGCACCCCTGCG
GTCAGTGGAAACCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCTCAAGTGCACATT
CAGATGACTTATCCTCTACAAGGCTTAACCCGGGAAGGGGACGCGCTTGAGTTAACATGTGAA
GCCATCGGGAAGCCCCAGCCTGTGATGGTAACTTGGGTGAGAGTCGATGATGAAATGCCTCAA
CACGCCGTACTGTCTGGGCCCCAACCTGTTTCATCAATAACCTAAACAAAACAGATAATGGTACA
TACCGCTGTGAAGCTTCAAACATAGTGGGGAAAGCTCACTCGGATTATATGCTGTATGTATAC
GATCCCCCACAACCTATCCCTCCTCCCACAACAACCACCACCACCACCACCACCACCACCACC
ACCATCCTTACCATCATCACAGATTCCCAGCAGGTGAAGAAGGCTCGATCAGGGCAGTGGAT
CATGCCGTGATCGGTGGCGTCGTGGCGGTGGTGGTGTTCGCCATGCTGTGCTTGCTCATCATT
CTGGGGCGCTATTTTGCCAGACATAAAGGTACATACTTCACTCATGAAGCCAAAGGAGCCGAT
GACGCAGCAGACGCAGACACAGCTATAATCAATGCAGAAGGAGGACAGAACAACCTCCGAAGAA
AAGAAAGAGTACTTCATCTAGATCAGCCTTTTTGTTTCAATGAGGTGTCCAACCTGGCCCTATT
TAGATGATAAAGAGACAGTGATATTGG

34/615

FIGURE 34

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39518
<subunit 1 of 1, 440 aa, 1 stop
<MW: 48240, pI: 4.93, NX(S/T): 7
MASVVLPSGSQCAAAAAAAPPGLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQ
VNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSELKVSLTNVSISDEGRYFCQLYT
DPPQESYTTITVLVPPRNLMDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTTELKGKSE
VEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQ
GLTREGDALELTCEAIGKPQPMVTWVRVDDEMPQHAVLSGPNLFINNLNKT DNGTYRCEASN
IVGKAHSDYMLYVYDPPTTIPPTTTTTTTTTTTTTTILTIITDSRAGEEGSIRAVDHA VIGGV
VAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI

Signal sequence.

amino acids 1-36

Transmembrane domain.

amino acids 372-393

N-glycosylation sites.amino acids 65-69, 99-103, 111-115, 163-167, 302-306, 306-310,
430-434**Tyrosine kinase phosphorylation sites.**

amino acids 233-240, 319-328

N-myristoylation sites.amino acids 9-15, 227-233, 307-313, 365-371, 376-382, 402-408,
411-417, 427-433, 428-432

35/615

FIGURE 35

GGTTGCCACAGCTGGTTTAGGGCCCCGACCACTGGGGCCCCCTTGTGAGGAGGAGACAGCCTCCCGGCCCGGGGAG
GACAAGTCGCTGCCACCTTTGGCTGCCGACGTGATTCCCTGGGACGGTCCGTTTCTGCCGTGAGCTGCCGGCCG
AGTTGGGTCTCCGTGTTTCAGGCCGGCTCCCCCTTCTGGTCTCCCTTCTCCGCTGGGCCGGTTATCGGGAGG
AGATTGPTTCCAGGGCTAGCAATTGGACTTTTGATGATGTTTGACCCAGCGGCAGGAATAGCAGGCAACGTGAT
TTCAAAGCTGGGCTCAGCCTCTGTTTCTCTCTCGTGAATCGCAAACCCATTTTGGAGCAGGAATCCAATCA
TGTCTGTGATGGTGGTGAGAAAGAAGGTGACACGGAAATGGGAGAAACTCCAGGCAGGAACACCTTTTGCTGTG
ATGGCCCGCTCATGATGGCCCGCAAAGGGCATTCTTCTACCTGACCCTTTTCTCATCCTGGGGACATGTACAC
TCTTCTTCGCCTTTGAGTCCGCTACCTGGCTGTTTCTGCTGTCTCCTGCCATCCCTGTATTTGCTGCCATGCTCT
TCCTTTTCTCCATGGCTACACTGTTGAGGACCAGCTTCAGTGACCCTGGAGTGATTCCTCGGGCGCTACCAGATG
AAGCAGCTTTATAGAAATGGAGATAGAAGCTACCAATGGTGGGTGCCCCAGGGCCAGCGACCACCGCCTCGTA
TCAAGAATTTCCAGATAAACCAACAGATTGTGAACTGAAATACTGTTACACATGCAAGATCTTCGGGCCTCCCC
GGGCCTCCCATTTGCAGCATCTGTGACAACTGTGTGGAGCGCTTCGACCATCACTGCCCCCTGGGTGGGGAATTGTG
TTGGAAGAGGAACTACCGCTACTTCTACCTCTTCATCCTTTCTCTCCTCCTCACAATCTATGTCTTCGCCT
TCAACATCGTCTATGTGGCCCTCAAATCTTTGAAATTTGGCTTCTTGGAGACATTGAAAGAACTCCTGGAAGT
TTCTAGAAGTCTCATTTGCTTCTTTACACTCTGGTCCGTGCTGGGACTGACTGGATTTTCTACTTTCTCGTGG
CTCTCAACCAGACAACCAATGAAGCATCAAAGGATCATGGACAGGGAAGAATCGCGTCCAGAATCCCTACAGCC
ATGGCAATATTGTGAAGAACTGCTGTGAAGTGTGTGGCCCCCTTGCCCCCAGTGTGCTGGATCGAAGGGGTA
TTTTGCCACTGGAGGAAAGTGGAAGTCGACCTCCAGTACTCAAGAGACCAGTAGCAGCCTCTTGCCACAGAGCC
CAGCCCCACAGAACACCTGAACTCAAATGAGATGCCGGAGGACAGCAGCACTCCCGAAGAGATGCCACCTCCAG
AGCCCCCAGAGCCACCACAGGAGGCAGCTGAAGCTGAGAAGTAGCCTATCTATGGAAGAGACTTTTGTGTTGTGTT
TAATTAGGCTATGAGAGATTTTCAAGTGAGAAGTTAAACCTGAGACAGAGAGCAAGTAAGCTGTCCCTTTTAACT
GTTTTTCTTTGGTCTTTTAGTCACCCAGTTGACACTGGCATTCTTTCTTGCTGCAAGCTTTTTTAAATTTCTGA
CAAGGCAGTGGCAGAAGATGTCAGTCACCTCTGATAACTGGAAAAATGGGTCTCTTGGGCCCTGGCACTGGTTCT
CCATGGCCTCAGCCACAGGGTCCCCCTTGGACCCCCTCTCTTCCCTCCAGATCCAGCCCTCCTGCTTGGGGTCAC
TGGTCTCATTTCTGGGGCTAAAAGTTTTTGGAGACTGGCTCAAATCCTCCCAAGCTGCTGCACGTGCTGAGTCCAGA
GGCAGTCACAGAGACCTCTGGCCAGGGGATCCTAACTGGGTCTTGGGGTCTTCAGGACTGAAGAGGAGGGAGAG
TGGGGTCAGAAGATTCTCTGGCCACCAAGTGCCAGCATTGCCCAAAATCCTTTTAGGAATGGGACAGGTACCT
TCCACTTGTGTANNNNNNNNNNNNNNNNNNNNNNNNTGTTTTTCTTTTGAATCCTGCTCCCATTAGGAG
CAGGAATGGCAGTAATAAAAGTCTGCACCTTTGGTCATTTCTTTTCCCTCAGAGGAAGCCCGAGTCTCACTTAAAC
ACTATCCCCTCAGACTCCCTGTGTGAGGCCTGCAGAGGCCCTGAATGCACAAATGGGAAACCAAGGCACAGAGAG
GCTCTCCTCTCCTCTCCTCTCCCCGATGTACCCTCAAAAAAATAATGCTAACCAGTTCTTCCATTAGCCCT
CGGCTGAGTGAGGGAAGCCAGCACTGCTGCCCTCTCGGGTAACTCACCTAAGGCCTCGGCCACCTCTGGCT
ATGGTAACCACACTGGGGGCTTCTCCAAGCCCCGCTCTCCAGCACTTCCACGGCAGAGTCCAGAGCCACTT
CACCTTGGGGGTGGGCTGTGCCCCCAGTCAGCTCTGCTCAGGACCTGCTCTATTTAGGGGAAGATTTATGT
ATTATATGTGGCTATATTTCTAGAGCACCTGTGTTTTCTCTTTCTAAGCCAGGGTCCTGTCTGGATGACTTAT
CGGTGGGGGAGTGTAACCGGAACCTTTTCTATCTATTTGAAGGCGATTAACTGTGTCTAATGCA

36/615

FIGURE 36

MSVMVVRKKVTRKWEKLPGRNTFCCDGRVMMARQKGFYLTFLILGTCTLFFAFECRYLAVQ
LSPAIPVFAAMLFLFSMATLLRTSFSDPGVIPRALPDEAAFIEMEIEATNGAVPQGQRPPRI
KNFQINNQIVKLKYCYTCKIFRPPRASHCSICDNCVERFDHCPWVGNCVGRNYRYFYLFIL
SLSLTIYVFAFNIVYVALKSLKIGFLETLKETPGTVLEVLCFFTLWSVVGLTGFHTFLVAL
NQTTNEDIKGSWTGKNRVQNPYSHGNIVKNCCEVLCGPLPPSVLDRRGILPLEESGSRPPSTQ
ETSSSLLPQSPAPTEHLNSNEMPEDSSTPEEMPPPEPPEPPQEAAEAEK

Putative transmembrane domains:

amino acids 36-55 (type II TM), 65-84, 188-208, 229-245

FIGURE 37

38/615

FIGURE 38

><subunit 1 of 1, 737 aa, 1 stop
><MW: 78475, pI: 5.09, NX(S/T): 11
MQPRRAQAPGAQLLPALALLLLLLLGAGPRGSSSLANPVPAAPLSAPGPCAAQPCRNGGVCTSRP
EPDPQHPAPAGEPGYSCTCPAGISGANQQLVADPCASNPCHHGNCSSSSSSSDGYLCICNEG
YEGPNCEQALPSLPATGWTESMAPRQLQPVPAEQEPDKILPRSQATVTLPTWQPKTGQKVEM
KWDQVEVIPDIACGNASSNSSAGGRLVSFEVPQNTSVKIRQDATASLILLWKVTATGFFQQCSL
IDGRSVTPLOASGGLVLEEMALGNNHFIGFVNDVTKSIVALRLTLVVKVSTCVPGESHAN
DLECSGKKGKCTTKPSEATFSCCTCEEQYVGTFCEEYDACQKPCQNNASCIDANEKQDGSNFTC
VCLPGYTGELCQSKIDYCLDPCRNGATCISSLSGFTCQCPEGYFGSACEEKVDPCASSPCQN
NGTCYVDGVHFTCNCSPGFTGPTCAQLIDFCALSPCAHGTCRSVGTSYKCLCDPGYHGLYCEE
EYNECLSAAPCLNAATCRDLVNGYECVCLAEYKGTHELYKDPCANVSCLNGATCDSGDLNGTC
ICAPGFTGEECDIDINECDSPCHHGGSCLDQPNGYNCHCPHGWVGANCEIHLQWKS GHMAES
LTNMPRHSLYIIIGALCVAFILMLIILIVGICRISRIEYQGSSRPAYEEFYNCRSIDSEFSNA
IASIRHAREFGKSRPAMYDVSPAIYEDYSPDDKPLVTLIKTKDL

Signal sequence.

amino acids 1-28

Transmembrane domain.

amino acids 641-660

N-glycosylation sites.amino acids 107-111, 204-208, 208-212, 223-227, 286-290, 361-365,
375-379, 442-446, 549-553, 564-568**Glycosaminoglycan attachment site.**

amino acids 320-324

Tyrosine kinase phosphorylation sites.

amino acids 490-498, 674-682

N-myristoylation sites.amino acids 30-36, 56-62, 57-63, 85-91, 106-112, 203-209,
373-379, 449-455, 480-486, 562-568, 565-571**Amidation site.**

amino acids 702-706

Aspartic acid and asparagine hydroxylation site.

amino acids 520-532, 596-608

EGF-like domain cysteine pattern signatures.amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466,
491-503, 529-541, 567-579, 605-617

FIGURE 39

GAGCCGCCGCCGCGCGCGCGCGCCGCGCACTGCAGCCCCAGGCCCGGCCCCCCACCCACGTCTG
CGTTGCTGCCCCGCCTGGGCCAGGCCCAAAGGCAAGGACAAAGCAGCTGTCAGGGAACCTCC
GCCGGAGTCGAATTTACGTGCAGCTGCCGGCAACCACAGGTTCCAAGATCGTTTTGCGGGGGCT
TCGCGTGTTCCAAGAACTGCCTGTGCGCCCTCAACCTGCTTTACACCTTGGTTAGTCTGCTGC
TAATTGGAATTGCTGCGTGGGGCATTGGCTTCGGGCTGATTTCCAGTCTCCGAGTGGTCGGCC
TGGTCATTGCAGTGGGCATCTTCTTGTTCTGATTGCTTTAGTGGGTCTGATTGGAGCTGTAA
AACATCATCAGGTGTTGCTATTTTTTTTATATGATTATTCTGTTACTTGTATTTATTGTTTCAGT
TTTCTGTATCTTGCGCTTGTTTAGCCCTGAACCAGGAGCAACAGGGTCAGCTTCTGGAGGTTG
GTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAATCTAAACTGCTGTGGGTTCC
GAAGTGTTAACCCAAATGACACCTGTCTGGCTAGCTGTGTTAAAAGTGACCACTCGTGCTCGC
CATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGAGATTTGTTGGTGGCATTGGCC
TGTTCTTTCAGTTTTTACAGAGATCCTGGGTGTTTGGCTGACCTACAGATACAGGAACCAGAAAG
ACCCCCGCGCGAATCCTAGTGCATTCTTTTGAATGAGAAAACAAGGAAGATTTCTTTTCGTATT
ATGATCTTGTTCACTTTCTGTAATTTTTCTGTTAAGCTCCATTTGCCAGTTTAAGGAAGGAAAC
ACTATCTGGAAAAGTACCTTATTGATAGTGGAATTATATATTTTTTACTCTATGTTTTCTCTACA
TGTTTTTTTTCTTTCCGTTGCTGAAAAATATTTGAAACTTGTGGTCTCTGAAGCTCGGTGGCAC
CTGGAATTTACTGTATTCATTGTGCGGGCACTGTCCACTGTGGCCTTTCTTAGCATTTTTTACCT
GCAGAAAAAATTTGTATGGTACCCTGTGTTGGTTATATGGTGAATCTGAACGTACATCTCAC
TGGTATAATTATATGTAGCACTGTGCTGTGTAGATAGTTCCTACTGGAAAAAGAGTGGAAATT
TATTAAAATCAGAAAGTATGAGATCCTGTTATGTTAAGGGAAATCCAAATTTCCCAATTTTTTT
TGGTCTTTTTTAGGAAAGATTGTTGTGGTAAAAAGTGTTAGTATAAAAATGATAATTTACTTGT
AGTCTTTTTATGATTACACCAATGTATTCTAGAAATAGTTATGTCTTAGGAAATTGTGGTTAA
TTTTTGACTTTTTACAGGTAAGTGCAAAAGGAGAAAGTGGTTTTCATGAAATGTTCTAATGTATAAT
AACATTTACCTTCAGCCTCCATCAGAATGGAACGAGTTTGTAGTAATCAGGAAGTATATCTAT
ATGATCTTGATATTGTTTTTATAATAATTTGAAGTCTAAAAGAGTCGATTTTTTAAACAAGTTAG
TATTAATGCGTTGGCCACGTAGCAAAAAGATATTTGATTATCTTAAAAAATGTTAAATACCG
TTTTTCATGAAATTTCTCAGTATTGTAACAGCAACTTGTCAAACCTAAGCATATTTGAATATGA
TCTCCCATAAATTTGAAATTGAAATCGTATTGTGTGGCTCTGTATATTCTGTTAAAAAATTTAA
GGACAGAAACCTTTCTTTGTGTATGCATGTTTGAATTTAAAGAAAGTAATGGAAG

40/615

FIGURE 40

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39979
><subunit 1 of 1, 204 aa, 1 stop
><MW: 22147, pI: 8.37, NX(S/T): 3
MVCGGFACSKNCLCALNLLYTLVSLLLIGIAAWGIGFGLISSLRVVGVVIAVGIFLFLIALVG
LIGAVKHHQVLLFFYMIILLVLFIVQFSVSCACLALNQEQQGQLLEVGNNTASARNDIQRL
NCCGFRSVNPNDTCLASCVKSDHSCSPCAPIIGEYAGEVLRVFGGIGLFFSFTEILGVWLTyr
YRNQKDPRANPSAFL
```

Signal Peptide:
amino acids 1-34

Transmembrane domains:
amino acids 47-63, 72-95 and 162-182

41/615

FIGURE 41

CAGTCACCAATGAAGCTGGGCTGTGTCTCATGGCCTGGGCCCTCTACCTTTCCCTTGGTGTGC
TCTGGGTGGCCAGATGCTACTGGCTGCCAGTTTTGAGACGCTGCAGTGTGAGGGACCTGTCT
GCACTGAGGAGAGCAGCTGCCACACGGAGGATGACTTGACTGATGCAAGGGAAGCTGGCTTCC
AGGTCAAGGCCTACACTTTCAGTGAACCCCTCCACCTGATTGTGTCTATGACTGGCTGATCC
TCCAAGGTCCAGCCAAGCCAGTTTTTGAAGGGGACCTGCTGGTTCTGCGCTGCCAGGCCTGGC
AAGACTGGCCACTGACTCAGGTGACCTTCTACCGAGATGGCTCAGCTCTGGGTCCCCCGGGC
CTAACAGGGAATTCTCCATCACCGTGGTACAAAAGGCAGACAGCGGGCACTACCACTGCAGTG
GCATCTTCCAGAGCCCTGGTCTGGGATCCCAGAAACAGCATCTGTTGTGGCTATCACAGTCC
AAGAACTGTTTCCAGCGCCAATTCTCAGAGCTGTACCCTCAGCTGAACCCCAAGCAGGAAGCC
CCATGACCCTGAGTTGTCAGACAAAGTTGCCCTGCAGAGGTGAGCTGCCCCGCTCCTCTTCT
CCTTCTACAAGGATGGAAGGATAGTGCAAAGCAGGGGGCTCTCCTCAGAATTCAGATCCCCA
CAGCTTCAGAAGATCACTCCGGGTCACTACTGGTGTGAGGCAGCCACTGAGGACAACCAAGTTT
GGAAACAGAGCCCCAGCTAGAGATCAGAGTGCAGGGTGCTTCCAGCTCTGCTGCACCTCCCA
CATTGAATCCAGCTCCTCAGAAATCAGCTGCTCCAGGAAGTCTCCTGAGGAGGCCCTGGGC
CTCTGCCTCCGCCGCCAACCCCATCTTCTGAGGATCCAGGCTTTTCTTCTCCTCTGGGGATGC
CAGATCCTCATCTGTATCACAGATGGGCCTTCTTCTCAAACACATGCAGGATGTGAGAGTCC
TCCTCGGTACCTGCTCATGGAGTTGAGGGAATTATCTGGCCACCAGAAGCCTGGGACCACAA
AGGCTACTGCTGAATTAGAAGTAAACAGTTCATCCATGATCTCACTTAACCACCCCAATAAATC
TGATTCTTTATTTTCTCTTCCTGTCCTGCACATATGCATAAGTACTTTTACAAGTTGTCCAG
TGTTTTGTTAGAATAATGTAGTTAGGTGAGTGTAATAAATTTATATAAAGTGAGAATTAGAG
TTTAGCTATAATTGTGTATTCTCTCTTAACACAACAGAATTCTGCTGTCTAGATCAGGAATTT
CTATCTGTTATATCGACCAGAATGTTGTGATTTAAAGAGAACTAATGGAAGTGGATTGAATAC
AGCAGTCTCAACTGGGGGCAATTTTGGCCCCCAGAGGACATTGGGCAATGTTTGGAGACATTT
TGGTCATTATACTTGGGGGGTTGGGGGATGGTGGGATGTGTGTCTACTGGCATCCAGTAAATA
GAAGCCAGGGGTGCCGCTAAACATCCTATAATGCACAGGGCAGTACCCCAACGAAAAATAA
TCTGGCCCAAAATGTCAGTTGTACTGAGTTTGAGAAACCCAGCCTAATGAAACCCTAGGTGT
TGGGCTCTGGAATGGGACTTTGTCCCTTCTAATTATTATCTCTTTCCAGCCTCATTGAGCTAT
TCTTACTGACATACCAGTCTTTAGCTGGTGTATGGTCTGTTCTTTAGTTCTAGTTTGTATCC
CCTCAAAGCCATTATGTTGAAATCCTAATCCCCAAGGTGATGGCATTAAAGAAGTGGGCCTTT
GGGAAGTGATTAGATCAGGAGTGCAGAGCCCTCATGATTAGGATTAGTGCCTTATTTAAAAA
GGCCCCAGAGAGCTAACTCACCTTCCACCATATGAGGACGTGGCAAGAAGATGACATGTATG
AGAACCAAAAAACAGCTGTCGCCAAACACCGACTCTGTCGTTGCCTTGATCTTGAACCTCCAG
CCTCCAGAATATGAGAAATAAAATTCTGGTTGTTTGTAGCCTAA

42/615

FIGURE 42

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40594
><subunit 1 of 1, 359.aa, 1 stop
><MW: 38899, pI: 5.21, NX(S/T): 0
MKLGCVLMAWALYLSLGV LWVAQM LLAASFETLQCEGPVCTEESSCHTEDDLTDAREAGFQVK
AYTFSEPFHLIVSYDWLILQGPAPVFEGLLVLRQAWQDWPLTQVTFYRDGSALGPPGPNR
EFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVAITVQELFPAPILRAVPSAEPQAGSPMT
LSCQTKLPLQRSAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQVWKQ
SPQLEIRVQGASSSAAPPTLNPAPQKSAAPGTAPEEAPGPLPPPPTPSSDPGFSSPLGMPDP
HLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHQKPGTTKATAE

Signal sequence:

amino acids 1-17

Leucine zipper pattern sequence:

amino acids 12-33

Protein kinase C phosphorylation site:

amino acids 353-355

43/615

FIGURE 43

GCGAGTGTCCAGCTGCGGAGACCCGTGATAATTCGTTAACTAATTCAACAAACGGGACCCTTC
TGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGGACAGGCGGATTGGAAGAGCGGGAA
GGTCTTGGCCAGAGCAGTGTGACACTTCCCTCTGTGACC**ATG**AAACTCTGGGTGTCTGCATT
GCTGATGGCCTGGTTTGGTGTCTGAGCTGTGTGCAGGCCGAATTCTTCACCTCTATTGGGCA
CATGACTGACCTGATTTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATCCTTGT
GGAGGAAGCCAAGCTTTCCAAGATTAAAGAGCTGGGCCAACAAAATGGAAGCCTTGACTAGCAA
GTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCTACAACTGGTGAAGCG
GCTAAACACAGACTGGCCTGCGCTGGAGGACCTTGTCTGCAGGACTCAGCTGCAGGTTTTAT
CGCCAACCTCTCTGTGCAGCGGCAGTTCTTCCCCACTGATGAGGACGAGATAGGAGCTGCCAA
AGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTTCCAGAGGGGA
TCCAGGAACCAAGTACCAGGCAATGCTGAGTGTGGATGACTGCTTTGGGATGGGCCGCTCGGC
CTACAATGAAGGGGACTATTATCATACGGTGTGTGGATGGAGCAGGTGCTAAAGCAGCTTGA
TGCCGGGGAGGAGGCCACCACAACCAAGTCACAGGTGCTGGACTACCTCAGCTATGCTGTCTT
CCAGTTGGGTGATCTGCACCGTGCCCTGGAGCTACCCGCCGCCTGCTCTCCCTTGACCCAAG
CCACGAACGAGCTGGAGGGAATCTGCGGTACTTTGAGCAGTTATTGGAGGAAGAGAGAGAAAA
AACGTTAAACAAATCAGACAGAAGCTGAGCTAGCAACCCAGAAAGGCATCTATGAGAGGCCTGT
GGACTACCTGCCTGAGAGGGATGTTTACGAGAGCCTCTGTCTGTTGGGAGGGTGTCAAACCTGAC
ACCCCGTAGACAGAAGAGGCTTTTCTGTAGGTACCACCATGGCAACAGGGCCCCACAGCTGCT
CATTGCCCCCTTCAAAGAGGAGGACGAGTGGGACAGCCCGCACATCGTCAGGTACTACGATGT
CATGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAACCTAAACTTGCACGAGCCAC
CGTTTCGTGATCCCAAGACAGGAGTCTCACTGTGCGCAGCTACCGGGTTTCCAAAAGCTCCTG
GCTAGAGGAAGATGATGACCCTGTTGTGGCCCGAGTAAATCGTCGGATGCAGCATATCACAGG
GTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAATTATGGAGTGGGAGGACAGTATGA
ACCGCACTTCGACTTCTCTAGGCGACCTTTTGACAGCGGCCTCAAAACAGAGGGGAATAGGTT
AGCGACGTTTCTTAACTACATGAGTGTGTAGAAGCTGGTGGTGCCACCGTCTTCCCTGATCT
GGGGGCTGCAATTTGGCCTAAGAAGGGTACAGCTGTGTTCTGGTACAACCTCTTGCGGAGCGG
GGAAGGTGACTACCGAACAAGACATGCTGCCTGCCCTGTGCTTGTGGGCTGCAAGTGGGTCTC
CAATAAGTGGTTCCATGAACGAGGACAGGAGTTCTTGAGACCTTGTGGATCAACAGAAGTTGA
CTGACATCCTTTTCTGTCTTCCCCCTCCTGGTCCTTCAGCCCATGTCAACGTGACAGACACC
TTTGTATGTTCCCTTTGTATGTTCCCTATCAGGCTGATTTTGGAGAAATGAATGTTTGTCTGGA
GCAGAGGGAGACCATACTAGGGCGACTCCTGTGTGACTGAAGTCCCAGCCCTTCCATTACGCC
TGTGCCATCCCTGGCCCCAAGGCTAGGATCAAAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGC
CTAGCAAGGTGCCCTTTGTACCTCAGGTGTTTTAGGTGTGAGATGTTTCAGTGAACCAAAGTTC
TGATACCTTGTTTACATGTTTGTGTTTTATGGCATTCTATCTATTGTGGCTTTACCAAAAAAT
AAAATGTCCCTACCAGAAAAA

44/615

FIGURE 44

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWAN
KMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALDVLQDSAAGFIANLSVQRQFFPTD
EDEIGAALKMRLQDTYRLDPGTISRGEIPGTYQAMLSVDDCFMGRSAYNEGDIYHTVLWM
EQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRRLSLDPSHERAGGNLRYFEQ
LLEEEREKTLTNQTEAELATPEGIYERPDVYLPEDVYESLCRGEVGLTPRRQKRLFCRYHH
GNRAPQLLIAPFKEEDEWDSPIVRYDVMSDEEIERIKEIAKPKLARATVRDPKTGVLTVAS
YRVSKSSWLEEDDPVVARVNRRMQHITGLTVKTAELLQVANYGVGGQYEPHFDPSRRPFDSG
LKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEVDYRTRHAACPV
LVGCKWVSNKWFHERGQEFRLPCGSTVD

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534**Tyrosine kinase phosphorylation site.**

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

45/615

FIGURE 45

GGGGCCTTGCCCTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGGG
CGGCGGGCGCGGGTGGCAGGGATCCCTGACGCCTCTGTCCCTGTTTCTTTGTGCTCCAGCC
TGTCTGTCGTGTTTTGGCGCCCCCGCCTCCCCGCGGTGCGGGGTGCACACCGATCCTGGGC
TTCGCTCGATTTGCCGCCGAGGCGCTCCCAGACCTAGAGGGGCGCTGGCCTGGAGCAGCGGG
TCGTCTGTGCTCTCTCTCTGCGCCGCGCCGGGGATCCGAAGGGTGCGGGGCTCTGAGGA
GGTGACGCGCGGGGCCTCCCGCACCTGGCCTTGCCCGCATTCTCCCTCTCTCCAGGTGTGA
GCAGCCTATCAGTCACCATGTCCGCAGCCTGGATCCCGGCTCTCGGCCTCGGTGTGTGTCTGC
TGCTGCTGCCGGGGCCCCGCGGGCAGCGAGGGAGCCGCTCCCATTGCTATCACATGTTTTACCA
GAGGCTTGACATCAGGAAAGAGAAAGCAGATGTCTCTGCCAGGGGGCTGCCCTCTTGAGG
AATTCTCTGTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGGGCTGCTGTCC
ACAGGGGAGTAATCAGCAACTCAGGGGGACCTGTACGAGTCTATAGCCTACCTGGTCGAGAAA
ACTATTCCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTTCTAGATGGTCTGCTTCTT
TCACAGTAACTAAAGGCAAAAGTAGTACACAGGAGGCCACAGGACAAGCAGTGTCCACAGCAC
ATCCACCAACAGGTAAACGACTAAAGAAAACACCCGAGAAGAAAACCTGGCAATAAAGATTGTA
AAGCAGACATTGCATTTCTGATTGATGGAAGCTTTAATATTGGGCAGCGCCGATTTAATTTAC
AGAAGAATTTTGTTGGAAAAGTGGCTCTAATGTTGGGAATTGGAACAGAAGGACCACATGTGG
GCCTTGTTCAAGCCAGTGAACATCCCAAATAGAATTTTACTTGAAAACTTTACATCAGCCA
AAGATGTTTTGTTTGCCATAAAGGAAGTAGGTTTTAGAGGGGGTAATCCAATACAGGAAAAG
CCTTGAAGCATACTGCTCAGAAATTCCTCACGGTAGATGCTGGAGTAAGAAAAGGGATCCCCA
AAGTGGTGGTGGTATTTATTGATGGTTGGCCTTCTGATGACATCGAGGAAGCAGGCATTGTGG
CCAGAGAGTTTGGTGTCAATGTATTTATAGTTTCTGTGGCCAAGCCTATCCCTGAAGAACTGG
GGATGGTTCAGGATGTCACATTTGTTGACAAGGCTGTCTGTGCGGAATAATGGCTTCTTCTCTT
ACCACATGCCCAACTGGTTTGGCACCACAAAATACGTAAAGCCTCTGGTACAGAAGCTGTGCA
CTCATGAACAAATGATGTGCAGCAAGACCTGTTATAACTCAGTGAACATTGCCTTTCTAATTG
ATGGCTCCAGCAGTGTGGAGATAGCAATTTCCGCCTCATGCTTGAATTTGTTTCCAACATAG
CCAAGACTTTTGAAATCTCGGACATTGGTGCCAAGATAGCTGCTGTACAGTTTACTTATGATC
AGCGCACGGAGTTCAGTTTCACTGACTATAGCACCAAAGAGAATGTCCTAGCTGTATCAGAA
ACATCCGCTATATGAGTGGTGGAAACAGCTACTGGTGATGCCATTTCCCTCACTGTTAGAAATG
TGTTTGGCCCTATAAGGGGAGAGCCCCAACAAGAACTTCCTAGTAATTGTCACAGATGGGCAGT
CCTATGATGATGTCCAAGGCCCTGCAGCTGCTGCACATGATGCAGGAATCACTATCTTCTCTG
TTGGTGTGGCTTGGGCACCTCTGGATGACCTGAAAGATATGGCTTCTAAACCGAAGGAGTCTC
ACGCTTTCTTCACAAGAGAGTTTACAGGATTAGAACCAATTGTTTCTGATGTCATCAGAGGCA
TTTGTAGAGATTTCTTAGAATCCAGCAATAATGGTAACATTTTGACAACCTGAAAGAAAAAGT
ACAAGGGGATCCAGTGTGTAAATTGTATTCTCATAATACTGAAATGCTTTAGCATACTAGAAT
CAGATACAAAACCTATTAAGTATGTCAACAGCCATTTAGGCAAATAAGCACTCCTTTAAAGCCG
CTGCCTTCTGGTTACAATTTACAGTGTACTTTGTTAAAAACACTGCTGAGGCTTCATAATCAT
GGCTCTTAGAACTCAGGAAAGAGGAGATAATGTGGATTAAAACCTTAAGAGTTCTAACCATG
CCTACTAAATGTACAGATATGCAAATTCATAGCTCAATAAAAGAATCTGATACTTAGACCAA
AAAAAAA

46/615

FIGURE 46

MSAAWIPALGLGVCLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPGGCPLLEFSVYG
NIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFVTKG
KSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIGQRRENLOKNFVG
KVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFAIKEVGFRGGNSNTGKALKHTA
QKFFTVDAGVRKGIPKVVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELGMVQDV
TFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLIDGSSSV
GDSNFRMLLEFVSNIAKTFEISDIGAKIAAVQFTYDQORTEFSFTDYSTKENVLAVIRNIRYMS
GGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAAHDAGITIFSVGVAVA
PLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532**N-myristoylation site.**amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449**Amidation site.**

amino acids 145-149

47/615

FIGURE 47

GCCCCGCGCCCGGCGCCGGGCGCCCCGAAGCCGGGAGCCACCGCCATGGGGGCCTGCCTGGGAG
CCTGCTCCCTGCTCAGCTGCGCGTCCTGCCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAGCT
GCTGCCCCGCCAGCCGCAACTCCACCGTGAGCCGCCCTCATCTTCACGTTCTTCCTCTTCCTGG
GGGTGCTGGTGTCCATCATTATGCTGAGCCCCGGGCGTGGAGAGTCAGCTCTACAAGCTGCCCT
GGGTGTGTGAGGAGGGGGCCGGGATCCCCACCGTCCTGCAGGGCCACATCGACTGTGGCTCCC
TGCTTGGCTACCGCGCTGTCTACCGCATGTGCTTCGCCACGGCGGCCTTCTTCTTCTTCTTTT
TCACCCTGCTCATGCTCTGCGTGAGCAGCAGCCGGGACCCCCGGGCTGCCATCCAGAATGGGT
TTTGGTTCTTTAAGTTCCTGATCCTGGTGGGCCTCACCGTGGGTGCCTTCTACATCCCTGACG
GCTCCTTCACCAACATCTGGTTCTACTTCGGCGTCGTGGGCTCCTTCCTCTTCATCCTCATCC
AGCTGGTGCTGCTCATCGACTTTGCGCACTCCTGGAACCAGCGGTGGCTGGGCAAGGCCGAGG
AGTGCGATTCCCGTGCCCTGGTACGAGGCCTCTTCTTCTTCACTCTCCTCTTCTACTTGCTGT
CGATCGCGGCCGTGGCGCTGATGTTCACTGTACTACACTGAGCCCAGCGGCTGCCACGAGGGCA
AGGTCTTCAGCATGCCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCTGCTGTCTGCCCA
AGGTCCAGGACGCCCCAGCCCAACTCGGGTCTGCTGCAGGCCTCGGTCATCACCTCTACACCA
TGTTTGTACCTGTGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCAACCCCCATTGCCCCA
CCCAGCTGGGCAACGAGACAGTTGTGGCAGGCCCCGAGGGCTATGAGACCCAGTGGTGGGATG
CCCCGAGCATTGTGGGCCTCATCATCTTCTCCTGTGCACCCTCTTCATCAGTCTGCGCTCCT
CAGACCACCGGCAGGTGAACAGCCTGATGCAGACCGAGGAGTGCCCACCTATGCTAGACGCCA
CACAGCAGCAGCAGCAGCAGGTGGCAGCCTGTGAGGGCCGGGCCTTTGACAACGAGCAGGACG
GCGTCACCTACAGCTACTCCTTCTTCCACTTCTGCCTGGTGCTGGCCTCACTGCACGTCATGA
TGACGCTCACCAACTGGTACAAGCCCGGTGAGACCCGGAAGATGATCAGCACGTGGACCGCCG
TGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCTCCTCTACCTGTGGACCCTGGTAGCCC
CACTCCTCCTGCGCAACCGCGACTTCAGCTTAGAGGCAGCCTCACAGCCTGCCATCTGGTGCCTC
CTGCCACCTGGTGCCTCTCGGCTCGGTGACAGCCAACCTGCCCCCTCCCCACACCAATCAGCC
AGGCTGAGCCCCCACCCTGCCCCAGCTCCAGGACCTGCCCTGAGCCGGGCCTTCTAGTCGT
AGTGCCCTTCAGGGTCCGAGGAGCATCAGGCTCCTGCAGAGCCCCATCCCCCGCCACACCCAC
ACGGTGGAGCTGCCTCTTCTTCCCCCTCCTCCCTGTTGCCATACTCAGCATCTCGGATGAAA
GGGCTCCCTTGTCTCAGGCTCCACGGGAGCGGGGCTGCTGGAGAGAGCGGGGAACCTCCACC
ACAGTGGGGCATCCGGCACTGAAGCCCTGGTGTTCCTGGTCACGTCCCCCAGGGGACCCTGCC
CCCTTCTGGACTTCGTGCCTTACTGAGTCTCTAAGACTTTTTCTAATAAACAAGCCAGTGCG
TGTAATAAAAAA

48/615

FIGURE 48

MGACLGACSLLSASCCLCGSAPCILCSCCPASRNSTVSRLLFTFFFLGVLVSIIMLSPGVES
QLYKLPWVCEEAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFFTLLMLCVSSSRDPR
AAIQNGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSFLFILIQLVLLIDFAHSWNQR
WLGKAEECDSRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTFVCVVS
IAAVLPKVQDAQPNSSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVAGPEGY
ETQWWDAPSIVGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQQVAACEGRA
FDNEQDGVITYSYSFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVVWKICASWAGLLLY
LWTLVAPLLLNRNDFS

Signal sequence:

amino acids 1-20

Transmembrane domains:amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,
272-283, 324-340, 391-406, 428-444

FIGURE 49

[illegible]

50/615

FIGURE 50

MAGIPGLLELLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDPFGAEAKLEVSS
SCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYIILSSSGDGAQHRDSGSSGKSRR
KRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGKTYVKGTQK
LRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKNANDIGMDYDYALLEL
KKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCDAQPGA
SGSGVYVRMWRQOQKWERKIIGIFSGHQWDMNGSPQDFNAVVRITPLKYAQICYWIKGNYL
DCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

51/615

FIGURE 51

GGGAGGGGGCTCCGGGCGCCGCGCAGCAGACCTGCTCCGGCCGCGCGCCTCGCCGCTGTCTCCGGGAGCGGCAG
CAGTAGCCCGGGCGGCGAGGGCTGGGGTTCTCGAGACTCTCAGAGGGGCGCCTCCCATCGGCGCCACCACCC
CAACCTGTTCTCGCGCGCCACTGCGCTGCGCCCCAGGACCCGCTGCCAACATGGATTTTCTCTGGCGCTGGT
GCTGGTATCCTCGCTCTACCTGCAGGCGGCCGCGGAGTTCGACGGGAGGTGGCCAGGCAAATAGTGTATCGAT
TGGCCTATGTCGTTATGGTGGGAGGATTGACTGCTGCTGGGGCTGGGCTCGCCAGTCTTGGGGACAGTGTACGCC
TGTGTGCCAACACGATGCAAACATGGTGAATGTATCGGGCCAAACAAGTGCAAGTGTATCCTGGTTATGCTGG
AAAAACCTGTAATCAAGATCTAAATGAGTGTGGCCTGAAGCCCCGGCCTGTAAGCACAGGTGCATGAACACTTA
CGGCAGCTACAAGTGCTACTGTCTCAACGGATATATGCTCATGCCGATGGTTCTGCTCAAGTGCCCTGACCTG
CTCCATGGCAAACCTGTAGTATGGCTGTGATGTTGTTAAAGGACAAATACGGTGCCAGTGCCCATCCCCTGGCCT
GCACCTGGCTCCTGATGGGAGGACCTGTGTAGATGTTGATGAATGTGCTACAGGAAGAGCCTCCTGCCCTAGATT
TAGGCAATGTGTCAACACTTTTGGGAGCTACATCTGCAAGTGTATAAAGGCTTCGATCTCATGTATATTGGAGG
CAAATATCAATGTGCATGACATAGACGAATGCTCACTTGGTCAGTATCAGTGCAGCAGCTTTGCTCGATGTTATAA
CGTACGTGGGTCCTACAAGTGCAAATGTAAAGAAGGATACCAGGGTGTGGACTGACTTGTGTGTATATCCCAAA
AGTTATGATTGAACCTTCAGGTCCAATTATGTACCAAAGGAAATGGTACCATTTTAAAGGGTGACACAGGAAA
TAATAATTGGATTCTGATGTTGGAAGTACTTGGTGGCCTCCGAAGACACCATATATTCCTCCTATCATTACCAA
CAGGCCTACTTCTAAGCCAACAACAAGACCTACACCAAAGCCAACCAATTCTACTCCACCACCACCACCACC
CCTGCCAACAGAGCTCAGAACACCTCTACCACCTACAACCCAGAAAGGCCAACCCCGGACTGACAACATATAGC
ACCAGCTGCCAGTACACCTCCAGGAGGGATTACAGTTGACAACAGGGTACAGACAGACCCTCAGAAACCCAGAGG
AGATGTGTTTCACTGTCTGGTACACAGTTGTAATTTTGACCATGGACTTTGTGGATGGATCAGGGAGAAAGACAA
TGACTTGCAGTGGGAACCAATCAGGGACCCAGCAGGTGGACAATATCTGACAGTGTGGCAGCCAAAGCCCCAGG
GGGAAAAGCTGCACGCTTGGTGCTACCTCTCGGCCGCTCATGCATTACAGGGACCTGTGCTGTCTCATTACAGGA
CAAGGTGACGGGGCTGCACTCTGGCACACTCCAGGTGTTTGTGAGAAAACACGGTGCCACGGAGCAGCCCTGTG
GGGAAGAAATGGTGGCCATGGCTGGAGGCAAACACAGATCACCTTGGCAGGGGCTGACATCAAGAGCGAATCACA
AAGATGATTAAAGGGTTGGAAAAAAGATCTATGATGGAATTAAGGAACTGGGATTATTGAGCCTGGAGAAG
AGAAGACTGAGGGGCAAACCATTTGATGTTTCAAGTATATGAAGGGTTGGCACAGAGAGGGTGGCGACCAGCTG
TTCTCCATATGCACTAAGAATAGAACAAGAGGAACTGGCTTAGACTAGAGTATAAGGGAGCATTTCTTGGCAGG
GGCCATTGTTAGAATACTTCATAAAAAAAGAGTGTGAAAATCTCAGTATCTCTCTCTCTTCTTCTAAAAAATTAGA
TAAAAATTTGTCTATTTAAGATGGTTAAAGATGTTCTTACCAAGGAAAAGTAACAAATTATAGAATTTCCCAAA
AGATGTTTTGATCTACTAGTAGTATGCAGTGAAAATCTTTAGAACTAAATAATTTGGACAAGGCTTAATTTAGG
CATTTCCCTCTTGACCTCCTAATGGAGAGGGATTGAAGGGGAAGAGCCCAACAAATGCTGAGCTCACTGAAATA
TCTCTCCCTTATGGCAATCCTAGCAGTATTAAGAAAAAAGGAACTATTTATTCCAAATGAGAGTATGATGGAC
AGATATTTTAGTATCTCAGTAATGTCTAGTGTGGCGGTGGTTTTTCAATGTTTCTTCATGGTAAAGGTATAAGCC
TTTCATTTGTTCAATGGATGATGTTTCAGATTTTTTTTTTTTTTAAAGAGATCCTTCAAGGAACACAGTTTCAAGAG
ATTTTCATCGGGTGATTCTCTCTGCTTCTGTGTGACAAGTTATCTTGGCTGCTGAGAAAGAGTGCCCTGCCCC
ACACCGGCAGACCTTTTCCTTACCTCATCAGTATGATTCAGTTTCTCTTATCAATTGGACTCTCCAGGTTCCAC
AGAACAGTAATATTTTTGAACAATAGGTACAATAGAAGGTCTTCTGTCAATTAACTGGTAAAGGCAGGGCTGG
AGGGGGAAAATAAATCATTAAGCCTTTGAGTAACGGCAGAATATATGGCTGTAGATCCATTTTAAATGGTTTCAAT
TCCTTTATGGTCATATAACTGCACAGCTGAAGATGAAAGGGGAAAATAAATGAAAATTTTACTTTTCGATGCCAA
TGATACATTGCACTAACTGATGGAAGAAGTTATCCAAAGTACTGTATAACATCTTGTATTATTTAATGTTTT
CTAAAATAAAAAATGTTAGTGGTTTCCAAATGGCCTAATAAAAAACAATTATTTGTAATAAAAAACACTGTTAGTAAT

52/615

FIGURE 52

MDFLALVLVSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQPR
CKHGECIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPDGS
CSSALTCSMANCQYGC DVVKGQIRCQCPSPGLHLAPDGRTCV DVDECATGRASCPRFRQCVNT
FGSYICKCHKGFDL MYIGGKYQCHDIDEC SLGQYQCSSFARCYNVRGSYKCKCKEGYQGDGLT
CVYIPKVMIEPSGPIHV PKNGTILKGD TGNNNWIPDVGSTWWPPKTPYIPPIITNRPTSKPT
TRPTPKPTPIPTPPPPPLPTELRTPLPPTT PERPTTGLTTIAPAASTPPGGITVDNRVQTD P
QKPRGDVFSVLVHSCNFDHGLCGWIREKDNDLHWEPIRDPAGGQYLTVSAAKAPGGKAARLVL
PLGRLMHSGDLCL SFRHKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQITLRGADIK
SESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482**Aspartic acid and asparagine hydroxylation site.**

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

53/615

FIGURE 53

CGGGCCGCCCCCGGCCCCATTTCGGGCCGGGCCTCGCTGCGGCGGGCGACTGAGCCAGGCTGGG
CCGCGTCCCTGAGTCCCAGAGTCGGCGCGGGCGGGCAGGGGCAGCCTTCCACCACGGGGAGCC
CAGCTGTCAGCCGCTCACAGGAAGATGCTGCGTCGGCGGGGCAGCCCTGGCATGGGTGTGCA
TGTGGGTGCAGCCCTGGGAGCACTGTGGTTCTGCCTCACAGGAGCCCTGGAGGTCCAGGTCCC
TGAAGACCCAGTGGTGGCACTGGTGGGCACCGATGCCACCCTGTGCTGCTCCTTCTCCCCTGA
GCCTGGCTTCAGCCTGGCACAGCTCAACCTCATCTGGCAGCTGACAGATACCAAACAGCTGGT
GCACAGCTTTGCTGAGGGCCAGGACCAGGGCAGCGCCTATGCCAACCGCACGGCCCTCTTCCC
GGACCTGCTGGCACAGGGCAACGCATCCCTGAGGCTGCAGCGCGTGCCTGTGGCGGACGAGGG
CAGCTTCACCTGCTTCGTGAGCATCCGGGATTTTCGGCAGCGCTGCCGTGAGCCTGCAGGTGGC
CGCTCCCTACTCGAAGCCCAGCATGACCTGGAGCCCAACAAGGACCTGCGGCCAGGGGACAC
GGTGACCATCACGTGCTCCAGCTACCAGGGCTACCCTGAGGCTGAGGTGTTCTGGCAGGATGG
GCAGGGTGTGCCCCCTGACTGGCAACGTGACCACGTGCGCAGATGGCCAACGAGCAGGGCTTGTT
TGATGTGCACAGCGTCCTGCGGGTGGTGTGGGTGCGAATGGCACCTACAGCTGCCTGGTGGC
CAACCCCGTGCTGCAGCAGGATGCGCACRGCTCTGTACCATCACAGGGCAGCCTATGACATT
CCCCCAGAGGCCCTGTGGGTGACCGTGGGGCTGTCTGTCTGTCTCATTGCACTGCTGGTGGC
CCTGGCTTTCTGTGTGCTGGAGAAAGATCAAACAGAGCTGTGAGGAGGAGAATGCAGGAGCTGA
GGACCAGGATGGGGAGGGAGAAGGCTCCAAGACAGCCCTGCAGCCTCTGAAACACTCTGACAG
CAAAGAAGATGATGGACAAGAAATAGCCTGACCATGAGGACCAGGGAGCTGCTACCCCTCCCT
ACAGCTCCTACCCTCTGGCTGCAATGGGGCTGCACTGTGAGCCCTGCCCCAACAGATGCATC
CTGCTCTGACAGGTGGGCTCCTTCTCCAAAGGATGCGATACACAGACCACTGTGCAGCCTTAT
TTCTCCAATGGACATGATTCCCAAGTCATCCTGCCTGCTGCCTTTTTTTCTTATAGACACAATGAACA
GACCACCCACAACCTTAGTTCTCTAAGTCATCCTGCCTGCTGCCTTATTTACAGTACATACA
TTTCTTAGGGACACAGTACACTGACCACATCACCACCTCTTCTTCCAGTGCTGCGTGGACCA
TCTGGCTGCCTTTTTTTCTCCAAAAGATGCAATATTCAGACTGACTGACCCCTGCCTTATTTT
ACCAAAGACACGATGCATAGTCACCCCGGCCCTTGTTTCTCCAATGGCCGTGATACACTAGTGA
TCATGTTTCAGCCCTGCTTCCACCTGCATAGAATCTTTTCTTCTCAGACAGGGACAGTGCGGCC
TCAACATCTCCTGGAGTCTAGAAGCTGTTTCCTTTCCCTCCTTCCCTGCCCAAGTGAA
GACAGGGCAGGGCCAGGAATGCTTTGGGGACACCGAGGGGACTGCCCCCACCACCATGG
TGCTATTCTGGGGCTGGGGCAGTCTTTTCTGGCTTGCTCTGGCCAGCTCCTGGCCTCTGGT
AGAGTGAGACTTCAGACGTTCTGATGCCTTCGGATGTCATCTCTCCTGCCCAAGGAATGGA
AGATGTGAGGACTTCTAATTTAAATGTGGGACTCGGAGGGATTTTGTAAGTGGGGGTATATT
TTGGGGAAAATAAATGTCTTTGTAAAAA

54/615

FIGURE 54

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41386
><subunit 1 of 1, 316 aa, 1 stop, 1 unknown
><MW: -1, pI: 4.62, NX(S/T): 4
MLRRRGSPGMGVHVGAAALGALWFCLTGALEVQVPEDPVVALVGTDATLCCSFSPPEPGFSLAQL
NLIWQLTDTKQLVHSFAEGDQGSAYANRTALFPDLLAQGNASRLRLQVRVADEGSFTCFVSI
RDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVITC SSYQGYPEAEVFWQDGQGVPLTGN
VTTSQMANEQGLFDVHSVLRVVLGANGTYSLVRNPVLQQDAHXSVTITGQPMTFPPEALWVT
VGLSVCLIALLLVALAFVCWRKIKQSCEENAGAEDQDGE GEGSKTALQPLKHSDSKEDDGQEIA

Important features:**Signal peptide:**

amino acids 1-28

Transmembrane domain:

amino acids 251-270

N-glycosylation site.

amino acids 91-94, 104-107, 189-192 and 215-218

Homologous region to Immunoglobulins and MHC

amino acids 217-234

55/615

FIGURE 55

GAGTCTTGACCGCCGCCGGGCTCTTGGTACCTCAGCGCGAGCGCCAGGCGTCCGGCCGCCGTG
GCTATGTTCGTGTCCGATTTCCGCAAAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCCTT
CTCTTCGTGGCCTCGGACGTGGATGCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTCCAG
TGTGACCACGTGCAATATACGCTGGTTCCAGTTTCTGGGTGGCAAGAACTTGAACTGCATTT
CTTGAGCATAAAGAACAGTTTCATTATTTTATTCTCATAACTGTGGAGCTAATGTAGACCTA
TTGGATATTCTTCAACCTGATGAAGACACTATATTCTTTGTGTGTGACTCCCATAGGCCAGTC
AATGTCGTCAATGTATACAACGATACCCAGATCAAATTACTCATTAACAAGATGATGACCTT
GAAGTTCCTCGCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATTTCAGGAAAT
GACAGTGATGGGTGACAGCCTTCTGAGAAGCGCACACGGTTAGAAGAGGAGATAGTGGAGCAA
ACCATGCGGAGGAGGCAGCGGCGAGAGTGGGAGGCCCGGAGAAGAGACATCCTCTTTGACTAC
GAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGATGTTTGAGCTGGCTTGGATGCTG
TCCAAGGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAACAGACCAGTGGGTGCAA
GACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGTCTGACGCGCCACGTTTCCCGC
CACAACCACCGGAACGAGGATGAGGAGAACACACTCTCCGTGGACTGCACACGGATCTCCTTT
GAGTATGACCTCCGCCTGGTGCTCTACCAGCACTGGTCCCTCCATGACAGCCTGTGCAACACC
AGCTATACCGCAGCCAGGTTCAAGCTGTGGTCTGTGCATGGACAGAAGCGGCTCCAGGAGTTC
CTTGCAGACATGGGTCTTCCCTGAAGCAGGTGAAGCAGAAGTTCCAGGCCATGGACATCTCC
TTGAAGGAGAATTTGCGGGAATGATTGAAGAGTCTGCAAATAAATTTGGGATGAAGGACATG
CGCGTGCAGACTTTTCAGCATTCATTTTGGGTTCAGCACAAAGTTTCTGGCCAGCGACGTGGTC
TTTGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGGATGGCTCAGGGACAGATCACTTCATC
CAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTGTACCATGGCCTGGAACCTCGCC
AAGAAGCAGCTGCGAGCCACCCAGCAGACCATTGCCAGCTGCCTTTGCACCAACCTCGTCATC
TCCCAGGGGGCCTTTCTGTACTGCTCTCTCATGGAGGGCACTCCAGATGTCATGCTGTTCTCT
AGGCCGGCATCCCTAAGCCTGCTCAGCAAACACCTGCTCAAGTCCTTTGTGTGTTTCGACAAAG
AACCGGCGCTGCAAACCTGCTGCCCCCTGGTGATGGCTGCCCCCTGAGCATGGAGCATGGCACA
GTGACCGTGGTGGGCATCCCCCAGAGACCGACAGCTCGGACAGGAAGAACTTTTTTGGGAGG
GCGTTTGAGAAGGCAGCGGAAAGCACCAGCTCCCGGATGCTGCACAACCATTTTGACCTCTCA
GTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTTCTGGACGCACTTATTTCCCTCCTGTCC
TAGGAAATTTGATTCTTCCAGAATGACCTTCTTATTTATGTAAGTGGCTTTCATTTAGATTGTA
AGTTATGGACATGATTTGAGATGTAGAAGCCATTTTTTATTAAATAAAATGCTTATTTAGGAAA

56/615

FIGURE 56

MFVSDFRKEFYEVVQSQRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQELETAFLEHKEQFHYFILINCGANVDLLDILQPDEDITFFVCDSHRPVNVVNVYNDTQIKLLIKQDDDLVPAYEDIFRDEEEDEEHSGNDSGDSEPSKRTREEEIVEQTMRRRQRREWEARRRDILFDYEQYEHGTSSAMVMFELAWMLSKDLNDMLWWAIVGLTDQWVQDKITQMKYVTDVGVLRHVSRHNHRNEDEENTLSVDCTRISFEYDLRLVLYQHWSLHDSL CNTSYTAARFKLWSVHGQKRLQEFLADMGLPLKQVKQKFQAMDISLKENLREMIEESANKFGMKDMRVQTF SIHFGFKHKFLASDVVFATMSLMESPEKDGSGTDHFIQALDSLRSNLDKLYHGLELAKKQLRATQQTIASCLCTNLVISQGPFLYCSLMEGTPDVMLFSRPASLSLLSKHLLKS FVCSTKNRRCKLLPLVMAAPLSMEHGTVTVVGIPPETDSSDRKNFFGRAFEKAAESTSSRMLHNHFDLSVIELKAEDRSKFLDALISLLS

57/615

FIGURE 57

CGCCGCCGTTGGGGCTGGAAGTTCCCGCCAGGTCCGTGCCGGGCGAGAGAGATGCTGCCCGGC
CCGCCTCGGCTTTGAGGCGAGAGAAGTGTCCCAGACCCATTTGCGCTTGCTGACGGCGTCGAG
CCCTGGCCAGACATGTCCACAGGGTTCTCCTTCGGGTCCGGGACTCTGGGCTCCACCACCGTG
GCCGCCGGCGGGACCAGCACAGGCGGCGTTTTCTCCTTCGGAACGGGAACGTCTAGCAACCCT
TCTGTGGGGCTCAATTTTGGAAATCTTGGAAAGTACTTCAACTCCAGCAACTACATCTGCTCCT
TCAAGTGGTTTTTGGAAACGGGGCTCTTTGGATCTAAACCTGCCACTGGGTTCACTCTAGGAGGA
ACAAATACAGGTGCCTTGCACACCAAGAGGCCTCAAGTGGTCACCAAATATGGAACCCTGCAA
GGAAAACAGATGCATGTGGGGAAGACACCCATCCAAGTCTTTTTAGGAGTCCCCTTCTCCAGA
CCTCCTCTAGGTATCCTCAGGTTTGCACCTCCAGAACCCCCGGAGCCCTGGAAAGGAATCAGA
GATGCTACCACCTACCCGCTGGATGGAGTCTCGCTCTGTGCGCCAGGCTGGAGTGCAGTGGCA
CGATCTCGGCTCACTGCAACCTCCGCCTCCCGGGTTCAAGCGAGTCTCCTGCCTCAGCCTCTG
AGTGTCTGGGGCTACAGGTGCCTGCAGGAGTCTGGGGCCAGCTGGCCTCGATGTACGTACGC
ACGCGGGAACGGTACAAGTGGCTGCGCTTCAGCGAGGACTGTCTGTACCTGAACGTGTACGCG
CCGGCGCGCGCGCCCGGGATCCCCAGCTGCCAGTGATGGTCTGGTTCCCGGGAGGCGCCTTC
ATCGTGGGCGCTGCTTCTTCGTACGAGGGCTCTGACTTGGCCGCGCGAGAAAGTGGTGCTG
GTGTTTTCTGCAGCACAGGCTCGGCATCTTCGGCTTCTGAGCACGGACGACAGCCACGCGCGC
GGGAAGTGGGGGCTGCTGGACCAGATGGCGGCTCTGCGCTGGGTGCAGGAGAACATCGCAGCC
TTCGGGGGAGACCCAGGAAATGTGACCCTGTTCGGCCAGTCGGCGGGGGCCATGAGCATCTCA
GGACTGATGATGTCACCCCTAGCCTCGGGTCTCTTCCATCGGGCCATTTCCCAGAGTGGCACC
GCGTTATTACAGACTTTTTCATCACTAGTAACCCACTGAAAGTGGCCAAGAAGGTGCCCCACCTG
GCTGGATGCAACCACAACAGCACACAGATCCTGGTAAACTGCCTGAGGGCACTATCAGGGACC
AAGGTGATGCGTGTGTCCAACAAGATGAGATTCCCTCCAACCTGAACTTCCAGAGAGACCCGGAA
GAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTGGTGATCCCAGATGACCCTTTGGTG
CTCCTGACCCAGGGGAAGGTTTCATCTGTGCCCTACCTTCTAGGTGTCAACAACCTGGAATTC
AATTGGCTCTTGCCTTATAATATCACCAAGGAGCAGGTACCACTTGTGGTGGAGGAGTACCTG
GACAATGTCAATGAGCATGACTGGAAGATGCTACGAAACCGTATGATGGACATAGTTCAAGAT
GCCACTTTCGTGTATGCCACACTGCAGACTGCTCACTACCACCGAGAAACCCCAATGATGGGA
ATCTGCCCTGCTGGCCACGCTACAACAAGGATGAAAAGTACCTGCAGCTGGATTTTACCACAA
GAGTGGGCATTGAAGCTCAAGGAGAAGAAGATGGCTTTTTTGGATGAGTCTGTACCAGTCTCAAA
GACCTGAGAAGCAGAGGCAATTCTAAGGGTGGCTATGCAGGAAGGAGCCAAAGAGGGGTTTGC
CCCCACCATCCAGGCCCTGGGGAGACTAGCCATGGACATACCTGGGGACAAGAGTTCTACCCA
CCCCAGTTTAGAACTGCAGGAGTCCCTGCTGCCTCCAGGCCAAAGCTAGAGCTTTTGCCTGT
TGTGTGGGACCTGCAGTGCCTTTCCAGCCTGACATCCCATGATGCCCCTCTACTTCACTGTT
GACATCCAGTTAGGCCAGGCCCTGTCAACACCACACTGTGCTCAGCTCTCCAGCCTCAGGACA
ACCTCTTTTTTTCCCTTCTTCAAATCCTCCCACCCTTCAATGTCTCCTTGTGACTCCTTCTTA
TGGGAGGTGACCCAGACTGCCACTGCCCCCTGTCACTGCACCCAGCTTGGCATTTACCATCCA
TCCTGCTCAACCTTGTTCCTGTCTGTTACATTGGCCTGGAGGCCTAGGGCAGGTTGTGACAT
GGAGCAAACCTTTTGGTAGTTTGGGATCTTCTCTCCCACCCACACTTATCTCCCCCAGGGCCAC
TCCAAAGTCTATACACAGGGGTGGTCTCTTCAATAAAGAAGTGTGATTAGAAAAAAAAAAAA

58/615

FIGURE 58

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44179
<subunit 1 of 1, 545 aa, 1 stop
<MW: 58934, pI: 9.45, NX(S/T): 4
MSTGFSFGSGTLGSTTVAAGGTSTGGVFSFGTGTSSNPSVGLNFGNLGSTSTPATTSAPSSGF
GTGLFGSKPATGFTLGGTNTGALHTKRPQVVTKYGTLQKGQMHVGKTPIQVFLGVPFSRPPLG
ILRFAPPEPPEPWKGIRDATTYPGWSLALSPGWSAVARSRLTATSASRVQASLLPQPLSVWG
YRCLQESWGLASMYVSTRERYKWLRFSEDCLYLNVPYAPARAPGDPQLPVMVWFPGGAFIVGA
ASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGNWGLLDQMAALRWVQENIAAFGGD
PGNVTILFGQSAGAMSISGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVAHLACN
HNSTQILVNCLRALSGTKVMRVSNNKMRFLQLNFQRPDEEIIWSMSPVVDGVVIPDDPLVLLTQ
GKVSSVPYLLGVNNLEFNWLLPYNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMDIVQDATFV
YATLQTAHYHRETPMMGICPAGHATTRMKSTCSWILPQEWA

Important features:**Signal peptide:**

amino acids 1-29

Carboxylesterases type-B serine active site.

amino acids 312-327

Carboxylesterases type-B signature 2.

amino acids 218-228

N-glycosylation sites.

amino acids 318-321, 380-383 and 465-468

59/615

FIGURE 59

CGGACGCGTGGGCTGGGCGCTGCAAAGCGTGTCCCGCCGGGTCCCCGAGCGTCCCGCGCCCTC
GCCCCGCCATGCTCCTGCTGCTGGGGCTGTGCCTGGGGCTGTCCCTGTGTGTGGGGTCGCAGG
AAGAGGCGCAGAGCTGGGGCCACTCTTCGGAGCAGGATGGACTCAGGGTCCCCGAGGCAAGTCA
GACTGTTGCAGAGGCTGAAAACCAAACCTTTGATGACAGAATTCTCAGTGAAGTCTACCATCA
TTTCCCGTTATGCCTTCACTACGGTTTCTCTGCAGAATGCTGAACAGAGCTTCTGAAGACCAGG
ACATTGAGTTCCAGATGCAGATTCCAGCTGCAGCTTTCATCACCAACTTCACTATGCTTATTG
GAGACAAGGTGTATCAGGGCGAAATTACAGAGAGAGAAAAGAAGAGTGGTGATAGGGTAAAAG
AGAAAAGGAATAAAAACCACAGAAGAAAATGGAGAGAAGGGGACTGAAATATTCAGAGCTTCTG
CAGTGATTTCCAGCAAGGACAAAGCCGCCTTTTTCTGAGTTATGAGGAGCTTCTGCAGAGGC
GCCTGGGCAAGTACGAGCACAGCATCAGCGTGCGGCCCCAGCAGCTGTCCGGGAGGCTGAGCG
TGGACGTGAATATCCTGGAGAGCGCGGGCATCGCATCCCTGGAGGTGCTGCCGCTTCAACA
GCAGGCAGAGGGGAGTGGGCGCGGGGAAGATGATTCTGGGCCTCCCCATCTACTGTCATTA
ACCAAAATGAAACATTTGCCAACATAATTTTTAAACCTACTGTAGTACAACAAGCCAGGATTG
CCCAGAATGGAATTTTGGGAGACTTTATCATTAGATATGACGTCAATAGAGAACAGAGCATTG
GGGACATCCAGGTTCTAAATGGCTATTTTGTGCACTACTTTGCTCCTAAAGACCTTCTCCTT
TACCCAAGAATGTGGTATTCGTGCTTGACAGCAGTGCTTCTATGGTGGGAACCAAACTCCGGC
AGACCAAGGATGCCCTCTTACAATTCTCCATGACCTCCGACCCAGGACCGTTTCAGTATCA
TTGGATTTTCCAACCGGATCAAAGTATGGAAGGACCACTTGATATCAGTCACTCCAGACAGCA
TCAGGGATGGGAAAGTGATACATTACCATATGTCACCCACTGGAGGCACAGACATCAACGGGG
CCCTGCAGAGGGCCATCAGGCTCCTCAACAAGTACGTGGCCACAGTGGCATTTGGAGACCGGA
GCGTGTCCCTCATCGTCTTCTGACGGATGGGAAGCCCACGGTCGGGGAGACGCACACCCCTCA
AGATCCTCAACAACACCCGAGAGGCCGCCGAGGCCAAGTCTGCATCTTCACCATTGGCATCG
GCAACGACGTGGACTTCAGGCTGCTGGAGAACTGTGCTGGAGAACTGTGGCCTCACACGGC
GCGTGCACGAGGAGGAGGACGCAGGCTCGCAGCTCATCGGGTTCTACGATGAAATCAGGACCC
CGCTCCTCTCTGACATCCGCATCGATTATCCCCCAGCTCAGTGGTGCAGGCCACCAAGACCC
TGTTCCCCAACTACTTCAACGGCTCGGAGATCATCATTTGCGGGGAAGCTGGTGGACAGGAAGC
TGGATCACCTGCACGTGGAGGTCACCGCCAGCAACAGTAAGAAATTCATCATCCTGAAGACAG
ATGTGCCTGTGCGGCCTCAGAAGGCAGGGAAAGATGTCACAGGAAGCCCCAGGCCTGGAGGCG
ATGGAGAGGGGGACACCAACCACATCGAGCGTCTCTGGAGCTACCTCACCACAAAGGAGCTGC
TGAGCTCCTGGCTGCAAAGTGACGATGAACCGGAGAAGGAGCGGCTGCGGCAGCGGGCCCAGG
CCCTGGCTGTGAGCTACCGCTTCCCTCACTCCCTTACCTCCATGAAGCTGAGGGGGCCGGTCC
CACGCATGGATGGCCTGGAGGAGGCCACGGCATGTGCGCTGCCATGGGACCCGAACCGGTGG
TGCAGAGCGTGCGAGGAGCTGGCACGCAGCCAGGACCTTTGCTCAAGAAGCCAAACTCCGTCA
AAAAAAAACAAAACAAAACAAAAAAGACATGGGAGAGATGGTGTTTTTCTCTCCACCACC
TGGGGATACGATGAAGATGGCCACCTGCAAGCCAGGAAGACGGCCCTCACCAGACACCATG
TCTGCTGGCACCTTGATCTTGACCTCCCAGCCTCCAGAACTGTGAGAAATAAATGTGTTTTG
TTTAAGCTAAA

60/615

FIGURE 60

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44192

<subunit 1 of 1, 694 aa, 1 stop

<MW: 77400, pI: 9.54, NX(S/T): 6

MLLLGLCLGLSLCVGSQEEAQSWGHSSEQDGLRVPRQVRLQLRLKTKPLMTEFSVKSTIISR
YAFTTVSCRMLNRRASEDQDIEFQMQUIPAAAFITNFTMLIGDKVYQGEITEREKKSGDRVKEKR
NKTTEENGEKGTEIFRASAVIPSKDKAAFFLSYEELLQRRLGKYEHSISVRPQQLSGRLSVDV
NILESAGIASLEVLPLHNSRQRGSGRGEDDSGPPPSTVINQNETFANIIFKPTVVQQARIAQN
GILGDFIIRYDVNREQSIGDIQVLNGYFVHYFAPKDLPLPKNVVFLDSSASMGVTKLRQTK
DALEFTHDLRPPQDRFSIIGFSNRKIVWKDHLISVTPDSIRDGKVYIHHMSPTGGTDINGALQ
RAIRLLNKYVAHSGIGDRSVSLIVFLTDGKPTVGETHTLKILNNTREAAARGQVCIFTIGIGND
VDFRLLEKLSLENCGLTRRVHEEEDAGSQLIGFYDEIRTPLLSDIRIDYPPSSVVQATKTLFP
NYFNGSEIIIAGKLVDKLDHLHVEVTASNSKKFIILKTDVPVRPQKAGKDVTSRPPGGDGE
GDTNHIERLWSYLTTKELLSSWLQSDDEPEKERLRQRAQALAVSYRELTPTFTSMKLRGVPRM
DGLLEEAHGMSAAMGPEPVVQSVRGAGTQPGPLLKKPNSVKKKQNKTKKRHGRDGVFPLHHLGIR

Signal sequence.

amino acids 1-14

N-glycosylation sites.

amino acids 97-101, 127-131, 231-235, 421-425, 508-512, 674-678

Glycosaminoglycan attachment sites.

amino acids 213-217, 391-395

N-myristoylation sites.

amino acids 6-12, 10-16, 212-218, 370-376, 632-638, 638-644

FIGURE 61

CAGGAACCCCTCTCTTTGGGTCTGGATTGGGACCCCTTTCCAGTACCATTTTTTCTAGTGAACC
ACGAAGGGGACGATACCAGAAAACACCCCTCAACCCAAAGGAAATAGACTACAGCCCAATTGGC
TGACTTTTGGCTATAGAAAAAGAAAGGACCAAGAGAGACAGTTTTTTTTTGGAAAGCTAAGT
TTCCTTTTATCGAGTCAAGAAACCCCTCTCTTGGAGTATTACAGCTTTTAAACAATTGAGT
AAAGTACGCTCCGGTCACC**ATGGT**GACAGCGCGCCTGGGTCCCGTCTGGGCAGCGCTCCTGCT
CTTTCTCCTGATGTGTGAGATCCGTATGGTGGAGCTCACCTTTGACAGAGCTGTGGCCAGCGG
CTGCCAACGGTGCTGTGACTCTGAGGAGCCCCCTGGATCCTGCCCATGTATCCTCAGCCTCTTC
CTCCGGCCGCCCCACGCCCCCTGCCTGAGATCAGACCCCTACATTAATATCACCATCCTGAAGG
TGACAAGGGGACCCAGGCCCAATGGGCTGCGCAGGGTACATGGGAGGGGAGGGTCCCCAAG
GGAGCCTGGCCCTCAGGGCAGCAAGGGTGACAAGGGGGAGATGGGCAGCCCCGGCGCCCCGTG
CCAGAAGCGCTTCTTCGCCTTCTCAGTGGGCGCAAGACGCGCCTGCACAGCGCGAGGACTT
CCAGACGCTGCTCTTCGAAAGGGTCTTTGTGAACCTTTGATGGTGCTTTTGACATGGCGACCGG
CCAGTTTGTCTGCTCCCTCGCTGGCATCTACTTCTTACGCTCAATGTGCACAGCTGGAATTA
CAAGGAGAGCTACGTGCACATTATGCATAACCCAGAAAGAGGCTGTATCCTGTACGCGCAGCC
CAGCGAGCGCAGCATCATGCAGAGCCAGAGTGTGATGCTGGACCTGGCCTACGGGGACCGCGT
CTGGGTGCGGCTCTTCAAGCGCCAGCGCGAGAACGCCATCTACAGCAACGACTTCGACACCTA
CATCACCTTCAGCGGCCACCTCATCAAGGCCGAGGACGAC**TGAGG**CTCTGGGCCACCTCC
CGGCTGGAGAGCTCAGGTGCTGGTCCCGTCCCTGCAGGGCTCAGTTTGCATGCTGTGAAGC
AGGAAGGCCAGGGAGGTCCCCGGGGACCTGGCATTCTGGGGAGACCCTGCTTCTATCTTGGCT
GCCATCATCCCTCCAGCCTATTTCTGCTCCTCTCTTCTCTCTTGGACCTATTTTAAAGAGCT
TGCTAACCTAAATATTCTAGAACTTTCCCGACCTCGTAGCCAGCACTTCTCAAACCTTGGAAA
TGCATTGCGAATCACC CGGGTTCGTGTTAAATGCAGATTCTGACTCAGCAGGCTGTAGTGGT
CCAGGATTCTGTGTTTCTCATATGTTCTTGGGTGATGCTGATGGGTGAGTCTATGAACCACA
CTGGAGCAACCAGGTTCTAGGACTTTCTCAATATTCTAGTACTTTCTGAACATTCTGGAATCC
TCCCCACATTCTAGAACTTCTCCCAACATTTTTTTTTTCTTGAGACAGAGTCTTGCTCTGTTGCC
CAGGCTAGAGTGCAAGTGGTGCATCTCAGTTACTGCAACCTCTGCCTCCCGGGTTCAAGCGA
TTCTTCTGCCTCAGCTCCCTAGTGGCTGGGATTACAGGCGCCTGCTACCATTGCTGGCTAAT
TTTTGTATTTTATAGTAGAGATGGGGTTTACCATATTGGCCAGGCTGGTCTTGAACCTCTGAC
TTCAGGTGACCCACCCGCTCTGGGCTCTCAAAATGCTGGGATTACAGGTGTGAGCCACCGTGC
CTGGCCCAATTCACCACTTTAAATTTCTCTATCCCTCCAGGGCTCCCCGTGCTATGTTCTCT
TTACCCCTTCCCCCTCTTCTCTTGTCTCAGGCTGCGACCACTGAGCCACCGTTCAATTATTCA
TTCATTAAACACTGAGCACTCACTCTGTGCTGGGTCCCGGGAAGGGTGAGGGGGTCAGACACA
GGCCCTGCCCCTGCCCTCAGTGACTGGCCAGTCCAGCCCAGGCGGGGAGAGATGTGTACATAG
GTTTTAAAGCAGACCCAGAGCTCATGGGGGGCTGTGTTCTGGGTGTTCAGGTGCTGCTGGTCC
TTCATTACCACCTGCTCCCCAAGGCTGGTGGGAGGGGTCCGGTGGCAGGGGAGGATATCTC
CTTCCCGTTCTCTATCCACCTGCCAGTGCTCATCGTTACAGCAAAACCCAGGGGGCTTGGC
CAGGTCAAGGGTTCTGTGAGGAGAGGACCCAGGAGTGTGGGGGCATTTGGGGGGTGAAGTGGC
CCCCGAAGAATGGAACCCACACCCATAGCTCTCCCCACAGCTGATACGGCATCTCGCAGAAG
ACCTGCCCTCTCTCACTGGGATCCCCCTTCTGCTCCTCTCCAGGGCTCTGCCAGGGCTTGTCTC
AGTCCCTTCCACCAAAGTCATCTGAACCTTCGGTTTCCCCAGGGCCTCCAGCTGCCCTCAGACA
CTGATGTCTGTCCCCAGGTGCTCTCTGCCCTCATGCCCTCTCACCGGCCAGTGCCCCGAC
TCTCCAGGCTTTATCAAGGTGCTAAGGCCCGGGTGGGAGCTCCTCGTCTCAGAGCCCTCCTC
CGGCTGGTGTGCTTTTACAAACACCTGCAGGAGAGAAGGGCCACGGAAGCCCCAGGCTTTAGA
GCCCTCAGCAGGCTCTGGGGAGCTAGAGCAAGAGGGGACCTCAGGCCTTCCGTTTCTTCTTCC
AGGGTGGGGTGGCCTGGTGTTCCTTAGCCTTCCAAACCCAGGTGGCCTGCCCTTCTCCCCAG
AGGGAGGCGGCCTCCGCCCATTTGGTGCTCATGCAGACTCTGGGGCTGAGGTGCCCCGGGGGGT
GATCTCTGGTGCTCAACAGCCGAGGGAGCGGTGGCTCCATGGCCAGATGACGGAAACAGGGTCT
GACCAAGTGCCACAGGAACCTGTGCTATAAACACCTGCCTGATCCTGCCCTGCCTGACCC
CGCCACGCCCCTGCCGTCCAGCATGATTAAGAATGCTGTCTCTCTTGGAAAAA

62/615

FIGURE 62

MVTAALGPVWAALLLFLLMCEIRMVELTFDRAVASGCQRCCDSEDPLDPAHVSSASSSSGRPHA
LPEIRPYINITILKGDKGDPGPMGLPGYMGREGPQGEPPQGSKGDKGEMGSPGAPCQKRFFA
FSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKETVH
IMHNQKEAVILYAQPSESRIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITFSGH
LIKAEDD

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 72-75

Clq domain proteins.

amino acids 144-178, 78-111 and 84-117

63/615

FIGURE 63

ATGGGAAGCCAGTAACACTGTGGCCTACTATCTCTTCCGTGGTGCCATCTACATTTTTTGGGAC
TCGGGAATTATGAGGTAGAGGTGGAGGCGGAGCCGGATGTCAGAGGTCTGAAATAGTCACCA
TGGGGGGAAAATGATCCGCCTGCTGTTGAAGCCCCCTTCTCATTCCGATCGCTTTTTTGGCCTTG
ATGATTTGAAAATAAGTCCTGTTGCACCAAGATGCAGATGCTGTTGCTGCACAGATCCTGTCAC
TGCTGCCATTGAAGTTTTTTCCAATCATCGTCATTGGGATCATTGCATTGATATTAGCACTGG
CCATTGGTCTGGGCATCCACTTCGACTGCTCAGGGAAGTACAGATGTCGCTCATCCTTTAAGT
GTATCGAGCTGATAGCTCGATGTGACGGAGTCTCGGATTGCAAAGACGGGGAGGACGAGTACC
GCTGTGTCCGGGTGGGTGGTCAGAATGCCGTGCTCCAGGTGTTACAGCTGCTTCGTGGAAGA
CCATGTGCTCCGATGACTGGAAGGGTCACACGCAAATGTTGCCTGTGCCAACTGGGTTTTCC
CAAGCTATGTGAGTTCAGATAACCTCAGAGTGAGCTCGCTGGAGGGGCAGTTCCGGGAGGAGT
TTGTGTCCATCGATCACCTCTTGCCAGATGACAAGGTGACTGCATTACACCACTCAGTATATG
TGAGGGAGGGATGTGCCTCTGGCCACGTGGTTACCTTGCAAGTGCACAGCCTGTGGTCATAGAA
GGGGCTACAGCTCACGCATCGTGGGTGGAACATGTCCCTGCTCTCGCAGTGGCCCTGGCAGG
CCAGCCTTCAGTTCCAGGGCTACCACCTGTGCGGGGGCTCTGTCATCACGCCCCCTGTGGATCA
TCACTGCTGCACACTGTGTTTATGACTTGTACCTCCCCAAGTCATGGACCATCCAGGTGGGTC
TAGTTTCCCTGTTGGACAATCCAGCCCCATCCCACTTGGTGGAGAAGATTGTCTACCACAGCA
AGTACAAGCCAAAGAGGCTGGGCAATGACATCGCCCTTATGAAGCTGGCCGGGGCCACTCACGT
TCAATGAAATGATCCAGCCTGTGTGCCTGCCAACTCTGAAGAGAACTTCCCCGATGGAAAAG
TGTGCTGGACGTGAGGATGGGGGGCCACAGAGGATGGAGGTGACGCCTCCCCTGTCTGAACC
ACGCGGCCGTCCCTTTGATTTCCAACAAGATCTGCAACCACAGGGACGTGTACGGTGGCATCA
TCTCCCCCTCCATGCTCTGCGCGGGCTACCTGACGGGTGGCGTGGACAGCTGCCAGGGGGACA
GCGGGGGGGCCCCTGGTGTGTCAAGAGAGGAGGCTGTGGAAGTTAGTGGGAGCGACCAGCTTTG
GCATCGGCTGCGCAGAGGTGAACAAGCCTGGGGTGTACACCCGTGTACCTCCTTCCTGGACT
GGATCCACGAGCAGATGGAGAGAGACCTAAAAACCTTGAAGAGGAAGGGGACAAGTAGCCACCT
GAGTTCCTGAGGTGATGAAGACAGCCCGATCCTCCCCTGGACTCCCGTGTAGGAACCTGCACA
CGAGCAGACACCCTTGGAGCTCTGAGTTCGGGCACCAGTAGCAGGCCCCGAAAGAGGCACCCTT
CCATCTGATTCCAGCACAACCTTCAAGCTGCTTTTTTGTGTTTTTGTGTTTTTGTAGGTGGAGTCT
CGCTCTGTTGCCAGGCTGGAGTGCAGTGGCGAAATCCCTGCTCACTGCAGCCTCCGCTTCCC
TGGTTCAAGCGATTCTCTTGCCCTCAGCTTCCCCAGTAGCTGGGACCACAGGTGCCCGCCACCA
CACCCAACTAATTTTTTGTATTTTTTAGTAGAGACAGGGTTTTACCATGTTGGCCAGGCTGCTCT
CAAACCCCTGACCTCAAATGATGTGCCTGCTTCAGCCTCCACAGTGTGGGATTACAGGCAT
GGGCCACCACGCCTAGCCTCACGCTCCTTTCTGATCTTCACTAAGAACAAGAGAGCAGCAAC
TTGCAAGGGCGGCCTTTCCCACTGGTCCATCTGGTTTTCTCTCCAGGGTCTTGCAAAATTCCT
GACGAGATAAGCAGTTATGTGACCTCACGTGCAAAGCCACCAACAGCCACTCAGAAAAGACGC
ACCAGCCCAGAAGTGCAGAACTGCAGTCACTGCACGTTTTTCATCTCTAGGGACCAGAACCAAA
CCCACCCTTTCTACTTCCAAGACTTATTTTACATGTGGGGAGGTTAATCTAGGAATGACTCG
TTTAAGGCCTATTTTCATGATTTCTTTGTAGCATTGGTGCTTGACGTATTATTGTCTTTGA
TTCCAAATAATATGTTTCCTTCCCTCATTGTCTGGCGTGTCTGCGTGGACTGGTGACGTGAAT
CAAAATCATCCACTGAAA

64/615

FIGURE 64

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45234
><subunit 1 of 1, 453 aa, 1 stop
><MW: 49334, pI: 6.32, NX(S/T): 1
MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALILAL
AIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLOVFTAASWK
TMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIHLLPDDKVLTALHHSVY
VREGCASGHVVTLOCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVITPLWI
ITAAHCVDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKLAGPLT
FNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAAVPLISNKICNHRDVYGGI
ISPSMLCAGYLTGGVDSCQGDSSGGLVCQERRLWKLVGATSTFGIGCAEVNKPGRVYTRVTSFLD
WIHEQMERDLKT
```

Signal Peptide:

amino acids 1-20

Transmembrane domain:

amino acids 240-284

65/615

FIGURE 65

CGGGCCAGCCTGGGGCGGCCGGCCAGGAACCCCGTTAAGGTGTCTTCTCTTTAGGGATGGT
GAGGTTGGAAAAAGACTCCTGTAACCCCTCCTCCAGGATGAACCACCTGCCAGAAGACATGGAG
AACGCTCTCACCGGGAGCCAGAGCTCCCATGCTTCTCTGCGCAATATCCATTCCATCAACCCC
ACACAACCTCATGGCCAGGATTGAGTCCATGAAGGAAGGGAAAAGAAAGGCATATCTGATGTC
AGGAGGACTTTCTGTTTGTGTTGTCACCTTTGACCTCTTATTCGTAACATTACTGTGGATAATA
GAGTTAAATGTGAATGGAGGCATTGAGAACACATTAGAGAAGGAGGTGATGCAGTATGACTAC
TATTCTTCATATTTTGATATATTTCTTCTGGCAGTTTTTCGATTTAAAGTGTTAATACTTGCA
TATGCTGTGTGCAGACTGCGCCATTGGTGGGCAATAGCGTTGACAACGGCAGTGACCAGTGCC
TTTTTACTAGCAAAAGTGATCCTTTTCAAGCTTTTCTCTCAAGGGGCTTTTGGCTATGTGCTG
CCCATCATTTTCATTCATCCTTGCCTGGATTGAGACGTGGTTCCTGGATTTCAAAGTGTTACCT
CAAGAAGCAGAAGAAGAAAACAGACTCCTGATAGTTCAGGATGCTTCAGAGAGGGCAGCACTT
ATACCTGGTGGTCTTTCTGATGGTCAGTTTTATTCCCCTCCTGAATCCGAAGCAGGATCTGAA
GAAGCTGAAGAAAAACAGGACAGTGAGAAACCACTTTTAGAACTATGAGTACTACTTTTGTTA
AATGTGAAAAACCCTCACAGAAAGTCATCGAGGCAAAAAGAGGCAGGCAGTGGAGTCTCCCTG
TCGACAGTAAAGTTGAAATGGTGACGTCCACTGCTGGCTTTATTGAACAGCTAATAAAGATTT
ATTTATTGTAATACCTCACAAACGTTGTACCATATCCATGCACATTTAGTGCCTGCCTGTGG
CTGGTAAGGTAATGTCATGATTCATCCTCTCTTCAGTGAGACTGAGCCTGATGTGTTAACAAA
TAGGTGAAGAAAGTCTTGTGCTGTATTCTTAATCAAAAGACTTAATATATTGAAGTAACACTT
TTTTAGTAAGCAAGATACCTTTTTTATTTCAATTACAGAATGGAATTTTTTTGTTTCATGTCT
CAGATTTATTTTGTATTTCTTTTTTAACACTCTACATTTCCCTTGTTTTTAACTCATGCACA
TGTGCTCTTTGTACAGTTTTTAAAAAGTGTAATAAAATCTGACATGTCAATGTGGCTAGTTTTA
TTTTTCTTGTTTTGCATTATGTGTATGGCCTGAAGTGTTGGACTTGCAAAAGGGGAAGAAAGG
AATTGCGAATACATGTAAATGTCACCAGACATTTGTATTATTTTTATCATGAAATCATGTTT
TTCTCTGATTGTTCTGAAATGTTCTAAATACTCTTATTTTGAATGCACAAAATGACTTAAACC
ATTCATATCATGTTTCCTTTGCGTTCAGCCAATTTCAATTAAATGAACTAAATTAAAAA

66/615

FIGURE 66

MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTFDL
LFVTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAI
ALTTAVTSAFLLAKVILSKLFSQGAFGYVLPPIISFILAWIETWFLDFKVLPPQEAEENRLLIV
QDASERAALIPGGLSDGQFYSPPESEAGSEEAEKQDSEKPLLEL

Important features of the protein:**Signal peptide:**

amino acids 1-20

Transmembrane domains:

amino acids 54-72, 100-118, 130-144, 146-166

N-myristoylation sites.

amino acids 14-20, 78-84, 79-85, 202-208, 217-223

67/615

FIGURE 67

AATAAAGCTTCCTTAATGTTGTATATGTCTTTGAAGTACATCCGTGCATTTTTTTTTTAGCATC
CAACCATTCCCTCCCTTGTAGTTCTCGCCCCCTCAAATCACCCCTCTCCCGTAGCCCAACCGACT
AACATCTCAGTCTCTGAAAATGACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCTCAC
GGGGCTCAGTCTCTTTTTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCACAGTACCTGC
CACCCCTCAACGTCTCAATGGCTCTGACGCCCGCCTGCCCTGCACCTTCAACTCCTGCTACAC
AGTGAACCACAAACAGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACCTGCTCTGAGGA
GATGTTCTCCAGTTCCGCATGAAGATCATTAACCTGAAGCTGGAGCGGTTTCAAGACCGCGT
GGAGTTCTCAGGGAACCCAGCAAGTACGATGTGTGGTGATGCTGAGAAACGTGCAGCCGGA
GGATGAGGGGATTTACAACCTGCTACATCATGAACCCCCCTGACCGCCACCGTGGCCATGGCAA
GATCCATCTGCAGGTCTCATGGAAGAGCCCCCTGAGCGGGACTCCACGGTGGCCGTGATTGT
GGGTGCCTCCGTGCGGGGCTTCTGGCTGTGGTCACTTGGTGCTGATGGTGGTCAAGTGTGT
GAGGAGAAAAAAGAGCAGAAGCTGAGCACAGATGACCTGAAGACCGAGGAGGAGGGCAAGAC
GGACGGTGAAGGCAACCCGGATGATGGCGCCAAGTAGTGGGTGGCCGGCCCTGCAGCCTCCCG
TGTCCTCGTCTCCTCCCCCTCTCCGCCCTGTACAGTGACCCTGCCTGCTCGCTCTTGGTGTGCTT
CCCGTGACCTAGGACCCCAGGGCCCACCTGGGGCCTCCTGAACCCCCGACTTCGTATCTCCCA
CCCTGCACCAAGAGTGACCCACTCTCTCCATCCGAGAAACCTGCCATGCTCTGGGACGTGTG
GGCCCTGGGGAGAGGAGAGAAAGGGCTCCACCTGCCAGTCCCTGGGGGGAGGCAGGAGGCAC
ATGTGAGGGTCCCCAGAGAGAAGGGAGTGGGTGGGCAGGGGTAGAGGAGGGGCCGTGTACAC
TGCCAGTGCTTGCCTGGCAGTGGCTTCAGAGAGGACCTGGTGGGGAGGGAGGGCTTTCTGT
GCTGACAGCGCTCCCTCAGGAGGGCCTTGGCCTGGCACGGCTGTGCTCCTCCCCTGCTCCAG
CCCAGAGCAGCCATCAGGCTGGAGGTGACGATGAGTTCTGAACTTGGAGGGGCATGTTAAA
GGGATGACTGTGCATTCCAGGGCACTGACGGAAAGCCAGGGCTGCAGGCAAAGCTGGACATGT
GCCCTGGGCCAGGAGGCCATGTTGGGCCCTCGTTTCCATTGCTAGTGGCCTCCTTGGGGCTCC
TGTTGGCTCCTAATCCCTTAGGACTGTGGATGAGGCCAGACTGGAAGAGCAGCTCCAGGTAGG
GGGCCATGTTTCCCAGCGGGGACCCACCAACAGAGGCCAGTTTCAAAGTCAGCTGAGGGGCTG
AGGGGTGGGGCTCCATGGTGAATGCAGGTGCTGCAGGCTCTGCCTTCTCCATGGGGTAACCA
CCCTCGCCTGGGCAGGGGCAGCCAAGGCTGGGAAATGAGGAGGCCATGCACAGGGTGGGGCAG
CTTTCTTTGGGGCTTCAGTGAGAACTCTCCAGTTGCCCTTGGTGGGGTTTCCACCTGGCTTT
TGGCTACAGAGAGGGAAGGGAAAGCCTGAGGCCGGCATAAGGGGAGGCCTTGGAACTGAGCT
GCCAATGCCAGCCCTGTCCCATCTGCGGCCACGCTACTCGCTCCTCTCCAACAACCTCCCTTC
GTGGGGACAAAAGTGACAATTGTAGGCCAGGCACAGTGGCTCACGCCTGTAATCCCAGCACTT
TGGGAGGCCAAGGCGGGTGGATTACCTCCATCTGTTTAGTAGAAATGGGCAAAACCCCATCTC
TACTAAAAATAACAAGAATTAGCTGGGCGTGGTGGCGTGTGCCTGTAATCCCAGCTATTTGGGA
GGCTGAGGCAGGAGAATCGCTTGAAGCCGGGAAGCAGAGGTTGCAGTGAAGTGAATAGTATGAT
AGTGCCACTGCAATTCAGCCTGGGTGACATAGAGAGACTCCATCTCAAAAAA

68/615

FIGURE 68

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45415
<subunit 1 of 1, 215 aa, 1 stop
<MW: 24326, pI: 6.32, NX(S/T): 4
MHRDAWLPRPAFSLTGLSLFFSLVPPGRSMEVTVPATLNVLNGSDARLPCTFNSCYTVNHKQF
SLNWTYQECNNCSEEMFLQFRMKIINLKLERFQDRVEFSGNPSKYDVSVMLRNVQPEDEGIYN
CYIMNPPDRHRGHGKIHLQVLMEEPPERDSTVAVIVGASVGGFLAVVILVLMVVKCVRKKKEQ
KLSTDDLKTEEEGKTDGEGNPDDGAK

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 161-179

Immunoglobulin-like fold:

amino acids 83-127

N-glycosylation sites.

amino acids 42-45, 66-69 and 74-77

69/615

FIGURE 69

GGCGCCTGGTTCGCGCTACTGGCTGTACGGAGCAGGAGCAAGAGGTCGCCGCCAGCCTCCGCCGCCGAGCCTC
GTTTCGTGTCCCCGCCCTCGCTCCTGCAGCTACTGCTCAGAAACGCTGGGGCGCCACCCTGGCAGACTAACGAA
GCAGCTCCCTTCCCACCCCAACTGCAGGTCTAATTTTGGACGCTTTGCCTGCCATTTCTTCCAGGTTGAGGGAGC
CGCAGAGGGCGGAGGCTCGCGTATTCCTGCAGTCAGCACCCACGTCGCCCCCGGACGCTCGGGTGTCTCAGGCCCTTC
GCGAGCGGGGCTCTCCGTCTGCGGTCCCTTGTGAAGGCTCTGGGCGGCTGCAGAGGCCGGCCGTCCGGTTTGGCT
CACCTCTCCCAGGAACTTCACACTGGAGAGCCAAAAGGAGTGGAAGAGCCTGTCTTGGAGATTTTCTTGGGGAA
ATCCTGAGGTCATTCAATATGAAGTGTACCGCGCGGGAGTGGCTCAGAGTAACCACAGTGTCTTTCATGGCTAGA
GCAATTCAGCCATGGTGGTTCCCAATGCCACTTTATTGGAGAACTTTTGGAAAATACATGGATGAGGATGGT
GAGTGGTGGATAGCCAAACAACGAGGGAAAAGGGCCATCACAGACAATGACATGCAGAGTATTTTGGACCTTCAT
AATAAATTACGAAGTCAGGTGTATCCAACAGCCTCTAATATGGAGTATATGACATGGGATGTAGAGCTGGAAAGA
TCTGCAGAAATCCTGGGCTGAAAGTTGCTTGTGGGAACATGGACCTGCAAGCTTGCTTCCATCAATTGGACAGAAT
TTGGGAGCACACTGGGGAAGATATAGGCCCGGACGTTTCATGTACAATCGTGGTATGATGAAGTGAAAGACTTT
AGCTACCCATATGAACATGAATGCAACCCATATTGTCCATTAGGTGTCTGGCCCTGTATGTACACATTATACA
CAGGTGCTGTGGGCAACTAGTAACAGAATCGGTTGTGCCATTAATTTGTGTACATAACATGAACATCTGGGGGCAG
ATATGGCCCAAAGCTGTCTACCTGGTGTGCAATTACTCCCCAAAGGGAAGTGGTGGGGCCATGCCCTTACAAA
CATGGGCGGCCCTGTTCTGCTTGGCCACCTAGTTTGGAGGGGGCTGTAGAGAAAATCTGTGTACAAAGAAGGG
TCAGACAGGTATTATCCCCCTCGAGAAGAGGAAACAAATGAAATAGAACGACAGCAGTCACAAGTCCATGACACC
CATGTCCGGACAAGATCAGATGATAGTAGCAGAAATGAAGTCATAAGCGCACAGCAAATGTCCCAAATTGTTTCT
TGTGAAGTAAGATTAAAGAGATCAGTGCAAGGAACAACCTGCAATAGGTACGAATGTCTGCTGGCTGTTTGGAT
AGTAAAGCTAAAGTTATTGGCAGTGTACATTATGAAATGCAATCCAGCATCTGTAGAGCTGCAATTCATTATGGT
ATAATAGACAATGATGGTGGCTGGGTAGATATCACTAGACAAGGAAGAAAGCATTATTTTCATCAAGTCCAATAGA
AATGGTATTCAAACAATTTGGCAAATATCAGTCTGCTAATTCCTTCACAGTCTCTAAAGTAACAGTTCCAGGCTGTG
ACTTGTGAACAACCTGTGGAACAGCTCTGTCCATTTTCATAAGCCTGCTTCACATTGCCCCAAGAGTATACTGTCT
CGTAACGTATGCAAGCAAATCCACATTATGCTCGTGAATTGGAACTCGAGTTTATTCTGATCTGTCCAGTATC
TGCAGAGCAGCAGTACATGCTGGAGTGGTTGCAATCACGGTGGTTATGTTGATGTAATGCCTGTGGACAAAAGA
AAGACCTACATTGCTTCTTTTCAGAATGGAATCTTCTCAGAAAGTTTACAGAATCCTCCAGGAGGAAAGGCATT
AGAGTGTTCGTGTTGTGTAAGTGAATCTTGGAAAGAGGACCATAAAGACTATTCCAAATGCAATATTTCTGA
ATTTTGTATAAACTGTAACATTACTGTACAGAGTACATCAACTATTTTCAGCCCAAAAAGGTGCCAAATGCATA
TAAATCTTGATAAAACAAAGTCTATAAAATAAAACATGGGACATTAGCTTTGGGAAAAGTAATGAAAATATAATGG
TTTTAGAAATCCTGTGTTAAATATGCTATATTTTCTTAGCAGTTATTTCTACAGTTAATTACATAGTCATGATT
GTTCTACGTTTCATATATTATATGGTGCTTTGTATATGCCACTAATAAAATGAATCTAAACATTGAATGTGAATG
GCCCTCAGAAAATCATCTAGTGCATTTAAAAATAATCGACTCTAAAACCTGAAAGAAACCTTATCACATTTTCCCC
AGTTCAATGCTATGCCATTACCAACTCCAATAATCTCAAATAATTTTCCACTTAATAACTGTAAAGTTTTTTTC
TGTTAATTTAGGCATATAGAATATTAATTTCTGATATTGCACTTCTTATTTTATATAAAATAATCCTTTAATATC
CAAATGAATCTGTTAAATGTTTGATTCTTGGGAATGGCCTTAAAAATAAATGTAATAAAGTCAGAGTGGTGGT
ATGAAAACATTCTAGTATCATGTAGTAAATGTAGGGTTAAGCATGGACAGCCAGAGCTTTCTATGTACTGTTA
AAATTGAGGTCACATATTTTCTTTTGTATCCTGGCAAATACCTGTCAGGCCAGGAAGTATAATAGCAAAAAGTT
GAACAAAGATGAACTAATGTATTACATTACCATTGCCACTGATTTTTTTTAAATGGTAAATGACCTTGTATATAA
ATATTGCCATATCATGGTACCTATAATGGTGATATATTTGTTTCTATGAAAATGTATTGTGCTTTGATACTAAA
AATCTGTAAATGTTAGTTTTGGTAATTTTTTTCTGCTGGTGGATTACATATTAAATTTTTTCTGCTGGTGGTA
TAAACATTAAATTAATCATGTTTCAAAAAA

70/615

FIGURE 70

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45417
<subunit 1 of 1, 500 aa, 1 stop
<MW: 56888, pI: 8.53, NX(S/T): 2
MKCTAREWLRVTTVLFMARAI PAMVVPNATLLEKLLEKYMDEDEGEWWIAKQRGKRAITDNDMQ
SILDHLNKLRSQVYPTASNMEYMTWDVELERSAESWAESCLWEHGPASLLPSIGQNLGAHWGR
YRPPTFHVQSWYDEVKDFSYPYEHECNPYCPFRCSGPVCTHYTQVVWATSNRIGCAINLCHNM
NIWGQIWPKAVYLVCNYSKGNWWGHAPYKHGRPCSACPPSFGGGCRENL CYKEGSDRYPPR
EEETNEIERQQSQVHDTHVTRSDSSRNEVIS AQQMSQIVSCEVRLRDQCKGTT CNRYECPA
GCLDSKAKVIGSVHYEMQSSICRAAIHYGIIDNDGGWVDITRQGRKHYFIKSNRNGIQTIGKY
QSANSFTVSKVTVQAVTCETTVEQLCPFHKPASHCPRVYCPRNCMQANPHYARVIGTRVYSDL
SSICRAAVHAGVVRNHGGYVDMPVDKRKTYIASFQNGIFSES LQNPPGGKA FRVFAVV
```

Important features:**Signal peptide:**

amino acids 1-20

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 protein

amino acids 165-186, 196-218, 134-146, 96-108 and 58-77

N-glycosylation site

amino acids 28-31

71/615

FIGURE 71

CAGCCCCGCGCGCCGGCCGAGTCGCTGAGCCGCGGCTGCCGGACGGGACGGGACCGGCTAGGC
TGGGCGCGCCCCCGGGCCCCGCGTGGGC**ATG**GGCGCACTGGCCCCGGCGCTGCTGCTGCCT
CTGCTGGCCAGTGGCTCCTGCGCGCCGCCCCGAGCTGGCCCCCGCGCCCTTACGCTGCCC
CTCCGGGTGGCGCGGCCACGAACCGCTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCC
GAGCGCCACGCCGACGGCTTGGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCC
GCCAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAG
ATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTT
GCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACA
TACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTT
GGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACT
ATTTTTGAATCAGAGAATTTCTTTTGGCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT
TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACACAA
GCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCTGGATCT
GGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAAGGAGACATC
TGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAATTGGAAATTGGA
GGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGC
ACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGGAAAGCTGTGGCCCCGCGCA
TCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAAT
TCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACCTGAGAGACGAGAACTCCAGC
AGGTCAATCCGTATCACAAATCCTGCCTCAGCTTTACATTCAGCCCATGATGGGGGCCGGCCTG
AATTATGAATGTTACCGATTTCGGCATTTCCCCATCCACAAATGCGCTGGTGATCGGTGCCACG
GTGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGC
CCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGAT
GTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTTAT
GCGCTCATGAGCGTCTGTGGAGCCATCCTCCTGTCTTAATCGTCCTGCTGCTGCTGCCGTTT
CGGTGTCAGCGTCGCCCCCGTGACCCTGAGGTGCTCAATGATGAGTCCTCTCTGGTCAGACAT
CGCTGGAAAT**TGA**ATAGCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCA
CATTTCCAGGGCAGCAGCCGGGATCGATGGTGGCGCTTCTCCTGTGCCCACCCGTCTTCAAT
CTCTGTTCTGCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTT
CAAATCCTCCCTACTTCCAAGAAAAATAATTAATAAAAAAACTTCATTCTAA

72/615

FIGURE 72

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45493
><subunit 1 of 1, 518 aa, 1 stop
><MW: 56180, pI: 5.08, NX(S/T): 2
MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGGPGTPAERHADGLALA
LEPALASPAGAAANFLAMVDNLQDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHSYI
DTYFDTERSSTYRSKGFDTVKYTGGSWTGFVGEDLVTPKGFNTSFLVNIATIFESENFFLP
GIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGSGTNGGSLVLG
GIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKAIVDSGTLLRLPQKV
FDAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISYLRDENSSRSFRITILPQ
LYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCAEIAGAAV
SEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCGAILLVLLVLLLLPFRQRRPRDPE
VVNDESSLVRHRWK

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 466-494

N-glycosylation sites.

amino acids 170-173 and 366-369

Leucine zipper pattern.

amino acids 10-31 and 197-118

Eukaryotic and viral aspartyl proteases

amino acids 109-118, 252-261 and 298-310

73/615

FIGURE 73

CGCGCGGCGAGAGCGCGCCAGCCCCGCGCGGATGCGCGCGCGCCAGGACGCCTCCTCCCGCTGCTGGCCCCGGC
CGGCGGCCCTGACTGCGCTGCTGCTGCTGCTGCTGGGCCATGGCGCGCGCGGGCGCTGGGGCGCCGGGCCCCAGG
AGGCGGCGGCGCGCGCGCGGACGGGCCCCCGCGGCGAGCGGCGAGGACGGACAGGACCCGACAGCAAGCACC
TGTACACGGCCGACATGTTTACGCACGGGATCCAGAGCGCGCGCACTTCGTTCATGTTCTTCGCGCCCTGGTGTG
GACACTGCCAGCGGCTGCAGCCGACTTGGAATGACCTGGGAGACAAATACAACAGCATGGAAGATGCCAAAGTCT
ATGTGGCTAAAGTGGACTGCACGGCCCACTCCGACGTGTGCTCCGCCCAGGGGGTGGGAGGATACCCACCTTAA
AGCTTTTCAAGCCAGGCCAAGAAGCTGTGAAGTACCAGGGTCTCGGGACTTCAGACACTGGAAAAGTGGATGC
TGCAGACACTGAACGAGGAGCCAGTGACACCAGAGCCGGAAGTGAACCGCCAGTGCCCCGAGCTCAAGCAAG
GGCTGTATGAGCTCTCAGCAAGCAACTTTGAGCTGCACGTTGCACAAGGCGACCACTTTATCAAGTTCTTCGCTC
CGTGGTGTGGTCACTGCAAAGCCCTGGCTCCAACCTGGGAGCAGCTGGCTCTGGGCCTTGAACATTCGAAACTG
TCAAGATTGGCAAGGTTGATTGTACACAGCACTATGAACCTGCTCCGGAACCAAGGTTCTGGCTATCCCACTC
TTCTCTGGTTCCGAGATGGGAAAAAGGTGGATCAGTACAAGGGAAGCGGGATTGGAGTCACTGAGGGAGTACG
TGGAGTCGCAGCTGCAGCGCACAGAGACTGGAGCGACGGAGACCGTCAAGCCCTCAGAGGCCCGGTGCTGGCAG
CTGAGCCCGAGGCTGACAAGGGCACTGTGTTGGCACTCACTGAAAATAAAGTTCAGTACACCACTTGCAGAAAGAA
TAACCTTCATCAAGTTTATGCTCCATGGTGTGGTCACTGTAAGACTCTGGCTCCTACTTGGGAGGAAGTCTCTA
AAAAGGAATTCCTGGTCTGGCGGGGTCAAGATCGCCGAAGTAGACTGCACTGCTGAACGGAATATCTGCAGCA
AGTATTCGGTACGAGGCTACCCACGTTATTGCTTTCCGAGGAGGGAAGAAAGTCACTGAGCACAGTGGAGGCA
GAGACCTTGACTCGTTACACCGCTTTGTCTGAGCCAAGCGAAAGACGAAGTCTAGGAACACAGTTGGAGGTCAC
CTCTCCTGCCAGCTCCCGCACCTGCGTTTAGGAGTTCAGTCCCACAGAGGCCACTGGGTTCCAGTGGTGGCT
GTTGAGAAAGCAGAACATACTAAGCGTGAGGTATCTTCTTGTGTGTGTGTTTCCAAAGCCAACACACTCTACAG
ATTCTTTATTAAGTTAAGTTTCTCTAAGTAAATGTGTAACCTCATGGTCACTGTGTAACATTTTTCAGTGGCGATA
TATCCCTTTTGACCTTCTCTTGATGAAATTTACATGGTTTCCCTTGAGACTAAAATAGCGTTGAGGGAAATGAAA
TTGCTGGACTATTTGTGGCTCCTGAGTTGAGTGATTTTGGTGAAAGAAAGCACATCCAAAGCATAGTTTACCTGC
CCACGAGTTCTGGAAAGGTGGCCTTGTGGCAGTATTGACGTTCTCTGATCTTAAGGTCACAGTTGACTCAATAC
TGTGTTGGTCCGTAGCATGGAGCAGATTGAAATGCAAAAACCCACACCTCTGGAAGATACTTTCACGGCCGCTGC
TGGAGCTTCTGTGTGCTGAATACTTCTCTCAGTGTGAGAGGTTAGCCGTGATGAAAGCAGCGTTACTTCTGACC
GTGCCTGAGTAAGAGAATGCTGATGCCATAACTTATGTGTCGATACTTGTCAAATCAGTTACTGTTGAGGGGAT
CCTTCTGTTTCTCACGGGTGAAACATGCTTTAGTTTCTCATGTTAACACGAAGCCAGAGCCACATGAAGTGT
TGGATGTCTTCTTAGAAAGGTTAGGCATGGAAAATTCACGAGGCTCATTCTCAGTATCTCATTAACTCATTGA
AAGATTCCAGTTGATTTGTACCTGGGGTGACAAGACCAGACAGGCTTTCCAGCGCTGGGTATCCAGGGAGGC
TCTGCAGCCCTGCTGAAGGGCCCTAACTAGAGTTCTAGAGTTTCTGATTCTGTTTCTCAGTAGTCCTTTTAGAGG
CTTGCTATACTTGGTCTGCTTCAAGGAGGTCGACCTTCTAATGTATGAAGAATGGGATGCATTTGATCTCAAGAC
CAAAGACAGATGTCAGTGGGCTGCTCTGGCCCTGGTGTGCACGGCTGTGGCAGCTGTTGATGCCAGTGTCTCTA
ACTCATGCTGTCTTGTGATTAAACACCTCTATCTCCCTTGGGAATAAGCACATACAGGCTTAAGCTCTAAGATA
GATAGGTGTTTGTCTTTTACCATCGAGCTACTTCCCATATAAACCCTTTGCATCCAACACTCTTACCCACCT
CCCATACGCAAGGGGATGTGGATACTTGGCCCAAAGTAACTGGTGGTAGGAATCTTAGAAACAAGACCACTTATA
CTGTCTGTCTGAGGCAGAAGATAACAGCAGCATCTCGACAGCCTCTGCCTTAAAGGAAATCTTTATTAATCAG
TATGGTTACAGATAATCTTTTTTTTAAAAAAACCCCACTCCTAGAGAAGCACAACTGTCAAGAGTCTTGTACA
CACAACCTCAGCTTTCATCACGAGTCTTGTATTCCAAGAAAATCAAAGTGGTACAATTTGTTTGTTTTACTAT
GATACTTTCTAAATAAAGTCTTTTTTTTTTAA

74/615

FIGURE 74

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46776
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47629, pI: 5.90, NX(S/T): 0
MPARPGRLLPLLARPAALTALLLLLLLGHGGGGRWGARAQEAAAAAADGPPAADGEDGQDPHSK
HLYTADMFTHGIQSAAHFVMFFAPWCGHCQRLQPTWN DLGDKYNSMEDAKVYVAKVDCTAHS D
VCSAQGVRGYPTLKLFPQGEAVKYQGPRDFQTLNWNMLQTLNEEPVTPEPEVEPPSAPELKQ
GLYELSA SNFELHVAQGDHFIKFFAPWCGHCKALAPTWEQLALGLEHSETVKIGKVDCTQH YE
LCSGNQVRGYPTLLWFRDGKKVDQYKGKRDLESLREYVESQLQRTETGATETVTPSEAPVLAA
EPEADKGTVLALTENNFD D TIAEGITFIKFYAPWCGHCKTLAPTWEELSKKEFPGLAGVKIAE
VDCTAERNICSKYSVRGYPTLLLFRGGKKVSEHSGGRDLDSLHRFVLSQAKDEL
```

Signal sequence:
amino acids 1-32

75/615

FIGURE 75A

CGGACGCGTGGGCGGACGCGTGGGCAAAAGAACTCGGAGTGCCAAAGCTAAATAAGTTAGCTGAGAAAACGCACG
CAGTTTGCAGCGCTGCGCCGGGTGCGCCAACTACGCAAGACCAAGCGGGCTCCGCGCGGACCGGCCGCGGGG
TAGGGACCCGGCTTTGGCCCTTCAGGCTCCCTAGCAGCGGGGAAAAGGAATTGCTGCCCGGAGTTTCTCGGAGGT
GGAGGGAGATCAGGAAACGGCTTCTTCTCACTTCGCCCGCTGGTGAGTGTCGGGGAGATTGGCAACGCCTAGG
AAAGGACTGGGGAATAAGCCCTGGGAAAGTGAGAAAGTGATCAGGAGGCCGTCCACTACGGCAGTTTATCTG
TCTGATCAGAGCCAGACGCGACGCGTCCACTTCGCAGTTCTTTCCAGGTGTGGGGACCGCAGGACAGACGGCCGA
TCCCGCCGCCCTCCGTACCAGCACTCCAGGAGAGTCAGCCTCGCTCCCCAACGTCGAGGGCGCTCTGGCCACGA
AAAGTTCCTGTCCACTGTGATTCTCAATTCCTTGCTTGGTTTTTTCTCCAGAGAACTTTGGGTGGAGATATTA
ACTTTTTTCTTTTTTTTTTCTTGGTGGAAGCTGCTTAGGGAGGGGGGAGGAGGAGGAGAAAGTGAAATGTGC
TGGAGAAGAGCGAGCCCTCCTTGTCTTCCGGAGTCCCATCCATTAAGCCATCACTTCTGGAAGATTAAAGTTGT
CGGACATGGTGACAGCTGAGAGGAGAGGAGGATTTCTTGCCAGGTGGAGAGTCTTACCCTCTGTTGGGTGCATG
TGTGCGCCCGCAGCGGCGCGGGGCGCGTGGTCTCCGCGTGGAGTCTCACCTGGGACCTGAGTGAATGGCTCCCA
GGGGCTGTGCGGGGCATCCGCCTCCGCCTTCTCCACAGGCCTGTGTCTGTCTGGAAAGATGCTAGCAATGGGG
CGCTGGCAGGATTCTGGATCCTCTGCCTCCTCACTTATGGTTACCTGTCTGGGGCCAGGCCTTAGAAGAGGAGG
AAGAAGGGGCCTTACTAGCTCAAGCTGGAGAGAACTAGAGCCAGCACAACTTCCACCTCCCAGCCCCATCTCA
TTTTCATCTAGCGGATGATCAGGGATTAGAGATGTGGGTACCACGGATCTGAGATTAAACACCTACTCTTG
ACAAGCTCGTCCGGAAGGAGTTAACTGGAGAATACTACTATGTCCAGCCTATTTGCACACCATCCAGGAGTCAGT
TTATTACTGGAAAGTATCAGATACACACCGGACTTCAACATTCTATCATAAGACCTACCCAACCCAAGTGTAC
CTCTGGACAATGCCACCCTACCTCAGAACTGAAGGAGGTTGGATATTCAACGCATATGGTGGGAAAATGGCACT
TGGGTTTTTAACAGAAAAGAATGCATGCCACCAGAAAGAGGATTTGATACCTTTTTTGGTTCCTTTTGGGAAGTG
GGGATTACTATACACTACAAATGTGACAGTCTGGGATGTGTGGCTATGACTTGTATGAAAACGACAATGCTG
CCTGGGACTATGACAAATGGCATATATACTCCACACAGATGTACACTCAGAGAGTACAGCAAATCTTAGCTTCCCAT
ACCCACAAAGCCTATATTTTTATATACTGCCTATCAAGCTGTTTCACTTACCCTGCAAGCTCCTGGCAGGTATT
TCGAACACTACCGATCCATTATCAACATAAACAGGAGAAGATATGCTGCCATGCTTTCCTGCTTAGATGAAGCAA
TCAACAACGTGACATTGGCTCTAAAGACTTATGGTTTTCTATAACAACAGCATATCATTACTCTTCAGATAATG
GTGGCCAGCCTACGGCAGGAGGGAGTAACTGGCCTCTCAGAGGTAGCAAAGGAACATATTGGGAAGGAGGGATCC
GGCTGTAGGCTTTGTGCATAGCCCACTTCTGAAAAACAAGGGAACAGTGTGTAAGGAACCTTGTGCACATCACTG
ACTGGTACCCCACTCTCATTTCCTGCTGAAGGACAGATTGATGAGGACATTCACTAGATGGCTATGATATCT
GGGAGACCATAAGTGAGGGTCTTCGCTCACCCGAGTAGATATTTGCATAACATTGACCCCTATACACCAAGGC
AAAAAATGGCTCCTGGGCAGCAGGCTATGGGATCTGGAACACTGCAATCCAGTCAGCCATCAGAGTGCAGCACTG
GAAATTGCTTACAGGAAATCCTGGCTACAGCGACTGGGTCCCCCTCAGTCTTTCAGCAACCTGGGACCGAACC
GTGGCACAATGAACGGATCACCTTGTCAACTGGCAAAAGATGTATGGCTTTTCAACATCACAGCCGACCCATGAG
GAGGGTGGACCTATCTAACAGGTATCCAGGAATCGTGAAGAAGCTCCTACGGAGGCTCTCACAGTTCAACAAAAC
TGCAGTGCCGGTCAGGTATCCCCCAAAGACCCAGAAAGTAACCTAGGCTCAATGGAGGGGTCTGGGGACCATG
GTATAAAGAGGAAACCAAGAAAAAGCAAGCAAAATCAGGCTGAGAAAAAGCAAAAGAAAAAGCAAAAAA
GAAGAAGAAACAGCAGAAAGCAGTCTCAGGTAAACCAGCAAATTTGGCTCGATAATATCGCTGGCCTAAGCGTCA
GGCTTGTTTTCATGCTGTGCCACTCCAGAGACTTCTGCCACCTGGCCGCCACACTGAAAACCTGCTGCTCAGTG
CCAAGGTGCTACTTGTGCAAGCCACACTTAGAGAGAGTGAGATGTTTATTTCTCTCGCTCCTTTAGAAAAACGTG
GTGAGTCTGAGTTCCTGCTGTGCTTCACTCAACTGACCAAAACACTGCTTTGAATTATAGGAGGAGAAACATA
ACCTACCATCCGCAAGCATGCTAATTTGATGGAAGTTACAGGGTAGCATGATTAAGTACCTTTGATAAATTAC
AGTCAAAGATTGTGTCACTCAAAGGCCCTGAAGAATATATTTCTTGGTGAATTTTTGTATGCTGTGCATATGA
CACTTGGGTTTTTAATTAATCTATTTATATATAAATATATGTTTCTTTCTGTGAAAAGCTGTTTTTCT
CACATGTGAACAGCTTGCACCTCATTTTACCATGCGTGAGGGAATGGCAAATAAGAAATGTTTGAGCACACTGCC
ACAATGAATGTAATATTTTCTAAACACTTTACTAGAAGAACATTTCACTATAAAAAACCTAATTTATTTTACA
GAAAAATATTTGTTGTTTTTATAAAAAGTTATGCAATGACTTTTTATTTTATTTCTGTCATACCATTAGAAGA
ATTTTATTTTCAATTTCTTCAAATTATCAAGCACTGTAATACTATAAATTAATGTAATACTGTGTGAATTCAGACTA
TAAAAACATCATTAGAAAACCTTTATAATCGTCATTGTTCAATCAAGATTTTGAATGTAATAAGATGAATATAT
ATTACTTGGAAATCAATGTTTGTGCGAGATTGAGACAACTTTATTGTTTCTATCATAAACTATTTATGTATCTT
AATTATTAATGATTTACTTTATGGCACTAGAAAATTTACTGTGGCTTTTCTGATCTAACTTCTAGCTAAAATT
GTATCATTTGGTCTAAAAAATAAAAACTTTTACTAATAGGCAATTGAAGGAATGGTTTGTACAACACACAGTAA
TATAATATGATTTTACAGATAGATGCTTCCCTTGGCTATGACATGGAGAAAGATTTTCCCATATAATAACTAA
TATTTATATTAGGTTGGTGCAAACTAGTTGCGGTTTTTCCCATTAAGTAATAACCTTACTCTTATACAAAGT
GGACATGTGGGGAGATACAGAGAAATGGAAGATACGGATCCTGCCTGGAGTAGGTAACCTTGCTTGGAAACCC
ACATGCAACCTCATGAGGAGAAATTAAGGAGTATTATCAGTAATGAAGTTTATCATGGGTCTCAATGAGCATA
GATTGGTGTGATCCTGTAGACCTGGTGTCTTTTGAAGTGCCCTCTCCTAATGCAGAGGCCTTGAAGCTTAC

77/615

FIGURE 76

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48296
><subunit 1 of 1, 515 aa, 1 stop
><MW: 56885, pI: 6.49, NX(S/T): 5
MAPRGCAGHPPPPSPQACVCPGKMLAMGALAGFWILCLLTGYLSWGQALEEEEEEGALLAQAGEKLEPSTTSTSQ
PHLIFILADDQGFRDVGYPHGSEIKTPTLDKLAEGVKLENYVQPICTPSRSQFITGKYQIHTGLQHSIIRPTQP
NCLPLDNATLPQKLKEVGYSTHVMVGKWHLGFNKECMPTRRGFDTFFGSLLGSGDYTHYKCDSPGMCYDLYEN
DNAAWDYDNGIYSTQMYTORVQOILASHNPTKPIFLYTAYQAVHSPLQAPGRYFEHYRSIININRRRYAAMLSC
DEAINNVTLALKTYGFYNNIIYSSDNGGQPTAGGSNWPLRGSKGTYWEGGIRAVGFVHSPLLKNKGTVCVELV
HITDWYPTLISLAEGQIDEDIQLDGYDIWETISEGLRSPRVDILHNIDPYTPRQKMAPGQQAMGSGTLQSSQPSE
CSTGNCLQEILATATGSPLSLSATWDRGTGTMNGSPCQLAKVYGFSTSQPTHMRGWYTLTG IQES
```

Important Features:**Signal Peptide:**

amino acids 1-37

Sulfatases signature 1.

amino acids 120-132

Sulfatases signature 2.

amino acids 168-177

Tyrosine kinase phosphorylation site.

amino acids 163-169

N-glycosylation sites.

amino acids 157-160, 306-309 and 318-321

78/615

FIGURE 77

AAAAAGCTCACTAAAGTTTCTATTAGAGCGAATACGGTAGATTTCCATCCCCTTTTGAAGAACAGTACTGTGGA
GCTATTTAAGAGATAAAACGAAATATCCTTTCTGGGAGTTCAAGATTGTGCAGTAATTGGTTAGGACTCTGAGC
GCCGCTGTTACCAATCGGGGAGAGAAAAGCGGAGATCTGCTCGCCTTGACAGCGCCTGAAGCACAAAGCAGAT
AGCTAGGAATGAACCATCCCTGGGAGTATGTGGAACAACGGGAGGAGCTCTGACTTCCCACTGTCCCATTTCTAT
GGGCGAAGGAACTGCTCCTGACTTCAGTGGTTAAGGGCAGAATTGAAAATAATTCTGGAGGAAGATAAGAATGAT
TCCTGCGCGACTGCACCGGGACTACAAAGGGCTTGCTCTGCTGGGAATCCTCCTGGGGACTCTGTGGGAGACCGG
ATGCACCCAGATACGCTATTAGTTCGGAAGAGCTGGAGAAAGGCTCTAGGGTGGGCGACATCTCCAGGGACCT
GGGGCTGGAGCCCCGGGAGCTCGCGGAGCGCGAGTCCGCATCATCCCCAGAGGTAGGACGCAGCTTTTCGCCCT
GAATCCGCGCAGCGGCAGCTTGGTCAAGGCGGGCAGGATAGACGGGAGGAGCTCTGTATGGGGGCCATCAAGTG
TCAATTAAATCTAGACATTCTGATGGAGGATAAGTGAAAATATATGGAGTAGAAGTAGAAGTAAGGGACATTAA
CGACAATCGCCCTTACTTTCGTGAAAGTGAATTAGAAATAAAAATTAAGTGAATAATGCAGCCACTGAGATGCGGTT
CCCTCTACCCACGCTGGGATCCGGATATCGGAAGAACTCTCTGCAGAGCTACGAGCTCAGCCCGAACACTCA
CTTCTCCCTCATCGTGCAAAATGGAGCCGACGGTAGTAAGTACCCCGAATTGGTGCTGAAACGCGCCCTGGACCG
CGAAGAAAAGGCTGCTCACCACCTGGTCTTACGGCTCCGACGGGGGCGACCCGGTGCGCACAGGCACCGCGCG
CATCCGCGTGATGGTTCTGGATGCGAACGACAACGCACACGCGTTTGCTCAGCCGAGTACCGCGCAGCGTTCC
GGAGAATCTGGCCTTGGGCGACGCGAGCTGTTGTAGTCAACGCTACCGACCTGACGAAGGAGTCAATGCGGAAGT
GAGGTATTCTTCCGGTATGTGGACGACAAGGCGGCCAAGTTTTCAAAGTAGATTGTAATTCAGGGACAATATC
AACAAATAGGGGAGTTGGACACGAGGAGTCAAGATTCTACCAGATGGAAGTGCAAGCAATGGATAATGCAGGATA
TTCTGCGCGAGCCAAAGTCTGATCACTGTTCTGGACGTGAACGACAATGCCCCAGAAGTGGTCTCACCTCTCT
CGCCAGCTCGGTTCCCGAAAATCTCTCCAGAGGGACATTAAATGCCCCTTTTAAATGTAAATGACCAAGATTCTGA
GAAAACGGACAGGTGATCTGTTTCATCCAGGAAATCTGCCCTTTAAATTAGAAAAATCTTACGGAAATTACTA
TAGTTTAGTCACAGACATAGTCTTGGATAGGGAACAGGTTCTAGCTACAACATCACAGTGACCGCCACTGACCG
GGGAACCCCGCCCTATCCACGGAACTCATATCTCGTGAACGTGGCAGACACCAACGACAACCGCGCGGTCTT
CCCTCAGGCCTCCTATTCCGCTTATATCCAGAGAACAATCCAGAGGAGTTTCCCTCGTCTCTGTGACCGCCCA
CGACCCGACTGTGAAGAGAACGCCCAGATCACTTATCCCTGGCTGAGAACACCATCCAAGGGGCAAGCCTATC
GTCCTACGTGTCCATCAACTCCGACACTGGGTAAGTGTATGCGCTGAGCTCCTTCGACTACGAGCAGTTCCGAGA
CTTGCAAGTGAAAGTGATGGCGGGGACAACGGGCACCCGCCCTCAGCAGCAACGTGTGCTTGAGCCTGTTCTGT
GCTGGACGAGAACGACAATGCGCCCGAGATCCTGTACCCGCGCTCCCCACGGACGGTTCCACTGGCGTGGAGCT
GGCTCCCCGCTCCGACAGAGCCCGGTACCTGGTGACCAAGGTGGTGGCGGTGGACAGAGACTCCGGCCAGAAGCG
CTGGCTGTCTACCGTCTGCTCAAGGCCAGCGAGCCGGGACTCTTCTCGGTGGGTCTGCACACGGGCGAGGTGCG
CACGGCGGAGCCCTGCTGGACAGAGACGCGCTCAAGCAGAGCCTCGTAGTGGCGCTCCAGGACCACGGCCAGCC
CCCTCTCTCCGCCACTGTACGCTCACCGTGGCGGTGGCCGACAGCATCCCCAAGTCTTGGCGGACCTCGGCAG
CCTCGAGTCTCCAGTAACTCTGAAACCTCAGACCTCACTCTGTACCTGGTGGTAGCGGTGGCCGCGGTCTCCTG
CGTCTTCTGGCCTTCGTATCTTGTGCTGGCGCTCAGGCTGCGGCGCTGGCACAAGTACCGCTGCTGCAGGC
TTCAGGAGGCGGCTTGACAGGAGCGCCGGCTCGCACTTTGTGGGCGTGGACGGGTGCAGGCTTTCTGACAGC
CTATTTCCACGAGGTTTCCCTCACCACGGACTCGCGGAAGAGTCACTGATCTTCCCCAGCCCAACTATGCAGA
CATGCTCGTCAGCCAGGAGAGCTTTGAAAAAGCGAGCCCCCTTTGCTGTGAGGTGATTGGGTATTTTCTAAAGA
CAGTCATGGGTAAATTGAGGTGAGTTTATATCAAATCTTCTTTCTTTTTTTTAAATTGCTCTGTCTCCCAAGC
TGGAGTGCAGCGGTACGATCATAGCTCACTGCGGCCCTCAAACCTCTAGGCTCAAGCAATTATCCACCTTTGCCT
CCGGTGTAAACAGGACTACAGGTGCAAGCCACCTACTGTCTGCCTATCTATCTATCTATCTATCTATCTATCT
CTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCT
CGAGGCGGGTGGATCACCTGAGGTGGGAGTTTGGAGCCAGCCTGACCAACATGGAGAAACCCGCTCTATACTAA
AAAAATACAAATTAGCCGGGCGTGGTGGTGCATGTCTGTAATCCAGCTACTTGGGAGGCTGAGTCAGGAGAAT
TGCTTTAACCTGGGAGGTGGAGGTTGCAATGAGCTGAGATTGTGCCATTGCACTCCAGCCTGGGCAACAAGAGT
AAACTCTATCTCA

79/615

FIGURE 78

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48306
><subunit 1 of 1, 916 aa, 1 stop
><MW: 100204, pI: 4.92, NX(S/T): 4
MIPARLHRDYKGLVLLGILLGLTLWETGCTQIRYSVPEELEKGSRVGDISRDLGLEPRELAERGVRIIPRGRTQLF
ALNPRSGSLVTAGRIDREELCMGAIKCOLNLDILMEDKVKIYGEVEVRDINDNAPYFRESELEIKISENAATEM
RFPLPHAWDPDIGKNSLQSYELSPNTHFSLIVQNGADGSKYPELVLRALDREEKAAHHLVLTASDGGDPVRTGT
ARIRVMVLANDANAPAFAPQPEYRASVPENLALGTQLLVVNATDPDEGVNAEVRYSFYVDDKAAQVFKLDCNSGT
ISTIGELDHEESGFYQMEVQAMDNAGYSARAKVLITVLDVNDNAPEVLTSLASSVPENSPRGTLIALLNVDNDQD
SEENGQVICFIQGNLFPKLEKSYGNYSLVTDIVLDREQVPSYNITVTATDRGTPPLSTETHISLNVADTNDNPP
VFPQASYSAYIPENNPRGVSLVSVTAHDPDCEENAQITYSLAENTIQQASLSSYVSINSDTGVLIALSSFDYEQF
RDLQVKVMARDNGHPPLSSNVSLSLFVLDQNDNAPEILYPALPTDGSTGVELAPRSAEPGYLVTKVVAVDRDSGQ
NAWLSYRLLKASEPGLFSVGLHTGEVVRTARALLDRDALKQSLVVAVQDHGQPPLSATVTLTVAVADSIPQVLADL
GSLESPANSETSDLTYLVVAVAAVSCVFLAFVILLALRLRRWHKSRLLQASGGGLTGAPASHFVGVDGVQAFI
QTYSHEVSLTTDSRKSHLIFPQPNYADMLVVSQESFEKSEPLLLSGDSVFSKDSHGLIEVSLYQIFFLFFFNCSVS
QAGVQRYDHSSLRPQTPRLKQLSHLCLRCNRDYRCKPPTVCLSIYLSIYLSIYLSIYLLLSCTDGS LTPVIPVLW
EAEAGGSPEVGS LRPA
```

Signal sequence:

amino acids 1-30

Transmembrane domains:

amino acids 693-711, 809-823, 869-888

80/615

FIGURE 79

AGCCGCTGCCCGGGCCGGGCGCCCGGGCGGCACCATGAGTCCCCGCTCGTGCCTGCGTTTCGCTGCGCCTCCTC
GTCTTCGCCGTCTTCTCAGCCGCGCGAGCAACTGGCTGTACCTGGCCAAGCTGTCGTGCGGTGGGGAGCATCTCA
GAGGAGGAGACGTGCCGAGAACTCAAGGGCCTGATCCAGAGGCAGGTGCAGATGTGCAAGCGGAACCTGGAAGTC
ATGGACTCGGTGCGCCGCGGTGCCAGCTGGCCATTGAGGAGTGCCAGTACCAGTTCGGAACCGGCGCTGGAAC
TGCTCCACACTCGACTCCTTGCCCGTCTTCGGCAAGGTGGTGACGCAAGGGACTCGGGAGGCGGCCCTTCGTGTAC
GCCATCTCTTCGGCAGGTGTGGCCTTTCAGTGACGCGGGCGTGCAGCAGTGGGGAGCTGGAGAAGTGGCGCTGT
GACAGGACAGTGATGGGTGAGCCACAGGGCTTCCAGTGGTCAGGATGCTCTGACAACATCGCCTACGGTGTG
GCCTTCTCACAGTCGTTTGTGGATGTGCGGGAGAGAAGCAAGGGGGCCTCGTCCAGCAGAGCCCTCATGAACCTC
CACACAATGAGGCCGCGCAGGAAGGCCATCCTGACACACATGCGGGTGGAATGCAAGTGCCACGGGGTGTGAGGC
TCCTGTGAGGTAAAGACGTGCTGGCGAGCCGTGCCGCCCTTCCGCCAGGTGGGTGACGCACTGAAGGAGAAGTTT
GATGGTGCCACTGAGGTGGAGCCACGCCGCGTGGGCTCCTCCAGGGCACTGGTACCACGCAACGCACAGTTCAAG
CCGCACACAGATGAGGACCTGGTGTACTTGGAGCCTAGCCCCGACTTCTGTGAGCAGGACATGCGCAGCGGCGTG
CTGGGCACGAGGGGGCCGCACATGCAACAAGACGTCCAAGGCCATCGACGGCTGTGAGCTGCTGTGCTGTGGCCGC
GGCTTCCACACGGCGCAGGTGGAGCTGGCTGAACGCTGCAGCTGCAAATTCCACTGGTGTGCTTCGTCAAGTGC
CGCAGTGCCAGCGGCTCGTGGAGTTGCACACGTGCCGATGACCGCCTGCCTAGCCCTGCGCCGGCAACCACTA
GTGGCCAGGGAAGGCCGATAATTTAAACAGTCTCCACCACCTACCCCAAGAGATACTGGTTGTATTTTTTGT
CTGGTTTGGTTTTTGGGTCTCATGTTATTTATTGCCGAAACCAGGCAGGCAACCCCAAGGGCACCACAGGGC
CTCCCCAAAGCCTGGGCTTGTGGCTGCCACTGACCAAGGGACCTTGCTCGTGCCGCTGGCTGCCCCGATGTG
GCTGCCACTGACCACTCAGTTGTTATCTGTGTCCGTTTTTCTACTTGACAGCCTAAGGTGGAGTAACAAGGAGTA
TTACCACCACATGGCTACTGACCGTGTGATCGGGGAAGAGGGGGCTTATGGCAGGGAATAGGTACCGACTTG
ATGGAAGTCACACCCTCTGGAAAAAAGAACTCTTAACCTCTCCAGCACACATACACATGGACTCCTGGCAGCTTGA
GCCTAGAAGCCATGTCTCTCAAATGCCCTGAGAAAGGGAACAAGCAGATACCAGGTCAAGGGCACCAGGTTTATT
TCAGCCCTTACATGGACAGCTAGAGGTTCGATATCTGTGGTCTTCCAGGCAAGAAGAGGGAGATGAGAGCAAG
AGACGACTGAAGTCCCACCCTAGAACCAGCCTGCCCCAGCCTGCCCCCTGGGAAGAGGAACTTAACCACTCCCC
AGACCCACCTAGGCAGGCATATAGGCTGCCATCCTGGACCAGGGATCCCGGCTGTGCCTTTGCAGTCATGCCCCG
GTCACCTTTTACAGCGCTGTTTCTCCATGAAACTGAAAACACACACACACACACACACACACACACACACAC
ACACACACACGGACACACACACACACCTGCGAGAGAGAGGGAGGAAAGGGCTGTGCCTTTGCAGTCATGCCCCG
TCACCTTTTACAGCACTGTTTCCTC

81/615

FIGURE 80

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48328
<subunit 1 of 1, 351 aa, 1 stop
<MW: 39052, pI: 8.97, NX(S/T): 2
MSPRSCLSRLRLLVFAVFSAAASNWLYLAKLSSVGSISEEETCEKLGKLIQRQVQMCKRNLEVMDSVRRGAQLAI
EECQYQFRNRRWNCSTLDSLPGKVVTTQGTREAAFYAISSAGVAFVAVTRACSSGELEKCGCDRTVHGVSPQGF
QWSGCSDNIAYGVAFSQSFVDVRERSKGASSSRALMNLHNNEAGRKAILTHMRVECKCHGVSGSCEVKTWCWRAVP
PFRQVGHALKEKFDGATEVEPRRVGSSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGRTCNKTS
KAIDGCELLCCGRGFHTAQVELAERCSCFHWCCFVKCRQCQRLVELHTCR

Important features:**Signal peptide:**

amino acids 1-22

N-glycosylation sites.

amino acids 88-91 and 297-300

Wnt-1 family signature.

amino acids 206-215

Homologous region to Wnt-1 family proteins

amino acids 183-235, 305-350, 97-138, 53-92 and 150 -174

82/615

FIGURE 81

CCGAGCCGGGCGCGCAGCGACGGAGCTGGGGCCGGCCTGGGACCATGGGCGTGAGTGCAATCTACGGATCAGTCT
CTGATGGTGGGTCGTTAACCTCAGTGGGGACTCCAAGATTTCCATGAAGAAAATCAGTTGTCTTCATTCAAGAAT
TGGGGTCTGGCTCAGAAATTCCTGCAGCTGGTGAAAATCTGTTTTCTAGAAGAGGTTTAATTAATGCCTGCAGTCT
GACATGTTCCCGATTTGAGGTGAAACCATGAAGAGAAAATAGAATACTTAATAATGCTTTTCCGCAACCGCTTCT
TGCTGCTGCTGGCCCTGGCTGCGCTGCTGGCCTTTGTGAGCCTCAGCCTGCAGTTCTTCCACCTGATCCCGGTGT
CGACTCCTAAGAATGGAATGAGTAGCAAGAGTCGAAAGAGAATCATGCCGACCCTGTGACGGAGCCCCCTGTGA
CAGACCCCGTTTATGAAGCTCTTTTGTACTGCAACATCCCCAGTGTGGCCGAGCGCAGCATGGAAGGTGATGCC
CGCATCATTTTAAGCTGGTCTCAGTGCAATGTGTTTCATTCGCCACGGAGACAGGTACCCACTGTATGTATTCCCA
AAACAAAGCGACCAGAAATGACTGCACTCTGGTGGCTAACAGGAAACCGTATCACCCAAAATGGAAGCTTTCA
TTAGTCACATGTCAAAGGATCCGGAGCCTCTTTCGAAAGCCCTTGAATCCTTGCCCTCTTACCCTAAATCACC
CATTTGTGTGAGATGGGAGAGCTCACACAGACAGGAGTTGTGCAGCATTTCAGAACGGTCAGCTGCTGAGGGATA
TCTATCTAAAGAAACACAACTCCTGCCAATGATTGGTCTGCAGACCAGCTCTATTTAGAGACCACTGGGAAA
GCCGGACCCTACAAAGTGGGCTGGCCTTGTCTTATGGCTTCTCCAGATTTTGACTGGAAGAAGATTTATTTCA
GGCACCAGCCAAGTGGCTGTTCTGCTCTGGAAGCTGCTATTGCCCGTAAGAAACAGTATCTGGAAGGAGC
AGCGTCGTGAGTACCTCCTACGTTTGAAGAACAGCCAGCTGGAGAAGACCTACGGGAGATGGCCAAGATCGTGG
ATGTCCCCACCAAGCAGCTTAGAGCTGCCAACCCCATAGACTCCATGCTCTGCCACTTCTGCCACAATGTGAGCT
TTCCCTGTACCAGAAATGGCTGTGTGACATGGAGCACTTCAAGGTAATTAAGACCCATCAGATCGAGGATGAAA
GGGAAAGACGGGAGAAAGAAATTTGACTTCGGGTATTCTCTCCTGGGTGCCACCCCATCCTGAACCAACCATCG
GCCGGATGCAGCGTGCCACCGAGGGCAGGAAAGAGCTCTTTGCCCTCTACTCTGCTCATGTGCTACTCTGT
CACCAGTTCTCAGTGCCCTTGGGCCTTTTCAAGCCAGGTTCCCAAGGTTTGCAGCCAGGTTGATCTTTGAGCTTT
GGCAAGACAGAGAAAAGCCAGTGAACATTCCTCCGATTTTACAATGGCGTCGATGTACATTTCCACACCT
CTTCTGCCAAGACCACCACAAGCTTCTCCCAAGCCATGTGCCCGCTTGAAACTTGGTCCGCTTTGTGAAA
GGGACATGTTTGTAGCCCTGGGTGGCAGTGGTACAAATATTATGATGCATGTACAGGGAAGGATTTCTAAAGG
TATGAGTACAGCAGTATAGAATCCATGCCAATACAGAGCATAGGGAAAGGTCCACTTCTAGTTTTGTCTGTTAC
TAAGGGTAGAAGATTATTGCTTTTTAAAGGCTAAATATTGTTTGTGGGAACACAGATGGTTGGGGTTGAACAGT
AAGCACATTGCTGCAATGTGGTACGTGAATTGCTTGGTACAAAATGGCCAGTTCACAGAGGAATAGAAGGTACTT
TATCATAGCCAGACTTCGCTTAGAATGCCAGAATAATATAGTTCAAGACCTGAAGTTGCCAATCCAAGTTTGCAC
TCTTCTGGCCTGCCCATGTTACTATGTGATGGAACAGCACACCTCAACCAAAATTTTTTAACTCTTAGACATT
TTTACCTTGTCTTGTAAAGATTTCTTGAAGTGATTATCTAAAATAAAGGTTGGCAAACTTTTCTGTAAAGG
GCCAGATTGTAATATTTTCACTGTGTGGACAAAAGGCCACATACAGTCTCTGTCTAATACTACTCAACTCTGT
TTCTGAAGCAGGAAAGCCACCACAGACAGTACATAAAGGAATATGTGTAGCTGGGTTCCAGGCCAGACAAAACA
GATGGTGACCAGACTTGGCCCCCTGGGCTGTAGTTTGTGACCCCTCATCTAAAAATAGGCTATACTACAATTGC
ACTTCCAGCACTTTGAGAACGAGTTGAATACCAAGAATTATTCAATGGTTCCTCCAGTAACTTCTGCTAGAAACA
CAGAATTTGGTCTGTATCTGACACTAGAACAAAATTTGAGGGTAAATAAACATTGAATTAGATGAATCATAGAA
AACTGATTAGAAGAATACTTGATGTTTATGATGATTGTGGTACAAGATAGTTTAAAGTATGTTCTAAATATTTGT
CTGCTGTAGTCTATTTGCTGTATATGCTGAATTTTTGTATGCCATTTAGTATTTTATAGTTTAGGAAAATATT
TTCTAAGACCAGTTTTAGATGACTCTTATTCTGTAGTAATATTCAATTTGCTGTACCTGCTTGGTGGTTAGAAG
GAGGCTAGAAGATGAATTCAGGCACCTTCTTCCAATAAACTAATTATGGCTCATTCCCTTGGACAAGCTGTAGA
ACTGGATTCAATTTTAAACATTTTCATCAGTTTCAAATGGTAAATTTCTGATTGATTTTTAAATGCGTTTTTGGGA
AGAACTTTGCTATTAGGTAGTTTACAGATCTTTATAAGGTGTTTTATATATTAGAAGCAATTATAATTACATCTG
TGATTTCTGAACATAATGGTGCTAATTCAGAGAAATGGAAAGTGAAAGTGAGATTCTCTGTTGTCATCGGCATTCC
AACTTTTTCTCTTTGTTTTGTCCAGTGTTGCATTGAATATGTCTGTTTCTATAAATAAATTTTTTAAAGATAA

83/615

FIGURE 82

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48329
><subunit 1 of 1, 480 aa, 1 stop
><MW: 55240, pI: 9.30, NX(S/T): 2
MLFRNRELLLLALAALLAFVSLSLQFFHLIPVSTPKNGMSSSKSRKRIMDPVTEPPVTDPVYEALLYCNIPSVAE
RSMEGHAPHHFKLVSVHVFIRHGDRYPLYVIPKTKRPEIDCTLVANRKPYPHPKLEAFISHMSKSGSGASFESPLNS
LPLYPNHPLCEMGELTQTGVVQHLQNGQLLRDIYLLKKHKLLPNDWSADQLYLETTGKSRTLQSGLALLYGFLPDF
DWKKIYFRHQPSALFCSGSCYCPVRNQYLEKEQRRQYLLRLKNSQLEKTYGEMAKIVDVPTKQLRAANPIDSMC
HFCHNVSEFPCTRNGCVDMEHFKVIKTHQIEDERERREKKLYFGYSLLGAHPILNQTIGRMQRATEGRKEELFALY
SAHDVTLSPVLSALGLSEARFPRFAARLTFELWQDREKPSSEHSVRILYNGVDVTFHTSFQDHHKRSPPKPMCPLE
NLVRFVKRDMFVALGGSGTNYDACHREGF
```

Signal sequence:
amino acids 1-18

FIGURE 83

TCTCGCAGATAGTAAATAAATCTCGGAAAGGCGAGAAAGAAGCTGTCTCCATCTTGTCTGTATCCGCTGCTCTTGT
GACGTTGTGGAGATGGGGAGCGTCTCTGGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAAGTGCC
CCGTGTTTGCATTCGCCAGTGTGCTCTGCTAGTGGAAACAACCTCCACTGTAACATAGATTGATCTATGCATTTTCTTG
CTTGTGTGGAGTATGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACAACCTGAATAAGATTCTCGGATTT
TGTGAGAAATGAGAAAGGTGTTGTCCTTTGAACATTTGGTTGGCTATAAAGTGTATATCGTTTGTGCTTTGGT
TTGGCTATGTTCTATCTCTCTCTCTCTTAACTAATGATCAAACTGAAGAGTAGACAGTGATCCCTAGAGCTGCAGTG
CACAAATGGATTTGGTTCTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGCATTCTTCATCCAGAAGGA
ACITTTACAACCTGTGTGTTTATGTAGGCATGGCAGGTGCCTTTGTTCATCTCTACACAACCTGATCTTAC
ATTGATTTTGCACATTCATGGAATGAATCGTGGTTGAAAAAATGGAAGAAGGAACTCGAGATGTTGGTATGCA
GCCCTGTTATCAGCTACAGCTCTGAATATCTGCTGTCTTTAGTTGCTATCTGCTGTCTTTGTCTACTACACT
CATCCAGCCAGTGTGTTTCAGAAAACAAGGCGTTCTCATGTTGCAACATGCTCTCTGCTTGGTGCTTCTGTAATG
TCTATACTGCCAAAAATCCAGAATACACAAACCAAGATCTGGTTTGTTCACGTCTTCAGTAATACAGCTCTACACA
ATGATATTTGACATGGTCAGCTATGACCAATGGAACCGAACAATAATGCAACCAAGCTCTACATGAACATAAATGGC
TACAATAACAAGCAAGCTGTCCCAAGAAGGAGGAGTCACTGCTGAGTGGTGGCATGCTCAAGGAATTATAGGACTA
ATTCTCTTTTTGTGTGTGTAATTTTATCCAGCATCCGTACTTCAAACAATAGTCAGGTTAATAAACTGACTCTA
ACAAGTGATGAATCTACATTAAATGAGATGGTGGAGCTAGAAGTATGGATCACTGGAGGATGGGACGATGTT
CACCGAGCTGTAGATAATGAAAGGATGGTGCTACATACAGTTATTCCTCTTTTCACTTCATGCTTTTCTGGCT
TCACTTTATATCATGATGACCCCTTACCAACTGGTCCAGGTATGAACCCCTCTCGTGAGATGAAAGTCAGTGGACA
GCTGTCTGGTGAAATCTCTTCCAGTTGGATGGCATCGTGTGTATGTTTGGACACTCGTGCGACCACTTGT
CTTACAAATCGTGATTTTGACTGAGTGAGACTTCTAGCATGAAAGTCCCATTGTTGATTATGCTTATTTGAAAC
AGTATTTCCCAACTTTTGTAAGTTGTGTATGTTTTGCTTCCCATTGTAACCTCTCCAGTGTTCTGGCATGAATTA
GATTTTACTGCTGTGCTATTTTGTATTTTCTTACCAAGTGCAATGTATGTAAGTAGAATGAATTCGACAGGAA
AGTTTTATGAATTTGGTGATGAGTTAGTAAAGTGGCCATTATGGGCTTATCTCTGCTCTATAGTTGTGAAAT
GAAGAGTAAAAACAATTTGTTTGACTATTTTAAATATATATAGACCTTAAGCTGTTTGTAGCAGCATAAAGC
AAATGTATGGCTGCCCTTTGAAATATTTGATGTGTTGCTGGCAGGATACGCAAGAACATGTTTATTTTAA
ATTTATAAACAAGTCACCTAAATGCCAGTTGTCTGAAAAATCTTAAAGGTTTACCCTTGATACGGAATTTACA
CAGGTAGGGAGTGTTTAGTGGACAATAGTGTAGGTTATGGATGGAGGTTGTCGCTACTAAATTAATAACGAGTAA
ATAATCTTACTTTGGTGAGAGATGGCCTTTGCCAACAAAGTGAACCTTTTGTGTTGTTTAACTCATGAAGTATG
GGTTCAGTGGAAATGTTTGAACCTCTGAAGGATTTAGACAAGGTTTGAAGGATAATCATGGGTTAGAAGGAA
GTGTTTTGAAGTCACTTTGAAAGTTAGTTTGGGCCCCAGCAGGTAGCTCACCTTGGTAAATCCCGACACTTTG
GGAGCTTAAGTGGGTAGATTACTTGAGCCAGGAATTCAGACAGGCTGGCATAGGTGAACCTGTTCTATAAAA
ATAATCTGGCTTTGAGCATATGCTTGCTGTCAGCACAGAGCTAGTGAAGATTGCTGAGCCAGAGCCAAAG
TTGTCAGTGAGCAAGTCAGTCACTGCACTAGCTGGCAGAGGTAAAGCCAAAAATATATATATTTGAAAT
CAAGGAGGCCAAAAATTTGACAGGGAAGGAAGTAAGTCAAAACCCTAGGCTTTAGTAGGTTACTTATATAAAATC
TAGTCCAGTTCTCTCATTTAAAAAAATGAAGACACTGAAATACAGACTTAAATAGCTCAGATAGCTAATTAGGAA
ATTTCAAGTTGGCCAAATAATAGCATCTCTCTGACATTTAAAAATAATTTCTATTCAAATACATGCATATTGAT
TTACACCTCATACTGTGATAATTAATGTGATGTGGATTGCTGGTGTCCAGCATGACCCATAAACAGGTGAGAAGA
ATGATGGAATGTTTGAATAAACTCCTGCTTATAGTATATACATACAGTTCAAAAGATGTTTAAATGCTTTTGT
ATTACTGCCATGTAATTAAGAAATATAGATTATTGTAACCTTTCAACCTGAAATCAAGCAGTATGAGAGTTTA
GTTATTTGTATGTGTCACTAGTGTCTAATGAAGCTTTTAAATCTACAATTTCTTCTTTAAAAATATTTATTAAT
GTGAATGGAATATAACAATTCAGCTTAATCCCCAACCTTATTTCTGTGTGTAGACATTGTATTCACAATTTTGA
ATGGCTGTGTTTACCTCTAAATAAATGAATTCAGAGAAAAAATAAAAAA

85/615

FIGURE 84

MGSVLGLCSMASWIPCLCGSAPCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGMEEQLNKIPGFCENE
KGVVPCNILVGKYKAVYRLCFGLAMFYLLSLLMIKVKSSSDPRAAVHNGFWFFKFAAAIAIIIGAFFIPEGTFTT
VWFYVGMAGAFCFILIQVLVLLIDFAHSWNESWVEKMEEGNSRCWYAALLSATALNYLLSLVAIVLFFVYYTHPAS
CSENKAFISVNMLLCVGASVMSILPKIQESQPRSGLLQSSVITVYTMYLTSAMTNEPETNCNPSLLSIIGYNTT
STVPKEGQSVQWWHAQGIIGLILFLLCVFYSSIRTSNNSQVNKLTLTSDESTLIEDGGARSDGSLEDGDDVHRAV
DNERDGVITYSYFFHFMLFLASLYIMMTLTNWSRYEPSREMKSQWTAVVWKISSSWIGIVLYVWTLVAPLVLTNRDFD

86/615

FIGURE 85

AACAAAGTTTCAGTGACTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGAGCTGCTGGGCAGA
GAGGGACTGTCCGGCTCCCAGATGCTGGGCCTCCTGGGGAGCACAGCCCTCGTGGGATGGATCACAGGTGCTGCT
GTGGCGGTCTGTGCTGCTGCTGCTGCTGGCCACCTGCCTTTTCCACGGACGGCAGGACTGTGACGTGGAGAGG
AACCGTACAGCTGCAGGGGGAAACCGAGTCCGCCGGGCCCAGCCTTGGCCCTTCCGGCGCGGGGCCACCTGGGA
ATCTTTCACCATCACCGTCATCCTGGCCACGTATCTCATGTGCCGAATGTGGGCCTCCACCACCACCACCC
CGCCACACCCCTCACCACTCCACCACCACCACCCACCCACCGCCACCATCCCGCCACGCTCGCTGAAGGCTGC
TGTCGCCGGTGCCTGTGGACAGCAGCTGCCCTGCCCTCCCATCTGTTCCCAGGACAAGTGGACCCCATGTTTCC
ATGTGGAAGGATGCATCTCTGGGGTGAACGAGGGGAACAATAGACTGGGGCTTGCTCCAGCTGCATTTGCATGGC
ATGCCCCAGTGTACTATGGCAGCAGAGAATGGAGGAACACTGGGTCTGCAGTGCTGAAGGGTTTGGGGAGTGGAG
AGCAAGGGTGCTCTTTCGGGGCTGGACAGCCCGTCTTGTGACAGTGACTCCAGTGAGCCCCAGAAATGACAAGC
GTGTCTTGGCAGAGCCAGCACACAAGTGGATGTGAAGTGCCCGTCTTGACCTCCTCATCAGGCTGCTGCAGGCCT
CTGGCGGGCAGGGCACTGGGAGAGGCCCTGAGAATGTCTTTTGGTTTGGAGAAGGCAGTGTGAGGCTGCACAGT
CAATTCATCGGTGCCTTAGTCCAAGAAAATAAAAACCACTAAGAAGCTTTAAAAAAAAAAAAAAAAAAAAA

87/615

FIGURE 86

MLGLLGSTALVGWITGA AVAVLLLLLLLATCLFHGRQDCDVERNRTAAGGNRVRRAPWPFRRRGHLGIFHHHRH
PGHVSHVFPNVGLHHHHHPRHTPHHLHHHHHPRHHPRHAR

88/615

FIGURE 87

CCCACGCGTCCGTCTAGTCCCCGGGCCAACTCGGACAGTTTGCTCATTATTATTGCAACGGTCAAGGCTGGCTTGT
GCCAGAACGGCGCGCGCGCGCGCACGCACACACACGGGGGAAACTTTTTTAAAAATGAAAGGCTAGAAGA
GCTCAGCGGGCGCGCGGGCGCTGCGCGAGGGCTCCGGAGCTGACTCGCCGAGGCAGGAAATCCCTCCGGTCGCGA
CGCCCGGCCCCGGCTCGGCGCCCCGCTGGGATGGTGCAGCGCTCGCCGCGGGCCCCGAGAGCTGCTGCACTGAAG
GCCGGCGACGATGCGAGCGCGCCCCGCTGCCCGTGTCCCCCGCCCGCGCCCTCCTGCTCGCCCTGGCCGGTGCTCT
GCTCGCGCCCTGCGAGGCCCCGAGGGGTGAGCTTATGGAACCAAGGAAGAGCTGATGAAGTTGTGAGTGCCTCTGT
TCGGAGTGGGGACCTCTGGATCCAGTGAAGAGCTTCGACTCCAAGAATCATCCAGAAGTGCTGAATATTCGACT
ACAACGGGAAAGCAAAGAACTGATCATAAATCTGGAAAGAAATGAAGGTCTCATTGCCAGCAGTTTCACGGAAAC
CCACTATCTGCAAGACGGTACTGATGTCTCCCTCGCTCGAAATTACACGGGTCACTGTTACTACCATGGACATGT
ACGGGGATATTCTGATTCAGCAGTCAGTCTCAGCACGTGTTCTGGTCTCAGGGGACTTATTGTGTTTGAAAATGA
AAGCTATGTCTTAGAACCAATGAAAAGTGCAACCAACAGATACAACTCTTCCCAGCGAAGAAGCTGAAAAGCGT
CCGGGGATCATGTGGATCACATCACACACACCAACCTCGCTGCAAAGAATGTGTTTCCACCACCTCTCAGAC
ATGGGCAAGAAGGCATAAAGAGAGACCTCAAGGCAACTAAGTATGTGGAGCTGGTGATCGTGGCAGACAACCG
AGAGTTTCAGAGGCAAGGAAAAGATCTGAAAAAGTTAAGCAGCGATTAAATAGAGATTGCTAATCACGTTGACAA
GTTTTACAGACCCTGAACATTTCGGATCGTGTGGTAGGCGTGGAAGTGTGGAATGACATGGACAAATGCTCTGT
AAGTCAGGACCCATTACACAGCCTCCATGAATTTCTGGACTGGAGGAAGATGAAGCTTCTACCTCGCAATCCCA
TGACAATGCGCAGCTTGTGAGTGGGTTTATTTCCAGGGACCACCATCGGCATGGCCCCAATCATGAGCATGTG
CACGGCAGACCAGTCTGGGGGAATTGTGATGGACCATTACAGACAATCCCCTTGGTGAGCCGTGACCTGGCACA
TGAGCTGGGCCACAATTTCCGGATGAATCATGACACACTGGACAGGGGCTGTAGCTGTCAAATGGCGGTTGAGAA
AGGAGGCTGCATCATGAACGCTTCCACCGGTTACCCATTTCCCATGGTGTTCAGCAGTGCAGCAGGAAGGACTT
GGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCTGTTTAACTGCCGGAAGTCAGGGAGTCTTTCGGGGCCA
GAAGTGTGGGAACAGATTTGTGGAAGAAGGAGAGGAGTGTGACTGTGGGGAGCCAGAGGAATGTATGAATCGCTG
CTGCAATGCCACCACCTGTACCCTGAAGCCGGACGCTGTGTGCGCACATGGGCTGTGCTGTGAAGACTGCCAGCT
GAAGCCTGCAGGAACAGCGTGCAGGGACTCCAGCAACTCCTGTGACCTCCCAGAGTTCTGCACAGGGGCCAGCCC
TCACTGCCAGCCAATGTGTACCTGCACGATGGGCACCTCATGTGAGGATGTGGACGGCTACTGCTACAATGGCAT
CTGCCAGACTCACGAGCAGCAGTGTGTGTCAGCTCTGGGGACCAGGTGCTAAACCTGCCCTGGGATCTGCTTTGA
GAGAGTCAATTTCTGCAGGTGATCCTTATGGCAACTGTGGCAAAGTCTCGAAGAGTTCCTTTGCCAAATGCGAGAT
GAGAGATGCTAAATGTGGAAAAATCCAGTGTCAAGGAGGTGCCAGCCGGCCAGTCATTGGTACCAATGCCGTTTC
CATAGAAACAAACATCCCTCTGCAGCAAGGAGGCCGGATTCTGTGCCGGGGGACCCACGTGTACTTGGGCGATGA
CATGCCGGACCCAGGGCTTGTGCTTGCAGGCACAAAGTGTGCAGATGGAAAAATCTGCCTGAATCGTCAATGTCA
AAATATTAGTGTCTTTGGGGTTACGAGTGTGCAATGCAGTGCCACGGCAGAGGGGTGTGCAACAACAGGAAGAA
CTGCCACTGCGAGGCCCACTGGGCACCTCCCTTCTGTGACAAGTTTGGCTTTGGAGGAAGCACAGACAGCGGCC
CATCCGGCAAGCAGAAGCAAGGCAGGAAGCTGCAGAGTCCAACAGGGAGCGCGGCCAGGGCCAGGAGCCCGTGGG
ATCGCAGGAGCATGCGTCTACTGCCTCACTGACACTCATCTGAGCCCTCCCATGACATGGAGACCGTGACCAAGTG
CTGCTGCAGAGGAGGTACGCGTCCCCAAGGCCTCCTGTGACTGGCAGCATTGACTCTGTGGCTTTGCCATCGTT
TCCATGACAACAGACACAACACAGTTCTCGGGGCTCAGGAGGGGAAGTCCAGCCTACCAGGCACGTCTGCAGAAA
CAGTGAAGGAAGGGCAGCGACTTCTGGTTGAGCTTCTGCTAAAACATGGACATGCTTCAGTGTGCTCTCTGAG
AGAGTAGCAGGTTACCACTCTGGCAGGCCCCAGCCCTGCAGCAAGGAGGAAGAGGACTCAAAAGTCTGGCCTTTC
ACTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTTGGGCCAGTGTCCCTTTCCCAAGTACACCTCAGCCT
TGGCAGCCCTGATGACTGGTCTCTGGCTGCAACTTAATGCTCTGATATGGCTTTTAGCATTATTATATGAAAAT
AGCAGGGTTTTAGTTTTTAATTTATCAGAGACCTGCCACCCATTCCATCTCCATCCAAGCAAACCTGAATGGCAA
TGAAACAACTGGAGAAGAAGGTAGGAGAAAGGGCGGTGAAGTCTGGCTCTTTGCTGTGGACATGCGTGACCAGC
AGTACTCAGGTTTGAAGGTTTGCAGAAAGCCAGGGAACCCACAGAGTCACCAACCCTTCATTTAACAAGTAAGAA
TGTTAAAAAGTGAACAATGTAAGACCTAACTCCATCCCCCGTGGCCATTACTGCATAAAATAGAGTGCATTT
GAAAT

89/615

FIGURE 88

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49624
><subunit 1 of 1, 735 aa, 1 stop
><MW: 80177, pI: 7.08, NX(S/T): 5
MAARPLPVSPARALLLALAGALLAPCEARGVSLWNQGRADEVVSASVRSGLWIPVKSFDKSNHPEVLNIRLQRE
SKELIINLERNEGLIASSFTETHYLQDGTDVSLARNYTGHCYYHGHVRGYSDSAVSLSTCSGLRGLIVFENESYV
LEPMKSATNRYKLFPAKKLKSVRGSCGSHHNTPNLAAKNVFPFPSQTWARRHKRETLKATKYVELVIVADNREFQ
RQKQDLEKVKQRLIEIANHVDFYRPLNIRIVLVGVEVWMDKCSVSQDPFTSLHEFLDWRKMKLLPRKSHDNA
QLVSGVYFQGTITIGMAPIMSMCTADQSGGIVMDHSDNPLGAAVTLAHELGHNFQGMNHDTLDRGCSCQMAVEKGGC
IMNASTGYFFPMVFSSCSRKDLETSLEKGMGVCLFNLPEVRESFQGGQKCGNRFVEEGEECDCEPEECMNRCNA
TTCTLKPDCAVCAHGLCCEDCQLKPAGTACRDSSNSCDLPEFCTGASPHCPANVYLHDGHSCQDQDGYCYNGICQT
HEQQCVTLWGPGAKPAPGICFERVNSAGDPYGNCGKVSXSSFAKCEMRDAKCGKIQCQGGASRPVIGTNAVSIET
NIPLQQGGRILCRGTHVYLGDDMPDPLVLVLAGTKCADGKICLNRCQCNISVFGVHECAMQCHGRGVCNNRKNCHC
EAHWAPPFCDKFGFGGSTDSGPRIQAEARQEAESNRERGGQEPVGSQEHASTSLTI
```

Signal peptide:
amino acids 1-28

90/615

FIGURE 89

CTGCTGCATCCGGGTGTCTGGAGGCTGTGGCCGTTTTGTTTTCTTGGCTAAAATCGGGGGAGTGAGGCGGGCCGG
CGCGGCGCGACACCGGGCTCCGGAACCACTGCACGACGGGGCTGGACTGACCTGAAAAAATGCTCTGGATTTCTA
GAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTA
CTATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCACCATGAAAGATTTCAACCACTCA
TACCATGCCTGTGGTGTTATAGCAACCATAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGT
GATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTGCTCGCATTGCGCTTTTCGTTGGTTTCATGTTGGCCTTT
GGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTATACCTGGA
ATTGCTGTATTTTTCCAGAATGCCTTCATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGACTTA
TGGCAGTGAACACATCTGATTTCCCACAGCACAAACAGCCCTGCATGGGTTTGTGTTTTTTTACTGCTCACTCC
CAACCTTTTGTAAATGCCATTTTCTAACTTATTTCTGAGTGTAGTCTCAGCTTAAAGTTGTGTAATACTAAAATC
ACGAGAACACCTAAACAACAACCAAAAATCTATTGTGGTATGCACTTGATTAACCTATAAAATGTTAGAGGAAAC
TTTCACATGAATAATTTTTGTCAAATTTTATCATGGTATAATTTGTAATAAATAAAGAAATTACAAAAGAAATT
ATGGATTTGTCAATGTAAGTATTTGTCTATCTGAGGTCCAAAACCAATGAAAGTGCTCTGAAGATTTAATGT
GTTTATTCAAATGTGGTCTCTTCTGTGTCAAATGTTAAATGAAATATAAACATTTTTTAGTTTTTAAATATTCC
GTGGTCAAAATCTTCTCACTATAATTGGTATTTACTTTTACCAAAAATTCTGTGAACATGTAATGTAAGTGGC
TTTTGAGGGTCTCCCAAGGGGTGAGTGGACGTGTTGGAAGAGAGAAGCACCATGGTCCAGCCACCAGGCTCCCTG
TGTCCCTTCCATGGGAAGGTCTTCCGCTGTGCCTCTCATTCCAAGGGCAGGAAGATGTGACTCAGCCATGACACG
TGGTTCTGGTGGGATGCACAGTCACTCCACATCCACCACTG

91/615

FIGURE 90

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLEFTGWWIIIDAAVIYPTMKDFNHSYHACGVIATIAFLMINAVSN
GQVRGDSYSEGCLGQTGARIWLFVGFMLAFGSLIASMWILFGGYVAKEKDIVYPGIAVFFQNAFIFFGGLVFKFG
RTEDLWQ

FIGURE 91

[illegible]

93/615

FIGURE 92

MWLPLVLLLAVALLLAVLCKVYLGLFSGSSPNPFSEDVKKRPPAPLVTDKEARKKVLKQAFSANQVPEKLDVVVIGS
GFGGLAAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNGLEFDGTGIHYIGRMEEGSIGRFILDQITEGQLDWAPLS
SPFDIMVLEGPNRKEYPMYSGEKAYIQGLKEKFPQEEAIIIDKYIKLVKVVSSGAPHAILLKFLPLPVVQLLDRC
GLLTRFSPFLQASTQSLAEVLQQLGASSELQAVLSYIFPTYGVTPNHSAFSMHALLVNHYMKGGFYPRGGSSEIA
FHTIPVIQRAGGAVLTATVQSVLLDSAGKACGVSVKKGHELVNIYCPIVVSNAGLENTYEHLLPGNARCLPGVK
QQLGTVRPGLGMTSVFICLRGTKEDLHLPSTNYYVYDMDQAMERYVSMPREEAAEHIPLLFFAFPSAKDPTW
EDRFPGRSTMIMLIPTAYEWFEWQAEKCKRGSDYETFKNSFVEASMSVVLKLPQLEGKVESVTAGSPLTNQF
YLAAPRGACYGADHDLGRLHPCVMASLRAQSPINLYLTGQDIFTGGLVGLQGALLCSSAILKRNLVSDLNLD
SRIRAQKKKN

94/615

FIGURE 93

GGGAAAGATGGCGGCGACTCTGGGACCCCTTGGGTCGTGGCAGCAGTGGCGGCGATGTTTGTGCGCTCGGGATGG
GTCCAGGATGTTACTCCTTCTTCTTTTGTGGGGTCTGGGCAGGGGCCACAGCAAGTCGGGGCGGGTCAAACGTT
CGAGTACTTGAACGGGAGCACTCGCTGTGCAAGCCCTACCAGGGTGTGGGCACAGGCAGTTCCTCACTGTGGAA
TCTGATGGGCAATGCCATGGTGATGACCCAGTATATCCGCCTTACCCAGATATGCAAAGTAAACAGGGTGCCTT
GTGGAACCGGGTGCCATGTTTCTGAGAGACTGGGAGTTGCAGGTGCACTTCAAAATCCATGGACAAGGAAGAA
GAATCTGCATGGGGATGGCTTGGCAATCTGGTACACAAAGGATCGGATGCAGCCAGGGCCTGTGTTTGGAAACAT
GGACAAATTTGTGGGGCTGGGAGTATTTGTAGACACCTACCCCAATGAGGAGAAGCAGCAAGAGCGGGTATTCCC
CTACATCTCAGCCATGGTGAACAACGGCTCCCTCAGCTATGATCATGAGCGGGATGGGCGGCCTACAGAGCTGGG
AGGCTGCACAGCCATTGTCCGCAATCTTACCTAGACACCTTCCCTGGTGATTCCGTACGTCAAGAGGCATTTGAC
GATAATGATGGATATTGATGGCAAGCATGAGTGGAGGGAGTGCATTGAAGTGCCCGGAGTCCGCCTGCCCGCGG
CTACTACTTCCGCACCTCCTCCATCACTGGGGATCTCTCAGATAATCATGATGTCATTTCCCTGAAGTTGTTGA
ACTGACAGTGGAGAGAACCCCAAGAGGAAAAGCTCCATCGAGATGTGTTCTTGCCTCAGTGGACAATATGAA
GCTGCCTGAGATGACAGCTCCACTGCCGCCCTGAGTGGCTGGCCCTCTTCTCATCGTCTTTTTCTCCCTGGT
GTTTTCTGTATTTGCCATAGTCATTGGTATCATACTCTACAACAAATGGCAGGAACAGAGCCGAAAGCGCTTCTA
CTGAGCCCTCCTGCTGCCACCACTTTTGTGACTGTCACCATGAGGTATGGAAGGAGCAGGCACTGGCCTGAGCA
TGCAGCCTGGAGAGTGTTCTTGTCTCTAGCAGCTGGTTGGGGACTATATTCTGTCACTGGAGTTTTGAATGCAGG
GACCCCGCATTCCCATGGTTGTGCATGGGGACATCTAACTCTGGTCTGGGAAGCCACCCACCCAGGGCAATGCT
GCTGTGATGTGCCTTTCCCTGCAGTCTTCCATGTGGGAGCAGAGGTGTGAAGAGAATTTACGTGGTTGTGATGC
CAAAATCACAGAACAGAATTTATAGCCCAGGCTGCCGTGTTGTTGACTCAGAAGGCCCTTCTACTTCAGTTTT
GAATCCACAAAGAATTAATACTGGTAACACCACAGGCTTTCTGACCATCCATTGTTGGGTTTTGCATTTGACC
CAACCTCTGCCTACCTGAGGAGCTTTCTTTGGAAACCAGGATGGAAACTTCTTCCCTGCCTTACCTTCCCTTCA
CTCCATTCAATTGCTCTCTGTGTGCAACCTGAGCTGGGAAAGGCATTTGGATGCCTCTCTGTTGGGGCCTGGGG
CTGCAGAACACACCTGCGTTTCACTGGCCTTCAATTAGGTGGCCCTAGGGAGATGGCTTTCTGCTTTGGATCACTG
TTCCCTAGCATGGGTCTTGGGTCTATTGGCATGTCCATGGCCTTCCCAATCAAGTCTCTTCAGGCCCTCAGTGAA
GTTTGGCTAAAGGTTGGTGTAATAATCAAGAGAAGCCTGGAAGACATCATGGATGCCATGGATTAGCTGTGCAAC
TGACCAGCTCCAGGTTTGATCAAACCAAAAGCAACATTTGTCATGTGGTCTGACCATGTGGAGATGTTTCTGGAC
TTGCTAGAGCCTGCTTAGCTGCATGTTTGTAGTTACGATTTTTTGAATCCCACTTTGAGTGCTGAAAGTGTAAG
GAAGCTTTCTTCTTACACCTTGGGCTTGGATATTGCCCAGAGAAGAAATTTGGCTTTTTTTTTCTTAATGGACAA
GAGACAGTTGCTGTTCTCATGTTCCAAGTCTGAGAGCAACAGACCCTCATCATCTGTGCCTGGAAGAGTTCACTG
TCATTGAGCAGCACAGCCTGAGTGCTGGCCTCTGTCAACCCTTATTCCACTGCCTTATTTGACAAGGGGTACAT
GCTGCTCACCTTACTGCCCTGGGATTAATCAGTTACAGGCCAGAGTCTCCTTGGAGGGCCTGGAACCTGAGTC
CTCCTATGAACCTCTGTAGCCTAAATGAAATTTCTTAAATCACCGATGGAACCAAAAAAAAAAAAAAAAAAGGGCG
GCCGCGACTCTAGAGTCGACCTGCAGTAGGGATAACAGGTAATAAGCTTGGCCGCCATGG

95/615

FIGURE 94

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50911
><subunit 1 of 1, 348 aa, 1 stop
><MW: 39711, pI: 8.70, NX(S/T): 1
MAATLGPLGSWQQWRRCLSARDGSRMLLLLLLLGSGQGPPQVAGQTFEYLKREHSLSKPYQGVGTGSSSLWNLM
GNAMVMTQYIRLTPDMQSKQGGALWNRVPCFLRDWELQVHFQKIHGQKKNLHGDGLAIWYTKDRMQPGPVFGNMDK
FVGLGVFVDYTPNEEKQQERVFPYISAMVNNGSLSYDHERDGRPTELGGCTAIVRNLYHDTFLVIRYVKRHLTIM
MDIDGKHEWRDCIEVPGVRLPRGYFYTSSITGDLSDNHDVISLKLFEFTVERTPEEEKLHRDVFLLPSVDNMKLP
EMTAPLPPLSGLALEFLIVFFSLVFSVFAIVIGIILYNKWQEQSRKRFY
```

Signal sequence:
amino acids 1-38

Transmembrane domain:
amino acids 310-329

96/615

FIGURE 95

CCTGTGTTAAGCTGAGGTTTCCCCTAGATCTCGTATATCCCCAACACATACCTCCACGCACACACATCCCCAAGA
ACCTCGAGCTCACACCAACAGACACACGCGCGCATACACACTCGCTCTCGCTTGTCCATCTCCCTCCCGGGGGAG
CCGGCGCGCGCTCCCACCTTTGCCGCACACTCCGGCGAGCCGAGCCCGCAGCGCTCCAGGATTCTGCGGCTCGGA
ACTCGGATTGCAGCTCTGAACCCCATGGTGGTTTTTAAACACTTCTTTTCCCTCTCTTCCCTCGTTTTGATTGC
ACCGTTTTCCATCTGGGGGCTAGAGGAGCAAGGCAGCAGCCTTCCCAGCCAGCCCTTGTGGCTTGCCATCGTCCA
TCTGGCTTATAAAAGTTTGCTGAGCGCAGTCCAGAGGGCTGCGCTGCTCGTCCCCTCGGCTGGCAGAAGGGGTG
ACGCTGGGCAGCGCGAGGAGCGCGCTGCTGCGGGCTTTCGGCTTGAGGGGCAAGGTGAAGAGCGCAC
CGGCCGTGGGGTTTACCGAGCTGGATTGTATGTTGCACCATGCTTCTTGGATCGGGGCTGTGATTCTTCCCCT
CTTGGGGCTGCTGCTCTCCCTCCC CGCGGGGCGGATGTGAAGGCTCGGAGCTGCGGAGAGGTCCGCCAGGCGTA
CGGTGCCAAGGGATTAGCCTGGCGGACATCCCCTACCAGGAGATCGCAGGGGAACACTTAAGAATCTGTCCTCA
GGAATATACATGCTGCACCACAGAAATGGAAGACAAGTTAAGCCAACAAAGCAAACCTCGAATTTGAAAACCTTGT
GGAAGAGACAAGCCATTTTGTGCGCACCACTTTTGTGTCCAGGCATAAGAAATTTGACGAATTTTCCGAGAGCT
CCTGGAGAATGCAGAAAAGTCACTAAATGATATGTTGTACGGACCTATGGCATGCTGTACATGCAGAATTCAGA
AGTCTTCCAGGACCTCTTACAGAGCTGAAAAGGTACTACACTGGGGGTAATGTGAATCTGGAGGAAATGCTCAA
TGACTTTTGGGCTCGGCTCCTGGAACGGATGTTTTACGCTGATAAACCCCTCAGTATCACTTCAGTGAAGACTACCT
GGAATGTGTGAGCAAATACACTGACCAGCTCAAGCCATTTGGAGACGTGCCCCGGAACCTGAAGATTGAGGTTAC
CCGCGCCTTCATTGCTGCCAGGACCTTTGTCCAGGGGCTGACTGTGGGCAGAGAAGTTGCAAACCGAGTTTCCAA
GGTCAGCCCACCCCAGGGTGTATCCGTGCCCTCATGAAGATGCTGTACTGCCCATACTGTGCGGGGCTTCCCAC
TGTGAGGCCCTGCAACAACCTACTGTCTCAACGTCATGAAGGGCTGCTTGGCAAATCAGGCTGACCTCGACACAGA
GTGGAATCTGTTTATAGATGCAATGCTCTTGGTGGCAGAGCGACTGGAGGGGCCATTCAACATTGAGTCGGTCAT
GGACCCGATAGATGTCAAGATTTCTGAAGCCATTATGAACATGCAAGAAAACAGCATGCAGGTGTCTGCAAAGGT
CTTTCAGGGATGTGGTCAGCCCAAACCTGCTCCAGCCCTCAGATCTGCCCGCTCAGCTCCTGAAAATTTTAATAC
ACGTTTCAGGCCCTACAATCCTGAGGAAAGACCAACAACCTGCTGCAGGCACAAGCTTGGACCGGCTGGTCACAGA
CATAAAAGAGAAATTGAAGCTCTCTAAAAAGGTCTGGTCAGCATTACCCTACACTATCTGCAAGGACGAGAGCGT
GACAGCGGGCACGTCCAACGAGGAGGAATGCTGGAACGGGCACAGCAAAGCCAGATACTTGCTGAGATCATGAA
TGATGGGCTCACCAACCAGATCAACAATCCCGAGGTGGATGTGGACATCACTCGGCCTGACACTTTCATCAGACA
GCAGATTATGGCTCTCCGTGTGATGACCAACAACTAAAAACGCCCTACAATGGCAATGATGTCAATTTCCAGGA
CACAAGTGATGAATCCAGTGGCTCAGGGAGTGGCAGTGGGTGCATGGATGACGTGTGTCCACGGAGTTTGAGTT
TGTCACCACAGAGGCCCCCGCAGTGGATCCCGACCGGAGAGAGGTGGACTCTTCTGCAGCCAGCGTGGCCACTC
CCTGCTCTCCTGGTCTCTCACCTGCATTGTCTTGGCACTGCAGAGACTGTGCAGATTAATCTTGGGTTTTTGGTCA
GATGAAACTGCATTTTAGCTATCTGAATGGCCAACCTCACTTCTTTTCTTACACTCTTGGACAATGGACCATGCCA
CAAAACTTACCGTTTTCTATGAGAAGAGAGCAGTAATGCAATCTGCCCTCCCTTTTTGTTTTCCCAAAGAGTACC
GGGTGCCAGACTGAACTGCTTCTTCTTCTCAGCTATCTGTGGGACCTTGTATTCTAGAGAGAATTCCTTA
CTCAAATTTTTCGTACCAGGAGATTTTCTTACCTTCATTTGCTTTTATGCTGCAGAAGTAAAGGAATCTCACGTT
GTGAGGGTTTTTTTTTCTCATTAAAAAT

97/615

FIGURE 96

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50914
><subunit 1 of 1, 555 aa, 1 stop
><MW: 62736, pI: 5.36, NX(S/T): 0
MPSWIGAVILPLLGLLLSLPAGADVKA RSCGEVRQAYGAKGFS LADIPYQEIAGEHLRICPQEYTCCTTEMEDKL
SQQSKLEFENLVEETSHFVRTTFVSRHKKFDEFFRELLENAEKSLNDMFVRTYGM LYMQNSEVFQDLFTELKRY Y
TGGNVNLEMLNDFWARLLERMFQLINPQYHFSE DYLEC VSKYTDQLKPF GDVPRK LKIQVTRAFIAARTFVQGL
TVGREVANRVSKVSPTPGCIRALMKMLYCPYCRGLPTVRPCNNYCLNVMKGCLANQADLDTEWNLFI DAMLLVAE
RLEGPFNIESVMDPIDVKISEAIMNMQENSMQVS AKVFQGC GQPKPAPALRSARSAPENFNTRFRPYNPEERPTT
AAGTSLDRLVTDIKEK LKLSKKVWSALPYTICKDES VTAGTSNEEECWNGH SKARYLPEIMNDGLTNQINNPEVD
VDITRPDTFIRQQIMALRVMTNKLKNAYNGNDVNFQDTSDESSGSGSGSGCMDDVCPTFEFEFVTTEAPAVDPDRR
EVDSSAAQRGHSLLSWSLTCIVLALQRLCR
```

Signal peptide:
amino acids 1-23

98/615

FIGURE 97

GGCGGCGTCCGTGAGGGGCTCCTTTGGGCAGGGGTAGTGTTTGGTGTCCCTGTCTTGCGTGATATTGACAACTG
AAGCTTTCCTGCACCACTGGACTTAAGGAAGAGTGTACTCGTAGGCGGACAGCTTTAGTGGCCGGCCGGCCGCTC
TCATCCCCCGTAAGGAGCAGAGTCCTTTGTACTGACCAAGATGAGCAACATCTACATCCAGGAGCCTCCCACGAA
TGGGAAGGTTTTATTGAAACTACAGCTGGAGATATTGACATAGAGTTGTGGTCCAAAGAAGCTCCTAAAGCTTG
CAGAAATTTTATCCAACCTTTGTTTGGAGCTTATTATGACAATACCATTTTTTCATAGAGTTGTGCCTGGTTTCAT
AGTCCAAGGCGGAGATCCTACTGGCACAGGGAGTGGTGGAGAGTCTATCTATGGAGCGCCATTCAAAGATGAATT
TCATTCACGGTTGCGTTTTAATCGGAGAGGACTGGTTGCCATGGCAAATGCTGGTTCTCATGATAATGGCAGCCA
GTTTTCTTCACACTGGGTCGAGCAGATGAACTTAACAATAAGCATACCATCTTTGGAAAGGTTACAGGGGGATAC
AGTATATAACATGTTGCGACTGTCAGAAGTAGACATTGATGATGACGAAAGACCACATAATCCACACAAAATAAA
AAGCTGTGAGGTTTTGTTAATCCTTTTGATGACATCATTCCAAGGGAAATTTAAAGGCTGAAAAAGAGAAACC
AGAGGAGGAAGTAAAGAAATTGAAACCCAAAGGCACAAAAATTTTAGTTTACTTTTCATTTGGAGAGGAAGCTGA
GGAAGAAGAGGAGGAAGTAAATCGAGTTAGTCAGAGCATGAAGGGCAAAGCAAAGTAGTCATGACTTGCTTAA
GGATGATCCACATCTCAGTTCTGTTCCAGTTGTAGAAAGTGAAAAAGGTGATGCACCAGATTTAGTTGATGATGG
AGAAGATGAAAGTGCAGAGCATGATGAATATATTGATGGTGTGATGAAAAGAACCCTGATGAGAGAAAGAATTGCCAA
AAAATTAAAAAAGGACACAAGTGCGAATGTAAATCAGCTGGAGAAGGAGAAGTGGAGAAGAAATCAGTCAGCCG
CAGTGAAGAGCTCAGAAAAAGCAAGACAATTAACCGGGAACCTCTTAGCAGCAAAACAAAAAAGTAGAAAA
TGCAGCAAAACAAGCAGAAAAAGAGTGAAGAGGAAGAAGCCCTCCAGATGGTGCTGTTGCCGAATACAGAAG
AGAAAAGCAAAAGTATGAAGCTTTGAGGAAGCAACAGTCAAAGAAGGGAACCTCCCGGGAAGATCAGACCTTGC
ACTGCTGAACCACTTTAAATCTAACTCACTCAAGCAATTGCTGAAACACCTGAAAATGACATTCCTGAAACAGA
AGTAGAAGATGATGAAGGATGGATGTCACATGTACTTCAGTTTGAGGATAAAAGCAGAAAAGTGAAAGATGCAAG
CATGCAAGACTCAGATACATTTGAAATCTATGATCCTCGGAATCCAGTGAATAAAAGAAGGAGGGAAGAAAGCAA
AAAGCTGATGAGAGAGAAAAAAGAAAGAAGATAAATGAGAATAATGATAACCAGAACTTGCTGGAATGTGCCT
ACAATGGCCTTGTAACAGCCATTGTTCCCAACAGCATCACTTAGGGGTGTGAAAAGAAGTATTTTGAACCTGTT
GTCTGGTTTTGAAAAACAATTATCTTTGCAAAATGTGGAATGATGTAAGCAAATGCTTTTGGTTACTGGTA
CATGTGTTTTTTCCTAGCTGACCTTTTATATTGCTAAATCTGAAATAAAATAACTTTCCTTCCACAAAAA
AAAAAAAAAAAAAAAAAAAA

99/615

FIGURE 98

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50919
><subunit 1 of 1, 472 aa, 1 stop
><MW: 53847, pI: 5.75, NX(S/T): 2
MSNIYIQEPPTNGKVLKTTAGDIDIELWSKEAPKACRNFIQLCLEAYDNTIFHRVVPGFIVQGGDPTGTGSGG
ESIYGAPFKDEFHSRLRFNRRGLVAMANAGSHDNGSQFFFTLGRADELNKHTIFGKVTGDTVYNMLRLSEVDID
DDERPHNPHKIKSCEVLFPFDDIIPREIKRLKKEKPEEEVKKLKPKGTKNFSLLSFGEEAEEEEEEVNVRVSQSM
KGKSKSSHDLKDDPHLSSVPVVESEKGDAPDLVDDGEDESAEHDEYIDGDEKNLMRERIAKKLKKDTSANVKSA
GEGEVEKKSVSRSEELRKEARQLKRELLAAKQKKVENAAKQAEKRSEEEAAPPDGAVAEYRREKQKYEALRKQOS
KKGTSREDQTLALLNQFKSKLTQAI AETPENDIPETEVEDDEGWMSHVLQFEDKSRKVKDASMQDSDTFEIYDPR
NPVNKRRREESKMLMREKKERR
```

Important features:**Signal peptide:**

amino acids 1-21

N-glycosylation sites:

amino acids 109-112 and 201-204

Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature.

amino acids 49-66

Homologous region to Cyclophilin-type peptidyl-prolyl cis-trans isomerase

amino acids 96-140, 49-89 and 22-51

100/615

FIGURE 99

CTTTTCTGAGGAACCCAGCAATGAATGGCTTTGCATCCTTGCTTCGAAGAAACCAATTTATCCTCCTGGTACTA
TTTCTTTTGCAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGTCTACCGCTGAAGTCTGTGCCACACACACA
ATTCACCAGGACCCAAAGGAGATGATGGTGAAAAAGGAGATCCAGGAGAAGAGGGAAAGCATGGCAAAGTGGGA
CGCATGGGGCCGAAAGGAATTAAAGGAGAACTGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCC
ATTGGGAAGAAGGGTGACAAAGGGGAAAAAGGTTTGCTTGGAAATACCTGGAGAAAAAGGCAAAGCAGGTACTGTC
TGTGATTGTGGAAGATACCGGAAATTTGTTGGACAACCTGGATATTAGTATTGCTCGGCTCAAGACATCTATGAAG
TTTGTCAAGAATGTGATAGCAGGGATTAGGGAAACTGAAGAGAAATTCTACTACATCGTGCAGGAAGAGAAGAAC
TACAGGGAATCCCTAACCCACTGCAGGATTCGGGGTGGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACA
CTCATCGCTGACTATGTTGCCAAGAGTGGCTTCTTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAAGGGAGGGA
CAGTACATGTCCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGCGACCCCTAT
GGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTGCCATCTTACCATGTACTTT
GTCTGTGAGTTCATCAAGAAGAAAAAGTAACTTCCCTCATCTACGTATTTGCTATTTTCCTGTGACCGTCATTA
CAGTTATTGTTATCCATCCTTTTTTTCCTGATTGTACTACATTTGATCTGAGTCAACATAGCTAGAAAATGCTAA
ACTGAGGTATGGAGCCTCCATCATCAAAAAAAAAAAAAAAAAA

101/615

FIGURE 100

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50980
><subunit 1 of 1, 277 aa, 1 stop
><MW: 30645, pI: 7.47, NX(S/T): 2
MNGFASLLRRNQFILLVLFLLQIQSLGLDIDSRPTAEVCATHTISPGPKGDDGEKGDPEEGKHGKVGRMGPKGI
KGELGDMGDQGNIGKTGPIGKKGDKGEKGLLGIPGEKGKAGTVCDGGRYRKFGQLDISIARLKTSMKFVKNVIA
GIRETEEFYYIVQEEKNYRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGFFRVFIGVNDLEREGQYMSTDN
TPLQNYSNWNEGEPSDPYGHEDCVEMLSGRWNDTECHLTMYFVCEFIKKKK
```

Signal peptide:
amino acids 1-25

102/615

FIGURE 101

GCAACCTCAGCTTCTAGTATCCAGACTCCAGCGCCGCCCGGGCGCGGACCCCAACCCCGACCCAGAGCTTCTCC
AGCGGCGGCGCAGCGAGCAGGGCTCCCCGCCTTAACCTTCCTCCGCGGGGGCCAGCCACCTTCGGGAGTCCGGGTT
GCCCACCTGCAAACCTCTCCGCCTTCTGCACCTGCCACCCCTGAGCCAGCGCGGGCCCCGAGCGAGTCA**ATG**GCCA
ACGCGGGGCTGCAGCTGTTGGGCTTCATTCTCGCCTTCCTGGGATGGATCGGCGCCATCGTCAGCACTGCCCTGC
CCCACTGGAGGATTTACTCCTATGCCGCGGACAACATCGTGACCGCCAGGCCATGTACGAGGGGCTGTGGATGT
CCTGCGTGTGCGAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACATTGC
AAGCAACCCGTGCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGA
AGTGATGAAGTGCTTGGAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGTGCCATATTTCTTC
TTGCAGGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCATGA
CCCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTCACTGGCTGGGCTGCTGCTTCTCTCGCCTTCTGG
GAGGTGCCCTACTTTGCTGTTCTGTCCCCGAAAAACAACCTCTTACCCAACACCAAGGCCCTATCCAAAACCTG
CACCTTCCAGCGGGAAAGACTACGTG**TGAC**CACAGAGGCAAAAGGAGAAAAATCATGTTGAAACAAACCGAAAATGG
ACATTGAGATACTATCATTAACATTAGGACCTTAGAATTTTGGGTATTGTAATCTGAAGTATGGTATTACAAAAC
AAACAAACAAACAAAAACCCATGTGTTAAAAATACTCAGTGCTAAACATGGCTTAATCTTATTTTATCTTCTTTT
CTCAATATAGGAGGGAAGATTTTCCATTTGTATTACTGTCTCCCATTTAGTAATCATACTCAAATGGGGGAAGG
GGTGCTCCTTAAATATATATAGATATGTATATATACATGTTTTTCTATTAAAAATAGACAGTAAATACTATTCT
CATTATGTTGATACTAGCATACTTAAATATCTCTAAATAGGTAAATGTATTTAATTCATATGATGAAGATG
TTTATTGGTATATTTTCTTTTCTGCTCTATATACATATGTAACAGTCAAATATCATTTACTCTTCTTCATTAGC
TTTGGGTGCCTTTGCCACAAGACCTAGCCTAATTTACCAAGGATGAATTCCTTCAATTCTTCATGCGTGCCCTTT
TCATATACTTATTTTATTTTACCATAATCTTATAGCACTTGCAATCGTTATTAAAGCCCTTATTTGTTTGTGTT
TCATTGGTCTCTATCTCCTGAATCTAACACATTTTATAGCCTACATTTTAGTTTCTAAAGCCAAGAAGATTTAT
TACAAATCAGAACTTTGGAGGCAATCTTCTGCAATGACCAAGTGATAAATTCCTGTTGACCTTCCACACAAT
CCCTGTACTCTGACCCATAGCACTCTTGTGCTTTGAAAATATTTGTCCAATTGAGTAGCTGCATGCTGTTCCC
CCAGGTGTTGTAACACAACCTTTATTGATTGAATTTTAAAGCTACTTATTCATAGTTTATATCCCCCTAAACTAC
CTTTTGTGTTCCCATTCCTTAATTGTATTGTTTTCCCAAGTGAATTATCATGCGTTTATATCTTCTTAATAAG
GTGTTGCTGTTTGTCTGAACAAAGTGCTAGACTTCTGGAGTGATAATCTGGTGACAAATATTCTCTGTAGC
TGTAAGCAAGTCATTAATCTTTCTACCTCTTTTTTCTATCTGCCAATTGAGATAATGATACTTAACAGTTAG
AAGAGGTAGTGTGAATATTAATTAGTTTATATTACTCTTATTCTTTGAACATGAACATATGCCTATGTAGTGTCTT
TATTGCTCAGCTGGCTGAGACACTGAAGAAGTCACTGAACAAAACCTACACACGTACCTTCATGTGATTCACTG
CCTTCTCTCTCTACCACTCTATTTCCACTGAACAAAACCTACACACATACCTTCATGTGGTTCAGTGCCTTCTCT
CTCTCTACCACTCTATTTCCACTGAACAAAACCTACGCACATACCTTCATGTGGCTCAGTGCCTTCTCTCTCTA
CCAGTCTATTTCCATTCTTTCAGCTGTGTCTGACATGTTTGTGCTCTGTTCCATTTTAAACACTGCTCTTACTTT
TCCAGTCTGTACAGAATGCTATTTCACTTGAGCAAGATGATGTAATGGAAAGGGTGTGGCACTGGTGTCTGGAG
ACCTGGATTGAGTCTTGGTGCTATCAATCACCGTCTGTGTTTGGCAAGGCATTTGGCTGCTGTAAGCTTATTG
CTTCATCTGTAAGCGTGGTGTGTAATTCCTGATCTTCCACCTCACAGTGATGTTGTGGGGATCCAGTGAGATA
GAATACATGTAAGTGTGGTGTGTAATTTAAAAAGTGCTATACTAAGGGAAGAATTGAGGAATTAAGTGCATAC
GTTTTGGTGTGCTTTTCAATGTTTGAAAATAAAAAAATGTTAAG

103/615

FIGURE 102

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52185
><subunit 1 of 1, 211 aa, 1 stop
><MW: 22744, pI: 8.51, NX(S/T): 1
MANAGLQLLGFI LAF LGWIGAIVSTALPQWRIYSYAGDNIVTAQAMYEG LWMSCVSQSTGQIQCKVFDSLNLSS
TLQATRALMVVGILLGVIAIFVATVGMKCMKCLEDDDEVQKMRMAVIGGAIFLLAGLAILVATAWYGNRIVQEFYD
PMTFPVNARYEFGQALFTGWAAASLCLLGGALLCCSCPRKTTSYPTPRPYPKPAPSSGKDYV
```

Important features:**Signal peptide:**

amino acids 1-21

Transmembrane domains:

amino acids 82-102, 118-142 and 161-187

N-glycosylation site.

amino acids 72-75

FMP-22 / EMP / MP20 family proteins

amino acids 70-111

ABC-2 type transport system integral membrane protein

amino acids 119-133

104/615

FIGURE 103

CCCACGCGTCCGCGGACGCGTGGGCTGGACCCAGGTCTGGAGCGAATTCCAGCCTGCAGGGCTGATAAGCGAGG
CATTAGTGAGATTGAGAGAGACTTTACCCCGCGTGGTGGTTGGAGGGCGCGCAGTAGAGCAGCAGCACAGGCGC
GGGTCCCGGGAGGCGCGCTCTGCTCGCGCCGAGATGTGGAATCTCCTTCACGAAACCGACTCGGCTGTGGCCACC
GCGCGCCGCGCGCTGGCTGTGCGCTGGGGCGCTGGTGTGGCGGGTGGCTTCTTTCTCCTCGGCTTCCTCTTC
GGGTGGTTTATAAATCCTCCAATGAAGCTACTAACATTACTCCAAAGCATAATATGAAAGCATTTTTGGATGAA
TTGAAAGCTGAGAACATCAAGAAGTTCTTACATAATTTTACACAGATACCACATTTAGCAGGAACAGAACAAAAC
TTTCAGCTTGCAAAGCAAATTCATCCAGTGGAAGAATTTGGCCTGGATTCTGTTGAGCTAGCTCATTATGAT
GTCCTGTTGTCTACCCAAATAAGACTCATCCCACTACATCTCAATAATTAATGAAGATGGAATGAGATTTTC
AACACATCATTATTTGAACCACCTCCTCCAGGATATGAAAATGTTTCGGATATTGTACCACCTTTTCACTGCTTC
TCTCCTCAAGGAATGCCAGAGGGCGATCTAGTGTATGTTAACTATGCACGAAGCTGAAGACTTCTTTAAATGGAA
CGGGACATGAAAATCAATTGCTCTGGGAAAATTGTAATTGCCAGATATGGGAAAGTTTCAGAGGAAATAAGGTT
AAAAATGCCCAGCTGGCAGGGGCCAAAGGAGTCATTCTCTACTCCGACCCTGCTGACTACTTTGCTCCTGGGGTG
AAGTCTATCCAGACGGTTGGAATCTTCTGGAGGTGGTGTCCAGCGTGGAAATATCCTAAATCTGAATGGTGCA
GGAGACCTCTCACACCAGGTTACCCAGCAAATGAATATGCTTATAGGCGTGGAATTGCAGAGGCTGTTGGTCTT
CCAAGTATTCTGTTTCATCCAATTGGATACATGATGCACAGAAGCTCCTAGAAAAAATGGGTGGCTCAGCACC
CCAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGGCTTTTACTGGAACCTTTTCTACA
CAAAAAGTCAAGATGCACATCCACTCTACCAATGAAGTGACGAGAATTTACAATGTGATAGGTACTCTCAGAGGA
GCAGTGGAACCAGACAGATATGTCATTCTGGGAGGTACCCGGGACTCATGGGTGTTGGTGGTATTGACCCCTCAG
AGTGGAGCAGCTGTTGTTTCATGAAATTGTGAGGAGCTTTGGAACACTGAAAAAGGAAGGGTGGAGACCTAGAAGA
ACAATTTTGTGTTGCAAGCTGGGATGCAGAAGAATTTGGTCTTCTTGGTTCTACTGAGTGGGCAGAGGAGAATTCA
AGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAATGCTGACTCATCTATAGAAGGAACTACACTCTGAGAGTT
GATTGTACACCGCTGATGTACAGCTTGTACACAACCTAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAA
GGCAAATCTCTTTATGAAAGTTGGACTAAAAAAGTCTTCCCCAGAGTTCAAGTGGCATGCCAGGATAAGCAAA
TTGGGATCTGGAATGATTTTGAAGGTGTTCTTCCAACGACTTGAATGCTTCAGGCAGAGCACGGTATACTAAA
AATTGGGAAACAAACAAATTCAGCGGCTATCCACTGTATCACAGTGTCTATGAAACATATGAGTTGGTGGAAAAG
TTTTATGATCCAATGTTTAAATATCACCTCACTGTGGCCAGGTTGAGGAGGGATGGTGTGTTGAGCTAGCCAAT
TCCATAGTGCTCCCTTTTGAATGTCGAGATTATGCTGTAGTTTTAAGAAAGTATGCTGACAAAATCTACAGTATT
TCTATGAAACATCCACAGGAAATGAAGCATACAGTGTATCATTTGATTCACTTTTTTCTGCAGTAAAGAATTTT
ACAGAAATTGCTTCCAAGTTCAGTGAGAGACTCCAGGACTTTGACAAAAGCAACCAATAGTATTAAGAATGATG
AATGATCAACTCATGTTTCTGGAAGAGCATTATTTGATCCATTAGGGTTACCAGACAGGCCTTTTATAGGCAT
GTCATCTATGCTCCAAGCAGCCACAACAAGTATGCAGGGGAGTCATTCCAGGAATTTATGATGCTCTGTTTGAT
ATTGAAAGCAAAGTGACCCCTTCCAAGGCTGGGGAGAAGTGAAGAGACAGATTTATGTTGCAGCCTTCACAGTG
CAGGCAGCTGCAGAGACTTTGAGTGAAGTAGCCTAAGAGGATTTTTTAGAGAATCCGTATTGAATTTGTGTGGTA
TGTCACCTAGAAAGAATCGTAATGGGTATATTGATAAATTTTAAATTTGGTATATTTGAAATAAAGTTGAATATT
ATATATAA

105/615

FIGURE 104

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA52756
><subunit 1 of 1, 750 aa, 1 stop
><MW: 84305, pI: 6.93, NX(S/T): 10
MWNLHETDSAVATARRPRWLCAGALVLAGGFLLGFLFGWFIKSSNEATNITPKHNMKAFLDELKAENIKKFLH
NETQIPHLAGTEQNFQLAKQIQSQWKEFGLDSVELAHYDVLLSYPNKTHPNYISIINEDGNEIFNTSLFEP PPPG
YENVSDIVPPFSAFSPQGMPEGDLVYVNYARTEDFFKLERDMKINCSGKIVARYGKVFRGNKVKNAGLAGAKGV
ILYSDPADYFAPGVKSYPDGWNLPGGGVQRGNIILNNGAGDPLTPGYPANAYARRGIAEAVGLPSIPVHPIGYY
DAQKLEKMGGSAPPDSSWRGSLKVPYNVGPFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRGAVEPDRYVILG
GHRDSWVFGGIDPQSGAAVVHEIVRSFGTLKKEGWRPRRTILFASWDAEEFLLGSTEWAEENSRLQERGVAI
NADSSIEGNYTLRV DCTPLMYSLVHNLTKELKSPDEGFEGKSLYESWTKKSPSEFSGMPRISKLGSGNDFEVFF
QRLGIASGRARYTKNWETNKFSGYPLYHSVYETYELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDY
AVVLRKYADKIYSISMKHPQEMKTYSVSFDLSFAVKNFTEIASKF SERLQDFDKSNPIVLRMMNDQLMFLERAF
IDPLGLPDRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESKVDPSKAWGEVKRQIYVAAFTVQAAAETLSEVA

Signal sequence:
amino acids 1-40

N-glycosylation sites.
amino acids 76-80, 121-125, 140-144, 153-157, 195-199, 336-340, 459-463,
476-480, 638-642

Tyrosine kinase phosphorylation sites.
amino acids 363-372, 605-613, 606-613, 617-626

N-myristoylation sites.
amino acids 85-91, 168-174, 252-258, 256-262, 282-288, 335-341, 360-366,
427-433, 529-535, 707-713

106/615

FIGURE 105

TGAAGAGTAATAGTTGGAATCAAAGAGTCAACGCAATGAAGTGTATTTACTGCTGCGTTTTATGTTGGGAATT
CCTCTCCTATGGCCTTGTCTTGGAGCAACAGAAACTCTCAAACAAAGAAAGTCAAGCAGCCAGTGCGATCTCAT
TTGAGAGTGAAGCGTGGCTGGGTGTGGAACCAATTTTTGTACCAGAGGAAATGAATACGACTAGTCATCACATC
GGCCAGCTAAGATCTGATTTAGACAATGGAACAATTTTCCAGTACAAGCTTTTGGGAGCTGGAGCTGGAAGT
ACTTTTATCATTGATGAAAGAACAGGTGACATATATGCCATACAGAAGCTTGATAGAGAGGAGCGATCCCTCTAC
ATCTTAAGAGCCCAGGTAATAGACATCGCTACTGGAAGGGCTGTGGAACCTGAGTCTGAGTTTGTCTCAAAGTT
TCGGATATCAATGACAATGAACCAAATTCCTAGATGAACCTTATGAGGCCATTGTACCAGAGATGTCTCCAGAA
GGAACATTAGTTATCCAGGTGACAGCAAGTGATGCTGACGATCCCTCAAGTGGTAATAATGCTCGTCTCCTCTAC
AGCTTACTTCAAGGCCAGCCATATTTTTCTGTTGAACCAACAGGAGTCATAAGAATATCTCTAAAATGGAT
AGAGAATGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGTCAGCCAGGAGCGTTGTCTGGA
ACAACAAGTGTATTAATTAACCTTTCAGATGTTAATGACAATAAGCCTATATTTAAAGAAAGTTTATACCGCTTG
ACTGTCTCTGAATCTGCACCCACTGGGACTTCTATAGGAACAATCATGGCATATGATATGACATAGGAGAGAAAT
GCAGAAATGGATTACAGCATTGAAGAGGATGATTCCGCAACATTTGACATTATTACTAATCATGAAACTCAAGAA
GGAATAGTTATATTAAGAAAGTGGATTTTGAAGCACCAGAACCTACGGTATTAGAGCAAAAGTTAAAAAC
CATCATGTTCTGAGCAGCTCATGAAGTACCACACTGAGGCTTCCACCCTTTCATTAAGATCCAGGTGGAAGAT
GTTGATGAGCCTCCTCTTTTCTCCTTCCATATTATGTATTTGAAGTTTTGAAGAAACCCACAGGGATCATT
GTAGGCGTGGTGTCTGCCACAGACCCAGACAATAGGAAATCTCCTATCAGGTATTCTATTACTAGGAGCAAAAGTG
TTCAATATCAATGATAATGGTACAATCACTACAAGTAACCTACTGGATCGTGAAATCAGTGCTTGGTACAACCTA
AGTATTACAGCCACAGAAAAATACAATATAGAACAGATCTCTTCGATCCCACTGTATGTGCAAGTTCTTAACATC
AATGATCATGCTCCTGAGTTCTCTCAATACTATGAGACTTATGTTTGTGAAAATGCAGGCTCTGGTCAGGTAATT
CAGACTATCAGTGAGTGGATAGAGATGAATCCATAGAAGAGCACCATTTTACTTTAATCTATCTGTAGAAGAC
ACTAACAATTCAAGTTTTACAATCATAGATAATCAAGATAACACAGCTGTCATTTTGACTAATAGAAGTGGTTTT
AACCTTCAAGAAGAACCTGTCTTCTACATCTCCATCTTAATTGCCGACAATGGAATCCCGTCACTTACAAGTACA
AACACCTTACCATCCATGTCTGTGACTGTGGTGACAGTGGGAGCACACAGACCTGCCAGTACCAGGAGCTTGTG
CTTTCCATGGGATTCAAGACAGAAGTTATCATTGCTATTCTCATTGTCATTATGATCATATTTGGGTTTATTTTT
TTGACTTTGGGTTTAAAAACAACGGAGAAAACAGATTCTATTTCTGAGAAAAGTGAAGATTTAGAGAGAAATATA
TTCCAATATGATGATGAAGGGGGTGGAGAAGAAGATACAGAGGCCTTTGATATAGCAGAGCTGAGGAGTAGTACC
ATAATGCCGGAACGCAAGACTCGGAAAACCAAGCGCTGAGATCAGGAGCCTATACAGGCAGTCTTTGCAAGTT
GGCCCCGACAGTGCCATATTCAGGAAATTCATTCTGGAAGAGCTCGAAGAAGCTAATACTGATCCGTGTGCCCT
CCTTTTGATTCCCTCCAGACCTACGCTTTTGAGGGAACAGGGTCATTAGCTGGATCCCTGAGCTCCTTAGAATCA
GCAGTCTCTGATCAGGATGAAAGCTATGATTACCTTAATGAGTTGGGACCTCGCTTTAAAGATTAGCATGCATG
TTTGGTCTGTCAGTGCAGTCAAATAATTAGGGCTTTTTACCATCAAATTTTTAAAGTGCTAATGTGTATTCTGA
ACCCAATGGTAGTCTTAAAGAGTTTTGTGCCCTGGCTCTATGGCGGGGAAAGCCCTAGTCTATGGAGTTTTCTGA
TTTCCCTGGAGTAAATACTCCATGGTTATTTAAGCTACCTACATGCTGTCTTGAACAGAGATGTGGGGAGAAA
TGTAACAATCAGCTCACAGGCATCAATACAACAGATTGGAAGTAAATAATGTAGGAAGATATTAAGTAGA
TGAGAGGACACAAGATGTAGTCGATCCTTATGCCGATTATATCATTATTTACTTAGGAAAGAGTAAAAATACCAAA
CGAGAAAATTTAAGGAGCAAAATTTGCAAGTCAAATAGAAATGTACAAATCGAGATAACATTTACATTTCTAT
CATATTGACATGAAAATTGAAAATGTATAGTCAGAGAAATTTTCATGAATTATCCATGAAGTATTGTTTCTTT
ATTTAAA

107/615

FIGURE 106

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906
><subunit 1 of 1, 772 aa, 1 stop
><MW: 87002, pI: 4.64, NX(S/T): 8
MNCYLLLRFMLGIPLLWPCLGATENSQTKKVKQPVRSHLRVKGWVWNQFFVPEEMNTTSHHIGQLRSDLNNGNN
SFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIATGRAVEPESEFVIKVSNDINDNEPKFLD
EPYEAIVPMSPEGTLVIQVTASDADDPSSGNNARLLYSLLQGQPYFSVEPTTGVIIRISSKMDRELQDEYWVIIQ
AKDMIGQPGALSGTTSVLIKLSVDNDNKPIFKESLYRLTVSESAPTGTSGTIMAYDNDIGENAEMDYSIEEDDS
QTFDIITNHETQEGIVILKKKVD FEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFLLPYY
VFEVFEETPQGSFVGVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDREISAWYNLSITATEKYNIEQ
ISSIPLYVQVLNINDHAPEFSQYYETVVCENAGSGQVIQTISAVDRDESEHHFYFNLSVEDTNNSSTIIDNQ
DNTAVILTNRGTGNLQEEPVFYISILIADNGIPSLTSTNTLTIHVDCGDSGSTQTCQYQELVLSMGFKTEVIIA
ILICIMIIFGFIFLTLGLKQRRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELRSTIMRERKTRKTTT
AEIRSLYRQSLQVGPDSAI FRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGS LAGSLSSLES AVSDQDESYDYL
NELGPRFKRLACMFGSAVQSNN
```

Important features:**Signal peptide:**

amino acids 1-21

Transmembrane domain:

amino acids 597-617

N-glycosylation sites.

amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518, 516-519 and 534-537

Cadherins extracellular repeated domain signature.

amino acids 136-146 and 244-254

108/615

FIGURE 107

ATCTGGTTGAACTACTTAAGCTTAATTTGTTAAACTCCGGTAAGTACCTAGCCCACATGATTTGACTCAGAGATT
CTCTTTTGTCCACAGACAGTCATCTCAGGGGCAGAAAGAAAAGAGCTCCCAAATGCTATATCTATTTCAGGGGCTC
TCAAGAACAATGGGAATATCATCCTGATTTAGAAAATTTGGATGAAGATGGATATACTCAATTACACTTCGACTCT
CAAAGCAATACCAGGATAGCTGTTGTTTCAGAGAAAGGATCGTGTGCTGCATCTCCTCCTTGGCGCCTCATTGCT
GTAATTTTGGGAATCCTATGCTTGGTAATACTGGTGATAGCTGTGGTCCTGGGTACCATGGGGGTTCTTTCCAGC
CCTTGTCTCTTAATTTGGATTATATATGAGAAGAGCTGTTATCTATTTCAGCATGTCACTAAATTCCTGGGATGGA
AGTAAAAGACAATGCTGGCAACTGGGCTCTAATCTCCTAAAGATAGACAGCTCAAATGAATTGGGATTTATAGTA
AAACAAGTGTCTTCCCAACCTGATAATTCATTTTGGATAGGCCTTTCTCGGCCCCAGACTGAGGTACCATGGCTC
TGGGAGGATGGATCAACATTCTCTTAACCTTATTTCAGATCAGAACACAGCTACCCAAGAAAACCATCTCCA
AATTGTGTATGGATTACGTGTCAGTCATTTATGACCAACTGTGTAGTGTGCCCTCATATAGTATTTGTGAGAAG
AAGTTTTCAATGTAAGAGGAAGGGTGGAGAAGGAGAGAGAAATATGTGAGGTAGTAAGGAGGACAGAAAACAGAA
CAGAAAAGAGTAACAGCTGAGGTCAAGATAAATGCAGAAAATGTTTAGAGAGCTTGGCCAACTGTAATCTTAACC
AAGAAATTGAAGGGAGAGGCTGTGATTTCTGTATTTGTGACCTACAGGTAGGCTAGTATATTTTTCTAGTTAG
TAGATCCCTAGACATGGAATCAGGGCAGCCAAGCTTGAGTTTTTATTTTTTATTTATTTATTTTTTGTAGATAGG
GTCTCACTTTGTACCCAGGCTGGAGTGCAGTGGCACAATCTCGACTCACTGCAGCTATCTCTCGCCTCAGCCCC
TCAAGTAGCTGGGACTACAGGTGCATGCCACCATGCCAGGCTAATTTTTGGTGTTTTTGTAGAGACTGGGTTTT
GCCATGTTGACCAAGCTGGTCTTAACCTCTGGGCTTAAGTGATCTGCCCGCCTTGGCCTCCCAAAGTGCTGGGA
TTACAGATGTGAGCCACCACACCTGGCCCCAAGCTGAATTTTCATCTGCCATTGACTTGGCATTACCTTGGG
TAAGCCATAAGCGAATCTTAATTTCTGGCTCTATCAGAGTTGTTTCATGCTCAACAATGCCATTGAAGTGACGG
TGTGTTGCCACGATTTGACCCCAACTTCTAGCAGTATATCAGTTATGAAGTGAAGGTGAATATATTTCTGAAT
AGCTAAATGAAGAAATGGGAAAAAATCTTACCACAGTCAGAGCAATTTTATTATTTTCATCAGTATGATCATAA
TTATGATTATCATCTTAGTAAAAAGCAGGAACCTCTACTTTTTCTTATCAATTAAATAGCTCAGAGAGTACATC
TGCCATATCTCTAATAGAATCTTTTTTTTTTTTTTTTTTTTTTGTAGACAGAGTTTCGCTCTTGTGCCCCAGGCTG
GAGTGCAACGGCACGATCTCGGCTCACCGCAACCTCCGCCCCCTGGGTTCAAGCAATTCCTCTGCCTCAGCCTCC
CAAGTAGCTGGGATTACAGTCAGGCACCACCACACCCGGCTAATTTTGTATTTTTTTAGTAGAGACAGGGTTTTCT
CCATGTCGGTCAGGGTAGTCCCGAACTCCTGACCTCAAGTGATCTGCCTGCCTCGGCCTCCCAAGTGCTGGGATT
ACAGGCGTGAGCCACTGCACCCAGCCTAGAATCTTGATATAATATGAATTGTAGGGAACTGCTCTCATAGGAAA
GTTTTCTGCTTTTTTAAATACAAAAATACATAAAAAATACATAAAATCTGATGATGAATATAAAAAAGTAACCAACC
TCATTGGAACAAGTATTAACATTTTGGAAATATGTTTTATTAGTTTTGTGATGTACTGTTTTACAATTTTTTACCAT
TTTTTTTCAGTAATTACTGTAAATGGTATTATTGGAAATGAAACTATATTTCTCATGTGCTGATTGTCTTATTT
TTTTTCATACTTTCCACTGGTGCTATTTTTATTTCGAATGGATATTTCTGTATTACTAGGGAGGCATTTACAGTC
CTCTAATGTTGATTAATATGTGAAAAGAAATGTACCAATTTTACTAAATTATGCAGTTTAAATGGATGATTTT
ATGTTATGTGGATTCATTTCAATAAAAAAAACTCTTATCAAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAA

109/615

FIGURE 108

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53912
<subunit 1 of 1, 201 aa, 1 stop
<MW: 22563, pI: 4.87, NX(S/T): 1
MEYHPDLENLDEDGYTQLHFDSQSNTRIAVSEKGSAAAPPWRLIAVILGILCLVILVIAVVLGTMGVLSSPCP
PNWIIYEKSCYLFMSLSNSWDGSKRQCWQLGSNLLKIDSSNELGFIVKQVSSQPDNSFWIGLSRPQTEVPWLWED
GSTFSSNLFQIRTTATQENFSPNCVWIHVSVIYDQLCSVPSYSICEKKFSM

Important features:**Type II transmembrane domain:**

amino acids 45-65

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 197-200

N-myristoylation sites.

amino acids 35-40 and 151-156

Homologous region to LDL receptor

amino acids 34-67 and 70-200.

110/615

FIGURE 109

CTGCAAGTTGTTAACGCCTAACACACAAGTATGTTAGGCTTCCACCAAAGTCTCAATATACCTGAATACGCACA
ATATCTTAACCTCTTCATATTTGGTTTTGGGATCTGCTTTGAGGTCCCATCTTCATTTAAAAAAAATACAGAGAC
CTACCTACCCGTACGCATACATATGTGTATATATATGTAACTAGACAAAAGATCGCAGATCATAAAGCAAG
CTCTGCTTTAGTTTCCAAGAAGATTACAAAGAATTTAGAGATGTATTTGTCAAGATCCCTGTGATTTCATGCCCT
TTGGGTTACGGTGTCTCAGTGATGCAGCCCTACCCCTTTGGTTTGGGGACATTATGATTTGTGTAAGACTCAGAT
TTACACGGAAGAAGGGAAAGTTTGGGATTACATGGCCTGCCAGCCGGAATCCACGGACATGACAAAATATCTGAA
AGTGAAACTCGATCTCCGGATATTACCTGTGGAGACCCCTCCTGAGACGTTCTGTGCAATGGGCAATCCCTACAT
GTGCAATAATGAGTGTGATGCGAGTACCCCTGAGCTGGCACACCCCTGAGCTGATGTTTGATTTGAAGGAAG
ACATCCCTCCACATTTTGGCAGTCTGCCACTTGAAGGAGTATCCCAAGCCTCTCCAGGTTAACATCACTCTGTC
TTGGAGCAAAACCATTGAGCTAACAGACAACATAGTTATTACCTTTGAATCTGGGCGTCCAGACCAAATGATCCT
GGAGAAGTCTCTCGATTATGGACGAACATGGCAGCCCTATCAGTATTATGCCACAGACTGCTTAGATGCTTTTCA
CATGGATCCTAAATCCGTGAAGGATTATCACAGCATACGGTCTTAGAAATCATTTGCACAGAAGAGTACTCAAC
AGGGTATACAACAAATAGCAAAATAATCCACTTTGAAATCAAAGACAGGTTCGCGCTTTTTGCTGGACCTCGCCT
ACGCAATATGGCTTCCCTCTACGGACAGCTGGATACAACCAAGAACTCAGAGATTTCTTTACAGTCACAGACCT
GAGGATAAGGCTGTTAAGACCAGCCGTTGGGAAATATTTGTAGATGAGCTACACTTGGCAGCCTACTTTTACGC
GATCTCAGACATAAAGGTGCGAGGAAGGTGCAAGTGTAACTCTCCATGCCACTGTATGTGTGTATGACAACAGCAA
ATTGACATGCGAATGTGAGCACAACACTACAGGTCCAGACTGTGGGAAATGCAAGAAGAATTATCAGGGCCGACC
TTGGAGTCCAGGCTCCTATCTCCCCATCCCCAAAGGCACTGCAAAATACCTGTATCCCAGTATTTCCAGTATTGG
TACGAATGTCTGCGACAACGAGCTCCTGCACTGCCAGAACGGAGGGACGTGCCACAACAACGTGCGCTGCCTGTG
CCGGCCGCATACACGGGCATCCTCTGCGAGAAGCTGCGGTGCGAGGAGGCTGGCAGCTGCGGCTCCGACTCTGG
CCAGGGCGCGCCCCGACGGCACCCCGAGCGCTGCTGTCTGCTGACCAACGCTGCTGGGAACCGCCAGCCCCCTGGT
GTTCTAGGTGTACCTCCAGCCACACCGGACGGGCTGTGCCGTGGGGAAGCAGACACAACCCAAACATTTGCTA
CTAACATAGGAAACACACATACAGACACCCCTCAGACAGTGTACAACTAAGAAGGCCTAAGTGAATAA
GCCATATTTATCACCCTGGACAGCACATCCGAGTCAAGACTGTTAATTTCTGACTCCAGAGGAGTTGGCAGCTG
TTGATATTATCACTGCAAAATCACATTGCCAGCTGCAGAGCATATTGTGGATTGGAAAGGCTGCGACAGCCCCCA
AACAGGAAAGCAAAAAACAAACAAATCAACCGACCTAAAAACATTGGCTACTCTAGCGTGGTGGCCCTAGTAC
GACTCCGCCCAGTGTGTGGACCAACCAATAGCATTCTTTGCTGTGAGGTGCATTGTGGGCATAAGGAAATCTGT
TACAAGCTGCCATATTGGCCTGCTCCGTCCCTGAATCCCTTCCAACCTGTGCTTTAGTGAACGTTGCTCTGTAA
CCCTCGTTGGTTGAAAGATTTCTTTGTCTGATGTTAGTGATGCACATGTGTAACAGCCCCCTCTAAAAGCGCAAG
CCAGTCATACCCCTGTATATCTTAGCAGCACTGAGTCCAGTGCGAGCACACACCCACTATACAAGAGTGGCTATA
GGAAAAAAGAAAGTGTATCTATCCTTTTGTATTCAAATGAAGTTATTTTCTTGAACCTACTGTAATATGTAGATT
TTTTGTATTATTGCCAATTTGTGTTACCAGACAATCTGTTAATGTATCTAATTGGAATCAGCAAAGACTGACATT
TTATTTTGTCTCTTTCTGTTCTGTTTGTCTTCACTGTGCAGAGATTTCTCTGTAAGGGCAACGAACGTGCTGGCA
TCAAAGAATATCAGTTTACATATATAACAAGTGTAATAAGATTCCACCAAAGGACATTCTAAATGTTTTCTTGT
GCTTTAACTGGAAGATTTAAAGAATAAAAACTCCTGCATAAACGATTTTCAAGGAATTTGTATTGCAATTTCTTA
AGATGAAAGGAACAGCCACCAAGCAGTTTCACACTCACTTTACTGATTTCTGTGTGGACTGAGTACATTACAGCTG
ACGAATTTAGTTCCAGGAAGATGGATTGATGTTCACTAGCTTGGACAACCTCTGCAAAATATGAGACTATTTCC
ACTTGGGAAAAATTACAACAGCAAAAAAAAAAAAAAAAAAAAAA

111/615

FIGURE 110

MYLSRSLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLKVKLDPPDITCGDP
PETFCAMGNPYMCNNECDASTPELAHPPELMFDFEGRHPSTFWQSATWKEYPKPLQVNITLSWSKTIELTDNIVI
TFESGRPDQMIKESLDYGRWQPYQYYATDCLDAFHMDPKSVKDLSQHTVLEIICTEEYSTGYTTNSKIIHFEI
KDRFALFAGPRLRNMASLYGQLDTTKKLRDFFTVDLRIRLLRPVAGEIFVDELHLARYFYAISDIKVRGRCKCN
LHATVCVYDNSKLTCECEHNTTGPDCGKCKKNYQGRFWSPGSYLPIPKGTANTCIPSISSIGTNVCDNELLHCQN
GGTCHNNVRCLCPAAYTGILCEKLRCEEAGSCGSDSGQAPPHGTPALLLLTTLLGTASPLVF

FIGURE 111

CGCTGCCGTACGCTCGCCGGGACCGCGGCCCTCGCCCTCGCCCTCCGCCCTGCGCCTGCACCGCGTAGACCGAC
CCCCCCTCCAGCGCGCCACCCGGTAGAGGACCCCCGCCCGTCCCCCGACCCGGTCCCCGCCCTTTTGTAAAACT
TAAAGCGGGCGCAGCATTAACGCTTCCCGCCCCGGTGACCTCTCAGGGGTCTCCCCGCCAAAGGTGCTCCGCCGC
TAAGGAACATGGCGAAGGTGGAGCAGGTCCTGAGCCTCGAGCCGCAGCAGCAGCTCAAATTCGAGGTCCTCTCA
CCGATGTTGTACCACCAACCTAAAGCTTGGCAACCCGACCGCAAGAAATGTGTGTTTAAGGTGAAGACTACAG
CACACCGTAGGTACTGTGTGAGGCCCAACAGCGGAATCATCGATGACAGGGGCCATAATTAATGTATCTGTGATGT
TACAGCCTTTTCGATTATGATCCCAATGAGAAAAGTAAACACAAGTTTATGGTTCAGTCTATGTTTGTCTCAACTG
ACACTTCAGATATGGAAGCAGTATGGAAGGAGGCAAAACCGGAAGACCTTATGGATTCAAACCTTAGATGTGTGT
TTGAATTCGCAGCAGAGAATGATAAACACCATGATGTAGAAATAAATAAAATTTATATCCACAATGCATCAAAGA
CAGAAACACCAATAGATGTCTAAGTCTCTGAGTCTCTTCTTTGGATGACACCGAAGTTAAGAAGGTTATGGAAGAT
GTAAGAGGCTCGAAGGTGAAGTTTCAGAGGCTACGGGAGGAGAACAAGCAGTTCAAGGAAGAAGATGGACTCGGGA
TGAGGAAGACAGTGCAGAGCAACAGCCCCATTTACGCATTAGCCCCAACTGGGAAGGAAGAAGGCCCTTAGCACCC
GGCTCTTGGCTCTGGTGGTTTTGTTCTTTATCGTTGGTGTAATTATTGGGAAGATTGCCTTGTAGAGGTAGCATG
CACAGGATGGTAAATTTGATTGGTGGATCCACCATATCATGGGATTTAAATTTATCATAACCATGTGTAAAAAGA
AATTAATGTATGATGACATCTCACAGGTCCTTGCCCTTTAAATTAACCTCCCTGCACACACACAGATACACA
CACACAAATATAATGTAACGATCTTTTAGAAGGTAAAAATGTATAGTAACTGATTGAGGGGGAAAAAGATGAT
CTTTATTAATGACAAGGGAAACCATGAGTAATGCCACAATGGCATATTGTAATGTCAATTTTAAACATTGGTAGG
CCTTGGTACATGATGCTGGATTACCTCTCTTAAATGACACCCCTTCTCGCCTGTTGGTGTCTGGCCCTTGGGGAG
CTGGAGCCCCAGCATGCTGGGGAGTGCGGTCACTCCACACAGTAGTCCCCAGTGGCCACTCCCGGCCAGGCT
GCTTTCGGTGTCTTCAGTCTCTGTCCAAGCCATCAGTCTCTGGGACTGATGAACAGAGTCAAGACGCCAAAGGAA
TGCTAGTGTGGCAGCATCAGACGTACTCGTATAAGTGAGAGCGGTGTGTTGACTGATTGACCCAGCGCTTTGGA
AATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACCTG
TTATTGAGAGATGTTTAATGCATATTTAACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTACAAGAGT
ACAGTTAATGCTGCGTCTGCTGCTGAACCTGTTGGGTGAACCTGGTATTGCTGCTGGAGGGCTGTGGGCTCCTCTGT
CTCTGGAGAGTCTGGCTCATGTGGAGTGGGTTTATTGGGATGCTGGGAAGAGCTGCCAGGAAGTGTTTTTCTT
GGGTGAGTAAATAACAACCTGTCATAGGGGAGGAAATTTCTCAGTAGTGACAGTCAACTCTAGGTTACCTTTTTTAA
TGAAGAGTAGTCAGTCTTCTAGATTGTTCTTATACCACCTCTCAACCATTACTCACACTTCCAGCGCCAGGTC
AAGTCTGAGCCTGACCTCCCCTTGGGGACCTAGCCTGGAGTCAGGACAAATGGATCGGGCTGCAGAGGGTTAGAA
GCGAGGGGCCACGACGAGTTGTGGGTGGGGAGCAAGGGAAGAGAGAACTCTTCAGCGAATCCTTCTAGTACTAGTT
GAGAGTTTGACTGTGAATTAATTTATGCCATAAAAGCAACCCAGTTCTGTTGACTATGTAGCATCTTGAAA
AGAAAAAATTATAATAAAGCCCCAAATTAAGAAAA

113/615

FIGURE 112

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53977

<subunit 1 of 1, 243 aa, 1 stop

<MW: 27228, pI: 7.43, NX(S/T): 2

MAKVEQVLSLEPQHLEKFRGPFTDVVTTNLKLGNPTRNVCFKVKTTAPRRYCVRPNSGIIDAGASINVSVMLQP
FDYDPNEKSKHKFMVQSMFAPDTSDMEAVWKEAKPEDLMDSKLRCVFELPAENDKPHDVEINKIISTTASKTET
PIVSKSLSSSLDDTEVKKVMEECKRLQGEVQRLREENKQFKEEDGLRMRKTVQSNSPISALAPTGKEEGLSTRLL
ALVVLFFIVGVIIGKIAL**Important features:****Transmembrane domain:**

amino acids 224-239

N-glycosylation site.

amino acids 68-71

N-myristoylation site.

amino acids 59-64, 64-69 and 235-240

114/615

FIGURE 113

CCCACGCGTCCGGGTGACCTGGGCCGAGCCCTCCCGGTCGGCTAAGATTGCTGAGGAGCGCGGGTAGCTGGCA
GGCGCCGACTTCCGAAGGCCCGCGTCCGGGCGAGGTGTCTCATGACTTCTCTGTGGACCATGTCCTGATCTT
TTTTGCCTGCGTGGTACGGGTAAGGGATGGACTGCCCCCTCTCAGCCTCTACTGATTTTACCACACCCAAGATTT
TTTGGAATGGAGGAGACGGCTCAAGAGTTTAGCCTTGCGACTGGCCCAGTATCCAGGTCGAGGTTCTGCAGAAGG
TTGTGACTTTAGTATACATTTTTCTTCTTTCGGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTCCAGC
AGCCATGGCCTTCTGCTTCTGAGACCCTGTGGTGGGAATTCACAGCTTCTATGACACTACCTGCATTGGCCT
AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTCAGAAAGTGAAGTGGCATTTTAACTATGTAAG
TTCTCTCAGATGGAGTGCAGCTTGGAAAAAATTCAGGAGGAGCTCAAGTTCAGCCTCCAGCGGTTCTCACTCT
GGAGGACACAGATGTGGCAAATGGGGTGATGAATGGTCACACACCGATGCACTTGGAGCCTGCTCCTAATTTCCG
AATGGAACCAGTGACAGCCCTGGGTATCCTCTCCCTCATTCCTCAACATCATGTGTGCTGCCCTGAATCTCATTCTG
AGGAGTTCACCTTGCAGAACATTCTTTACAGGATCCAAGGAGCTGGTTCTGCTGGTTGGACCAAACCTCGTGAAGC
CAGCCACCCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCATCCGGGAGCAGTGATGTCAAACCTTCTGCTGCTG
GGGAAATCTCATCAGCAGGGAGCCTGTGGAAAAGGGCATGTCAAGTGAATCTGGGAATGGCTGGATTCCGGAACA
TCTGCCCATGTGTATTGATGGCAGAGCTGTTGCCACAAGCGCCTTTATTTAGGGTAAAATTAACAAATCCATT
CTATTCTCTGACCCATGCTTAGTACATATGACCTTTAACCCTTACATTTATATGATTCTGGGGTTGCTTCAGAA
GTGTTATTTTCATGAATCATTCATATGATTGATCCCCCAGGATTCTATTTTGTTTAATGGGCTTTTCTACTAAAA
GCATAAAATACTGAGGCTGATTTAGTCAGGGCAAACCATTTACTTTACATATTCGTTTTCAATACTTGCTGTTC
ATGTTACACAAGCTTCTTACGGTTTTCTTGTAAACAATAAATATTTTGTAGTAAATAATGGGTACATTTTAACAAAC
TCAGTAGTACAACCTAACTTGTATAAAAGTGTGTAAAAATGTATAGCCATTTATATCCTATGTATAAATTAAT
GAGGTGGCTTCAGAAATGGCAGAATAAATCTAAAGTCTTTATTAATAAAAAAAAAAAAAAAAAAAAAAG

115/615

FIGURE 114

MSVIFACVVRVDRDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFSIHFSSFGDVACMAICS
CQCPAAMAFCFLET LWWEFTASYDTTCIGLASRPYAFLEFDSIIQVKWHFNYVSSSQMECSLEKIQEELKLQPP
AVLTLEDTDVANGVMNGHTPMHLEPAPNFRMEPV TALGILSLILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLDQTS

116/615

FIGURE 115

CTCAGCGGCGCTTCCTCGTAGCGAGCCTAGTGGCGGGTGTTTGCATTGAAACGTGAGCGCGACCCGACCTTAAAG
AGTGGGGAGCAAAGGGAGGACAGAGCCCTTTAAACGAGGCGGGTGTTGCTGCCCTTTAAGGGCGGGGCGTCC
GGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTTTCTGTGCGAGGCTGCGAGGAAAGGCCCTAGGCTGGGTC
TGGGTGCTTGGCGGGCGGGGCTTCCTCCCCGCTCGTCCCTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCT
GAGCAGAGTATGGAAGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAG
TGTATTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCCTGACCCGCTTCAAGAAGCCT
GCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGCCTCGAGCTGTGCACCTTTACCTG
GCAATTGCCCTGGGTGCTGTCTGCTCCTGCCCTTCTCCATCATCAGCAATGAGGTGCTGCTCCTCGCTCGG
AACTACTACATCCAGTGGCTCAACGGCTCCCTCATCCATGGCCTCTGGAACCTTGTTTTCTCTTCCCCAACCTG
TCCCTCATCTTCCTCATGCCCTTTGCATATTTCTTCACTGAGTCTGAGGGCTTTGCTGGCTCCAGAAAGGGTGTC
CTGGGCGGGTCTATGAGACAGTGGTGATGTTGATGCTCCTCACTCTGCTGGTGCTAGGTATGGTGTTGGGTGGCA
TCAGCCATTGTGGACAAGAACAAGGCCAACAGAGAGTCACTCTATGACTTTTGGGAGTACTATCTCCCTACCTC
TACTCATGCATCTCCTTCCCTGGGGTCTGCTGCTCCTGGTGCTACTCCACTGGGTCTCGCCCGCATGTTCTCC
GTCAGTGGGAAGCTGCTAGTCAAGCCCCGGCTGCTGGAAGACCTGGAGGAGCAGCTGTACTGCTCAGCCTTTGAG
GAGGCAGCCCTGACCCGCGAGGATCTGTAATCCTACTTCTGCTGGCTGCCTTTAGACATGGAGCTGTACACAGA
CAGGTCTGGCTCTGCAGACACAGAGGGTCTGCTGGAGAAGAGGCGGAAGGCTTACGCTGGCAACGGAACCTG
GGCTACCCCTGGCTATGCTGTGCTTGTGCTGCTGACGGGCTGTCTGTGCTCATTGTGGCCATCCACATCCTG
GAGCTGCTCATCGATGAGGCTGCCATGCCCCGAGGCATGCAGGGTACCTCCTTAGGCCAGGTCTCCTTCTCCAAG
CTGGGCTCCTTTGGTGCCGTCATTCAGGTTGTACTCATCTTTTACCTAATGGTGCTCCTCAGTTGTGGGCTTCTAT
AGCTCTCCACTCTTCCGGAGCCTGCGGCCAGATGGCACGACACTGCCATGACGCAGATAATTGGGAAGTGTGTC
TGTCTCCTGGTCTTAAGCTCAGCACTTCTGTCTTCTCTCGAACCTGGGGCTCACTCGCTTTGACCTGCTGGGT
GACTTTGGACGCTTCACTGGCTGGGCAATTTCTACATTGTGTTCTCTACACGCAGCCTTTGCAGGCCTCACC
ACACTCTGTCTGGTGAAGACCTTCACTGCAGCTGTGCGGCAGAGCTGATCCGGGCCTTTGGGCTGGACAGACTG
CCGCTGCCCCGTCTCCGTTTTCCCCAGGCATCTAGGAAGACCCAGCACCAGTGAACCTCCAGCTGGGGGTGGGAAG
GAAAAAAGTGGACACTGCCATCTGCTGCCTAGGCCTGGAGGGAAGCCCAAGGCTACTTGGACCTCAGGACCTGGA
ATCTGAGAGGGTGGGTGGCAGAGGGGAGCAGGCCATCTGCATATTGCATAATCTGAGCCAGAGTTTGGGACCA
GGACCTCCTGCTTTTCCATACTTAAGTGGCCTCAGCATGGGGTAGGGCTGGGTGACTGGGTCTAGCCCTGAT
CCCAAATCTGTTTACACATCAATCTGCCTCACTGCTGTTCTGGGCCATCCCCATAGCCATGTTTACATGATTTGA
TGTGCAATAGGGTGGGTAGGGGAGGAAAGGACTGGGCCAGGGCAGGCTCGGGAGATAGATTGTCTCCCTTGC
CTCTGGCCAGCAGAGCCTAAGCACTGTGCTATCCTGGAGGGCTTTGGACCACCTGAAAGACCAAGGGGATAGG
GAGGAGGAGGCTTACGCCATCAGCAATAAGTTGATCCAGGGAAAAAA

117/615

FIGURE 116

MEAPDYEVLSVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDDATVNKIALELCFTFLAIA
LGAVLLLPFSIISNEVLLSLPRNYIIQWLNGSLIHGLWNLVFLFPNLSLIFLMPFAYFFTESEGFAGSRKGV LGR
VYETVVMMLLLTLLVLGMVWVASAIVDKNKANRESLYDFWEYYPYLYSCISFLGVLLLLLVCTPLGLARMF SVTG
KLLVKPRILLEDLEEQLYCSAFEEAALTRRICNPTSCWLPLDMELLHRQVLALQTQRV LLEKRRKASAWQRNLGYP
LAMLCLLVLTGLSVLIVAIHILELLIDEAAMP RGMQGTSLGQVSFSKLG SFGAVIQVVLIFYLMVSSVVG FYSSP
LFRSLRPRWHD TMTQIIGNCVCLLV LSSALPVFSRTLGLTRFDLLGDFGRFNWLG NFIYVFLYNAAFAGLT TLC
LVKTFTA AVRAELIRAFGLDRLPLPVSGFPQASRKTQH Q

FIGURE 117

[illegible]

119/615

FIGURE 118

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA54002
><subunit 1 of 1, 544 aa, 1 stop
><MW: 60268, pI: 9.53, NX(S/T): 3
MLLPILLSLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSPYPRQDWTGSTPAYGYWFKAVTETTKGAPVAT
NHQSREVEEMSTRGRFQLTGDPKAGNCSLVIRDAQMQDESQYFFRVERGSYVTYNFMNDGFFLKVTVLSFTPRPQD
HNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPP
ATLSWVLQNRVLSSSHWPWGPRLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTV
LENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGS
QHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLEFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINNVPT
AGPLAQKRNQKATPNSPRTPPPPGAPSPESKKNQKKYQLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPR
PEARMPKGTQADYAEVKFQ
```

Important features:**Signal peptide:**

amino acids 1-15

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 100-103, 297-300 and 306-309

Immunoglobulins and major histocompatibility complex proteins signature.

amino acids 365-371

120/615

FIGURE 119

CTCGCGCAGGGATCGTCCCATGGCCGGGGCTCGGAGCCGCGACCCTTGGGGGGCCTCCGGGATTGCTACCTTTT
TGGCTCCCTGCTCGTGAACCTGCTCTTCTACGGGCTGTGCGCTTCAATCTGGACGTGATGGGTGCCTTGCGCAA
GGAGGGCGAGCCAGGCAGCCTCTTCGGCTTCTCTGTGGCCCTGCACCGGCAGTTGCAGCCCCGACCCAGAGCTG
GCTGCTGGTGGGTGCTCCCCAGGCCCTGGCTCTTCTGGGCAGCAGGCGAATCGCACTGGAGGCCTCTTCGCTTG
CCCGTTGAGCCTGGAGGAGACTGACTGCTACAGAGTGGACATCGACCAGGGAGCTGATATGCAAAAGGAAAGCAA
GGAGAACCAGTGGTTGGGAGTCAGTGTTCGGAGCCAGGGGCTGGGGGCAAGATTGTTACCTGTGCACACCGATA
TGAGGCAAGGCAGCGAGTGGACCAGATCCTGGAGACGCGGGATATGATTGGTCGCTGCTTTGTGCTCAGCCAGGA
CCTGGCCATCCGGGATGAGTTGGATGGTGGGGAATGGAAGTTCTGTGAGGGACGCCCCAAGGCCATGAACAATT
TGGGTTCTGCCAGCAGGGCACAGCTGCCGCCTTCTCCCTGATAGCCACTACCTCCTCTTTGGGGCCCCAGGAAC
CTATAATTGGAAGGGCACGGCCAGGGTGGAGCTCTGTGCACAGGGCTCAGCGGACCTGGCACACCTGGACGACGG
TCCCTACGAGCGGGGGGAGAGAAGGAGCAGGACCCCGCCTCATCCGGTCCCTGCCAACAGCTACTTTGGCTT
CTCTATTGACTCGGGGAAAGTCTGGTGCCTGCAGAAGAGCTGAGCTTTGTGGCTGGAGCCCCCGCGCCAACCA
CAAGGGTGCTGTGGTTCATCCTGCCAAGGACAGCGCCAGTCGCCTGGTGCCCGAGGTTATGCTGTCTGGGGAGCG
CCTGACCTCCGGCTTTGGCTACTCACTGGCTGTGGCTGACCTCAACAGTGATGGCTGGCCAGACCTGATAGTGGG
TGCCCCCTACTTCTTTGAGCGCCAAGAAGAGCTGGGGGGTGTGTGTATGTGTAATTGAACAGGGGGGTCACTG
GGCTGGGATCTCCCTCTCCGGCTCTCGGGCTCCCTGACTCCATGTTTCGGGATCAGCCTGGCTGTCTGGGGGA
CCTCAACCAAGATGGCTTTCCAGATATTGCAGTGGGTGCCCCCTTTGATGGTGATGGGAAAGTCTTCATCTACCA
TGGGAGCAGCCTGGGGGTTGTGCCAAACCTTCACAGGTGCTGGAGGGCGAGGCTGTGGGCATCAAGAGCTTCGG
CTACTCCCTGTCCAGGCAGCTTGGATATGGATGGGAACCAATACCCTGACCTGCTGGTGGGCTCCCTGGCTGACAC
CGCAGTGCTCTTCAGGGCCAGACCCATCCTCCATGCTCTCCATGAGTCTCTATTGCTCCAGGAAGCATCGACCT
GGAGCAGCCCAACTGTGTGGCGGCCACTCGGTCTGTGTGGACCTAAGGGTCTGTTTCAGCTACATTGCAGTCCC
CAGCAGCTATAGCCCTACTGTGGCCCTGGACTATGTGTTAGATGCGGACACAGACCGGAGGCTCCGGGGCCAGGT
TCCCCGTGTGACGTTCTGAGCCGTAACCTGGAAGAACCAGCACCAGGCTCGGGCACCGTGTGGCTGAAGCA
CCAGCATGACCGAGTCTGTGGAGACGCCATGTTCCAGCTCCAGGAAAATGTCAAAGACAAGCTTCGGGCCATTGT
AGTGACCTTGTCTACAGTCTCCAGACCCCTCGGCTCCGGCGACAGGCTCCTGGCCAGGGGCTGCCTCCAGTGGC
CCCCATCCTCAATGCCACCAGCCAGCACCAGCGGCCAGAGATCCACTTCTGAAGCAAGGCTGTGGTGAAGA
CAAGATCTGCCAGAGCAATCTGCAGCTGGTCCACGCCGCTTCTGTACCCGGGTGAGCGACACGGAATTCCAACC
TCTGCCCATGGATGTGGATGGAAACAACAGCCCTGTTGCACTGAGTGGGCAGCCAGTCATTGGCCTGGAGCTGAT
GGTCACCAACCTGCCATCGGACCCAGCCAGCCCAAGGCTGATGGGGATGATGCCCATGAAGCCCAGCTCCTGGT
CATGCTTCTGACTCACTGCACTACTCAGGGGTCCGGGCCCTGGACCTGCGGAGAAGCCACTCTGCCTGTCCAA
TGAGAATGCCTCCCATGTTGAGTGTGAGCTGGGGAAACCCATGAAGAGAGGTGCCAGGTGACCTTCTACCTCAT
CCTTAGCACCTCCGGGATCAGCATTGAGACCACGGAAGTGGAGGTAGAGCTGCTGTTGGCCACGATCAGTGAGCA
GGAGCTGCTCCAGTCTCTGCACGAGCCCGTGTCTTATTGAGCTGCCACTGTCCATTGCAGGAATGGCCATTCC
CCAGCAACTCTTCTTCTGCTGGTGTGGTGGAGGGCGAGAGAGCCATGCAGTCTGAGCGGGATGTGGGCAGCAAGGT
CAAGTATGAGTACGGGTTTCCAACCAAGGCCAGTGCCTCAGAACCCTGGGCTCTGCCTTCTCAACATCATGTG
GCCTCATGAGATTGCCAATGGGAAGTGGTTGCTGTACCCAATGCAGGTTGAGCTGGAGGGCGGGCAGGGGCTGG
GCAGAAAGGGCTTTGCTCTCCAGGCCCAACATCCTCCACTGGATGTGGACAGTAGGGATAGGAGGCGGGGGA
GCTGGAGCCACCTGAGCAGCAGGAGCCTGGTGAGCGGCAGGAGCCAGCATGTCTGGTGGCCAGTGTCTCTGC
TGAGAAGAAGAAAAACATCACCTGGACTGCGCCCGGGGCACGGCCAAGTGTGTGGTGTTCAGCTGCCACTCTA
CAGCTTTGACCGCGCGGCTGTGCTGCATGTCTGGGGCCGTCTCTGGAACAGCACCTTTCTGGAGGAGTACTCAGC
TGTGAAGTCCCTGGAAGTGATTGTCCGGGCCAACATCACAGTGAAGTCCCTCCATAAAGAACTTGATGCTCCGAGA
TGCTTCCACAGTGATCCAGTGATGGTATACTTGACCCCATGGCTGTGGTGGCAGAAGGAGTGCCCTGGTGGGT
CATCCTCCTGGCTGTACTGGCTGGCTGCTGGTGTGCTAGCACTGCTGGTGTGCTCCTGTGGAAGATGGGATTCTT
CAAACGGGCGAAGCACCCGAGGCCACCGTGCCCCAGTACCATGCGGTGAAGATTCTCGGGAAGACCGACAGCA
GTTCAAGGAGGAGAAGACGGGCACCATCCTGAGGAACAAGTGGGGCAGCCCCGGCGGGAGGGCCCCGATGCACA
CCCCATCCTGGCTGCTGACGGGCATCCCGAGCTGGGCCCGAGTGGGCATCCAGGGCCAGGCACCGCCTAGGTTCC
CATGTCCCAGCCTGGCCTGTGGCTGCCCTCCATCCCTTCCCCAGAGATGGCTCCTTGGGATGAAGAGGGTAGAGT
GGGCTGCTGGTGTGCGCATCAAGATTTGGCAGGATCGGCTTCTCAGGGGCACAGACCTCTCCACCCACAAGAAC
TCCTCCCACCAACTTCCCCTTAGAGTGCTGTGAGATGAGAGTGGGTAAATCAGGGACAGGGCCATGGGGTAGGG
TGAGAAGGGCAGGGGTGCTGATGCAAAGGTGGGGAGAAGGGATCCTAATCCCTTCTCCATTCACCTGT
GTAACAGGACCCCCAAGGACCTGCCTCCCCGGAAGTGCTTAACCTAGAGGGTGGGGAGGAGTTGTGTCACTGA
CTCAGGCTGCTCCTTCTCTAGTTTCCCTCTCATCTGACCTTAGTTTGTGCTGCCATCAGTCTAGTGGTTTCGTGGT
TTCGTCTATTTATTAAAAATATTTGAGAACAAAAA

121/615

FIGURE 120

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA55737
><subunit 1 of 1, 1141 aa, 1 stop
><MW: 124671, pI: 5.82, NX(S/T): 5
MAGARSRDPWGASGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHRQLQPRPQSWLLVGAP
QALALPGQANRTGGFLFACPLSLEETDCYRVDIDQGADMOKESKENQWLGVSVRSQGPGGKIVTCAHRYEARQRV
DQILETRDMIGRCFVLSQDLAIRDELDDGGGEWKFCGRPQGHEQFGFCQOQTAAAFSPDSHYLLFGAPGTYNWKG
ARVELCAQGSADLAHLDDGPYEAGGEKEQDPRLLIPVPANSYFGFSIDSGKGLVRAEELS FVAGAPRANHKGAVVI
LRKDSASRLVPEVMSLGERLTSGFGYSLAVADLNSDGWPD LIVGAPYFFERQEELGGAVYVYLNQGGHWAGISPL
RLCGSPDSMFGISLAVLGDLDNQDGFDPDIAGAPFDGDGKVFIYHGSSSLGVVAKPSQVLEGEAVGIKSGYSLSGS
LDMDGNQYPDLLVGS LADTAVLFRARPILHVSHEVSIAPRSIDLEQPN CAGGHSVCVDLRVCF SYIAVPSSYSPT
VALDYVLDADTDRLRLRGQVPRVTFLSRNLEEPKHQASGTVWLKHQHDRVCGDAMFQLQENVKDKLRAIVVTL SYS
LQTPRLRRQAPGQGLPPVAPILNAHQPSQRAEIHFLKQCGGEDKICQSNLQLVHARFCTRVSDTEFQPLPMDVD
GTTALFALSGQP VIGLELMVTNLPSDPAQFQADGDDAHEAQLLVM LPSDLHYSGVRALDPAEKPICLSNENASHV
ECELGNPMKRGAQVTFYLILSTSGIS IETTELEVELL LATISEQELHPVSARARVFIELPLSIAGMAIPQQLFFS
GVVRGERAMQSERDVGSKVKYEVTVSNQGQSLR TLGSAFLNIMWPHEIANGKWL LYPMQVELEGQGPQKGLCS
PRPNILHLDVDSDRRRRRRELEPPEQQEPGERQEPSMSWVPVSSAEKKKNITLDCARGTANCVVFSCPLYSFDR AA
VLHVWGRLWNSTFLEEYS AVKSLEVIVRANITVKSSIKNLMLRDASTVIPVMVYLDPM AVVAEGVPWWVILLAVL
AGLLVLALLVLLWLKMGFFKRAKHPEATVPQYHAVKIPREDRQQFKEEKTGTILRNNWGS PRREGPD AHPILAAD
GHPELGPDPGHPGPGTA
```

Important features:**Signal peptide:**

amino acids 1-33

Transmembrane domain:

amino acids 1040-1062

N-glycosylation sites.

amino acids 86-89, 746-749, 949-952, 985-988 and 1005-1008

Integrins alpha chain proteins.

amino acids 1064-1071, 384-408, 1041-1071, 317-346, 443-465, 385-407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408 and 1031-1047

122/615

FIGURE 121

GGCACGAGGCGGCGGGGAGTTCGCGGGATGCGCCCGGGAGCCACAGCCTGAGGCCCTCAGGTCTCTGCAGGTGTC
GTGGAGGAACCTAGCACCTGCCATCCTCTTCCCAATTTGCCACTTCCAGCAGCTTTAGCCCATGAGGAGGATGT
GACCGGGACTGAGTCAGGAGCCCTCTGGAAGCATGGGAGACTGTGGTGATTGTTGCCATAGGTGTGCTGGCCACCA
TCTTTCTGGCTTCGTTTGCAGCCTTGGTGCTGGTTTGCAGGCAGCGCTACTGCCGGCCGCGAGACCTGCTGCAGC
GCTATGATTCTAAGCCCATTTGTGGACCTCATTGGTGCCATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAAGTGG
ACGATGTCGTTATCACCAACCCCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATCGAAGATGCCTCGGGTC
TCATGTCCCAGTGCATTGCCATCTTGAAGATTTGTCACACTCTGACAGAGAAGCTTGTTGCCATGACAATGGGCT
CTGGGGCCAAGATGAAGACTTCAGCCAGTGTGAGCGACATCATTGTGGTGGCCAAGCGGATCAGCCCCAGGGTGG
ATGATGTTGTGAAGTCGATGTACCCTCCGTTGGACCCCCAACTCCTGGACGCACGGACGACTGCCCTGCTCCTGT
CTGTCAGTCACCTGGTGCTGGTGACAAGGAATGCCTGCCATCTGACGGGAGGCCCTGGACTGGATTGACCAGTCTC
TGTCGGCTGCTGAGGAGCATTGGAAGTCCTTCGAGAAGCAGCCCTAGCTTCTGAGCCAGATAAAGGCCTCCCAG
GCCCTGAAGGCTTCCTGCAGGAGCAGTCTGCAATTTAGTGCCTACAGGCCAGCAGCTAGCCATGAAGGCCCTGC
CGCCATCCCTGGATGGCTCAGCTTAGCCTTCTACTTTTTCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTT
CAGCTGTGTGTGCATAGTAAAGCAGGAGATCCCCGTGAGTTTATGCCTCTTTTGCAGTTGCAAACCTGGCTGGT
GAGTGGCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACTCTCTGCAAGAGGAGTATTGAAAACCTGGTGGAC
TGTCAGCTTTTATTAGCTCACCTAGTGTTTTCAAGAAAATTGAGCCACCGTCTAAGAAATCAAGAGGTTTCACAT
TAAATTAGAATTTCTGGCCTCTCTCGATCGGTGAGAATGTGTGGCAATCTGATCTGCATTTTCAGAAGAGGAC
AATCAATTGAAACTAAGTAGGGGTTTCTTCTTTTGGCAAGACTTGACTCTCTCACCTGGCCTGTTTCATTTATT
TGTATTATCTGCCTGGTCCCTGAGGCGTCTGGGTCTCTCCTCTCCCTTGAGGTTTGGGTTTGAAGCTGAGGAAC
TACAAAGTTGATGATTTCTTTTTATCTTTATGCCTGCAATTTTACCTAGCTACCACTAGGTGGATAGTAAATTT
ATACTTATGTTTCCCTCAAAAAAAAAAAAAA

123/615

FIGURE 122

METVVIVAIGVLATIFLASFAALVLVCRQRYCRPRDLLQRYDSKPIVDLIGAMETQSEPSELELDDVVITNPHE
AILENEDWIEDASGLMSHCIAILKICHTLTEKLVAMTMGSGAKMKTSASVSDIIVVAKRISPRVDDVVKSMYPPL
DPKLLDARTTALLLSVSHLVLVTRNACHTTGGLDWIDQSLSAEEHLEVLREAALASEPDKGLPGPEGFLQEQSAI

124/615

FIGURE 123

CCCTTACATCCTCCTAGGACCCGGTCGGTAGTCGTCGCCCCAGCCCGCCGGGGGCGCAGCGCCCGAGCCGCGGCC
CTCGAGACGGGACCGAGAGCATCATGGGCAGCACTGTCCCGCGCTCCGCCTCCGTGCTGCTTCTGCTGCTGCTCC
TGCGCCGGGCGGAGCAGCCCTGCGGGGCCGAGCTCACCTTCGAGCTGCCGACAACGCCAAGCAGTGCTTCCACG
AGGAGGTGGAGCAGGGCGTGAAGTTCTCCCTGGATTACCAGGTCATCACTGGAGGCCACTACGATGTTGACTGCT
ATGTAGAGGACCCCAAGGGGAACACCATCTACAGAGAAACGAAGAAGCAGTACGACAGCTTCACGTACCGGGCTG
AAGTCAAGGGCGTTTATCAGTTTGTCTTCAGTAATGAGTTTTCCACCTTCTCTCACAAGACCGTCTACTTTGACT
TTCAAGTGGGCGATGAGCCTCCCATTTCTCCAGACATGGGGAACAGGGTCACAGCTCTACCCAGATGGAGTCCG
CCTGCGTGACCATCCATGAGGCTCTGAAAACGGTGATTGACTCCCAGACGCATTACCGGCTGCGGGAGGCCCCAGG
ACCGGGCCCGAGCGGAAGACCTTAATAGCCGAGTCTCTTACTGGTCTGTTGGCGAGACGATTGCCCTGTTCTGTGG
TCAGCTTCAGTCAGGTGCTACTGTTGAAAAGCTTCTTCACAGAAAACGACCCATCAGCAGGGCAGTCCACTCCT
AGCCCCGGCATCCTGCTCTAGGGCCCTCATGCCCCAGGCTGGAGCAGCTCTCCTAGGTCACAGCCTGCTGGGCT
GGGTGCGGTAGCCAGGGTGGAGGCAGAACGATGCTGCTGTGGTAGCCCTTTGCCTTTCATGCCATGCTTGATT
CTTGACCTCAGCAGCTGAAGGTCTCAGAGACCAGTAATCAGAAGGCATCCGACTGCATTAAAGTGTGCAGCGCTG
AAAAGACATTTACAAGTAGGCCAGGGATTAGCCACTGTGGGAGGGTGGACAGGCAATGGTTCAGTGGCCTGGCTG
TTGGCAGGAAGTCCAAGTGCCAGGCCTCTTGGGCAGCTTAGGGCCCTGCCTCTGTTTCATGATGCATGGGTGAT
TTGTCTGGGTGTCCTATCCCATATGGAGAAGAAAGGGGCTCTAAGTTCTGGCTCTTCTTTCTTTGGGGTTCTCT
GTACCTGAGGAAACCAGGCCCTGGGTGACTTTGCAGATCTGCTCACCTCGGTGAGCAACAGTGTGAGCCATGCA
AGCAGGACAGAATGGTGACTGGGTGCCCTTGGTGAGCTGTGTATTTCTAGGAGGTAGAAAACCTGTGGGAAACTG
TGGCTAATAAAAACTAAGTGTGAGCGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

125/615

FIGURE 124

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56052

<subunit 1 of 1, 217 aa, 1 stop

<MW: 24777, pI: 5.55, NX(S/T): 0

MGSTVPRSASVLLLLLLRRAEQPCGAELTFELPDNAKQCFHEEVEQGVKFSLDYQVITG
GHYDVDCYVEDPQGNTIYRETKKQYDSFTYRAEVKGVYQFCFSNEFSTFSHKTVYFDFQV
GDEPPILPDMGNRVTAQTQMESACVTIHEALKTVIDSQTHYRLREAQDRARAEDLNSRVS
YWSVGETIALFVVSFSQVLLKSFTEKRPISRAVHS

Important features:**Signal peptide:**

amino acids: 1-23

Transmembrane domain:

amino acids: 187-201

N-myristoylation sites:

amino acids: 26-32, 48-54, 131-137

Tyrosine kinase phosphorylation site:

amino acids: 82-91

Glycosyl hydrolases family 25 proteins:

amino acids: 53-61

126/615

FIGURE 125

GGCACGAGGCGCTGTCCACCCGGGGGCGTGGGAGTGAGGTACCAGATTGAGCCCATTTGGCCCCGACGCCTCTGT
TCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGTTCTTACGGACTGCAAGATGGAGGAAGCGGGGAACCTAG
GAGGCCTGATTAAGATGGTCCATCTACTGGTCTTGTCAGGTGCCTGGGGCATGCAAATGTGGGTGACCTTCGTCT
CAGGCTTCCTGCTTTCCGAAGCCTTCCCCGACATACCTTCGGACTAGTGCAGAGCAAACCTTCCCCTTCTACT
TCCACATCTCCATGGGCTGTGCCTTCATCAACCTCTGCATCTTGGCTTCACAGCATGCTTGGGCTCAGCTCACAT
TCTGGGAGGCCAGCCAGCTTTACCTGCTGTTCTGAGCCTTACGCTGGCCACTGTCAACGCCCCGCTGGCTGGAAC
CCCGCACCACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGAGCGAGGCCTGGGTGGGGAGGTACCAGGCA
GCCACCAGGGTCCCGATCCCTACCGCCAGCTGCGAGAGAAGGACCCCAAGTACAGTGCTCTCCGCCAGAATTTCT
TCCGCTACCATGGGCTGTCTCTCTTTGCAATCTGGGCTGCGTCCTGAGCAATGGGCTCTGTCTCGCTGGCCTTG
CCCTGGAAATAAGGAGCCTCTAGCATGGGCCCTGCATGCTAATAAATGCTTCTCAGAAATGAAAAAAAAAAAAA
AAAAAA

127/615

FIGURE 126

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56107
<subunit 1 of 1, 231 aa, 1 stop
<NX(S/T): 0
MEEGGNLGGGLIKMVHLLVLSGAWGMQMWVTFVSGFLLFRSLPRHTFGLVQSKLFFYFHHISMGCAFINLCILASQ
HAWAQLTFWEASQLYLLFLSLTLATVNARWLEPRTTAAMWALQTVEKERGLGGEVPGSHQGPDPYRQLREKDPKY
SALRQNFRRYHGLSSLCNLGCVLSNGLCIAGLALEIRSL
```

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 86-103, 60-75

Casein kinase II phosphorylation site.

amino acids 82-86

Tyrosine kinase phosphorylation site.

amino acids 144-151

N-myristoylation site.

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 54-65

G-protein coupled receptors proteins.

amino acids 44-85

128/615

FIGURE 127

GCTTCATTTCTCCCGACTCAGCTTCCCACCCCTGGGCTTTCGAGGTGCTTTCGCCGCTGTCCCCACCACTGCAGC
CATGATCTCCTTAACGGACACGCAGAAAATTGGAATGGGATTAACAGGATTTGGAGTGTTTTCTGTCTTTGG
AATGATTCTCTTTTTTGACAAAGCACTACTGGCTATTGGAAATGTTTTATTGTAGCCGGCTTGGCTTTTGTAAAT
TGGTTTAGAAAGAACATTCAGATTCTTCTTCCAAAAACATAAAATGAAAGCTACAGGTTTTTTCTGGGTGGTGT
ATTTGTAGTCCTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTCTCTTGTTCAGGGG
CTTCTTTCCTGTCGTTGTTGGCTTTATTAGAAGAGTGCCAGTCCTTGGATCCCTCCTAAATTTACCTGGAATTAG
ATCATTGTAGATAAAGTTGGAGAAAGCAACAATATGGTATAACAACAAGTGAATTTGAAGACTCATTTAAATA
TTGTGTTATTTATAAAGTCATTTGAAGAATATTCAGCACAAAATTAAATTACATGAAATAGCTTGTAAATGTTCTT
TACAGGAGTTTAAAACGTATAGCCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTGAAAACAGGCTTCTA
CTCAAGTGAAGTAAAGAAGAGTCAGCAAGCAAAGTGAAGAGAGGTGAAATCCATGTTAATGATGCTTAAGAACTC
TTGAAGGCTATTTGTGTTGTTTTTCCACAATGTGCCAAACTCAGCCATCCTTAGAGAACTGTGGTGCCTGTTTCT
TTTCTTTTTATTTTGAAGGCTCAGGAGCATCCATAGGCATTTGCTTTTTTAGAAGTGTCCACTGCAATGGCAAAA
TATTTCCAGTTGCACTGTATCTCTGGAAGTGATGCATGAATTCGATTGGATTGTGTCATTTTAAAGTATTAAAC
CAAGGAAACCCCAATTTTGATGTATGGATTACTTTTTTTTGNCGNCAGGGCC

129/615

FIGURE 128

MISLTDQKIGMGLTGFGVFFLFFGMILFFDKALLAIGNVLFVAGLAFVIGLERTFRFFFQKHMKATGFFLGGV
FVVLIGWPLIGMIFEIYGFFLLFRGFFPVVVGFIIRVPVLGSLNLPGIRSFVDKVGESNNMV

Important features:

Transmembrane domains:

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

N-myristoylation sites.

amino acids 11-16, 51-56 and 116-121

Aminoacyl-transfer RNA synthetases class-II protein.

amino acids 49-59

130/615

FIGURE 129

AATTCAGATTTTAAAGCCATTCTGCAGTGAATTTTCATGAAGTAGCAAGAGGACACCATCTTCTGTATTATACA
AGAAAGGAGTGTACCTATCACACACAGGGGGAAAAATGCTCTTTTGGGTGCTAGGCCTCCTAATCCTCTGTGGTT
TTCTGTGGACTCGTAAAGGAAAACTAAAGATTGAAGACATCACTGATAAGTACATTTTATCACTGGATGTGACT
CGGGCTTTGGAACTTGGCAGCCAGAACTTTTGATAAAAAGGGATTTTCATGTAATCGCTGCCTGTCTGACTGAAT
CAGGATCAACAGCTTTAAAGGCAGAAACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAGAGA
ATGTCAAGAGGACTGCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGGTCTGATCAATAATGCTG
GTGTTCCCGGCGTGCTGGCTCCCACTGACTGGCTGACACTAGAGGACTACAGAGAACCTATTGAAGTGAACCTGT
TTGGACTCATCAGTGTGACACTAAATATGCTTCCTTTGGTCAAGAAAGCTCAAGGGAGAGTTATTAATGTCTCCA
GTGTTGGAGGTGCGCTTGCAATCGTTGGAGGGGGCTATACTCCATCCAAATATGCAGTGGAAGGTTTCAATGACA
GCTTAAGACGGGACATGAAAGCTTTTGGTGTGCACGTCTCATGCATTGAACCAGGATTGTTCAAAACAAACTTGG
CAGATCCAGTAAAGTAATTGAAAAAACTCGCCATTTGGGAGCAGCTGTCTCCAGACATCAAACAACAATATG
GAGAAAGTTACATTGAAAAAGTCTAGACAACTGAAAGGCAATAAATCCTATGTGAACATGGACCTCTCTCCGG
TGGTAGAGTGCATGGACCACGCTCTAACAAGTCTCTTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAAA
TTTTCTGGATACCTCTGTCTCATGCCCAGCAGCTTTGCAAGACTTTTATTGTTGAAACAGAAAGCAGAGCTGG
CTAATCCCAAGGCAGTGTGACTCAGCTAACCACAAATGTCTCCTCCAGGCTATGAAATTGGCCGATTTCAAGAAC
ACATCTCCTTTTCAACCCCATTCCTTATCTGCTCCAACCTGGACTCATTATAGATCGTGCTTATTTGGATTGCAAA
AGGGAGTCCCACCATCGCTGGTGGTATCCAGGGTCCCTGCTCAAGTTTCTTTGAAAAGGAGGGCTGGAATGGT
ACATCACATAGGCAAGTCTGCCCCTGTATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGGAAATTGAAAGACTT
GCCCATTCAAATGATCTTTACCGTGGCCTGCCCCATGCTTATGGTCCCCAGCATTTACAGTAACTTGTGAATGT
TAAGTATCATCTCTTATCTAAATATTTAAAGATAAGTCAACCCAAAAA
AA
AAAAAAA

131/615

FIGURE 130

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56406
><subunit 1 of 1, 319 aa, 1 stop
><MW: 35227, pI: 8.97, NX(S/T): 3
MLFWVLGLLILCGFLWTRKGKLIKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIAACLTESGSTALKAETSE
RLRTVLLDVTDPENVKRTAQWVKVQVGEKGLWGLINNAGVPGVLAPTDWLTLEDYREPIEVNLFGLISVTLNMLP
LVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGFNDLRRDMKAFGVHVSCEPGLFKTNLADPVKVEKKLA
IWEQLSPDIKQQYGEgyIEKSLDKLKGKNSYVNMDSLSPVVECMDHALTSLEPKTHYAAGKDAKIFWIPLSHMPAA
LQDFLLLLKQKAE LANPKAV
```

Important features of the protein:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 136-152

N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

132/615

FIGURE 131

AGACAGTACCTCCTCCCTAGGACTACACAAGGACTGAACCAGAAGGAAGAGGACAGAGCAAAGCCATGAACATCA
TCCTAGAAATCCTTCTGCTTCTGATCACCATCATCTACTCCTACTTGGAGTCGTTGGTGAAGTTTTTCATTCCCTC
AGAGGAGAAAAATCTGTGGCTGGGGAGATTGTTCTCATTACTGGAGCTGGGCATGGAATAGGCAGGCAGACTACTT
ATGAATTTGCAAAACGACAGAGCATATTGGTTCTGTGGGATATTAATAAGCGCGGTGTGGAGGAACTGCAGCTG
AGTGCCGAAAACTAGGCGTCACTGCGCATGCGTATGTGGTAGACTGCAGCAACAGAGAAGAGATCTATCGCTCTC
TAAATCAGGTGAAGAAAGAAGTGGGTGATGTAACAATCGTGGTGAATAATGCTGGGACAGTATATCCAGCCGATC
TTCTCAGCACCAAGGATGAAGAGATTACCAAGACATTTGAGGTCAACATCCTAGGACATTTTTGGATCACAAAAG
CACTTCTTCCATCGATGATGGAGAGAAATCATGGCCACATCGTCACAGTGGCTTCAGTGTGCGGCCACGAAGGGA
TTCCTTACCTCATCCCATATTGTTCCAGCAAATTTGCCGCTGTTGGCTTTCACAGAGGTCTGACATCAGAACTTC
AGGCCTTGGGAAAACTGGTATCAAAACCTCATGTCTCTGCCAGTTTTTGTGAATACTGGGTTACCAAAAATC
CAAGCACAAGATTATGGCCTGTATTGGAGACAGATGAAGTCGTAAGAAGTCTGATAGATGGAATACTTACCAATA
AGAAAATGATTTTTGTTCCATCGTATATCAATATCTTTCTGAGACTACAGAAGTTTCTTCTGAACGCGCCTCAG
CGATTTTAAATCGTATGCAGAATATTCAATTTGAAGCAGTGGTTGGCCACAAAATCAAATGAAATGAATAAATA
AGCTCCAGCCAGAGATGTATGCATGATAATGATATGAATAGTTTCGAATCAATGCTGCAAAGCTTTATTTACAT
TTTTTCAGTCCTGATAATATTAATAACATTGGTTTGGCACTAGCAGCAGTCAAACGAACAAGATTAATTACCTGT
CTTCTGTTTCTCAAGAATATTTACGTAGTTTTTTCATAGGTCTGTTTTTCTTTTCATGCCTCTTAAAACTTCTG
TGCTTACATAAACATACTTAAAGGTTTTCTTTAAGATATTTTATTTTCCATTTAAAGGTGGACAAAAGCTACC
TCCCTAAAAGTAAATACAAAGAGAACTTATTTACACAGGGAAGGTTTAAAGACTGTTCAAGTAGCATTTCCAATCTG
TAGCCATGCCACAGAATATCAACAAGAACACAGAATGAGTGCACAGCTAAGAGATCAAGTTTCAGCAGGCAGCTT
TATCTCAACCTGGACATATTTTAAGATTGAGCATTTGAAAGATTTCCCTAGCCTCTTCTTTTTCATTAGCCCAA
AACGGTGCAACTCTATTCTGGACTTTATTACTTGATTCTGTCTTCTGTATAACTCTGAAGTCCACAAAAGTGGA
CCCTCTATATTTCTCCCTTTTATAGTCTTATAAGATACATTATGAAAGGTGACCGACTCTATTTTAAATCTCA
GAATTTTAAGTTCTAGCCCCATGATAACCTTTTCTTTGTAATTTATGCTTTTCATATATCCTTGGTCCCAGAGAT
GTTTAGACAATTTTAGGCTCAAAAATTAAGCTAACACAGGAAAAGGAAGTGTACTGGCTATTACATAAGAAACA
ATGGACCCAAGAGAAGAA

133/615

FIGURE 132

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56409

<subunit 1 of 1, 300 aa, 1 stop

<MW: 33655, pI: 9.31, NX(S/T): 1

MNIILEILLLLITIIYSYLESIVKFFIPQRRKSVAGEIVLITGAGHGIGRQTTYEFAKRQSILVLWDINKRGVEE
TAAECRKLGVTAHAYVVDCSNREEIYRSLNQVKKEVGDTVIVVNNAGTVYPADLLSTKDEEITKTFEVNILGHFW
ITKALLPSMMERNHGHIVTVASVCGHEGIPYLIPYCSSKFAAVGFHRGLTSELQALGKTGIKTSCLCPVFVNTGF
TKNPSTRLWPVLETDEVVRSIDGILTNNKMIFVPSYINIFLRLQFLPERASAILNRMQNIQFEAVVGHKIKMK

Important features:**Signal peptide:**

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-33 and 58-61

Short-chain alcohol dehydrogenase family protein

amino acids 165-202, 37-49, 112-122 and 210-219

134/615

FIGURE 133

CTGAGCGGGCGGTAGCATGGAGGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCGGCGCACTCGCTTT
CCAGCACCTCAACACGGGACTCGGACACGGAAGGTTTTCTTCTTGGGGAAGTAAAGGTGAAGCCAAGAACAGCAT
TACTGATTCCCAATGGATGATGTTGAAGTTGTTTATACAATTGACATTGAGAAATATATTCCATGCTATCAGCT
TTTGTAGCTTTTATAATTCTTCAGGCGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAA
TGTGGTAGGTTGGTACAAATCCGTCGTCATTGAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAAAAA
CTTGCAGGAGCATTTTTCAAACCAAGACCTTGTTTTCTGCTATTAACACCAAGTATAATAACAGAAAGCTGCTC
TACTCATCGACTGGAACATTCCTTATATAAACCTCAAAAAGGACTTTTTTCACAGGGTACCTTTAGTGGTTGCCAA
TCTGGGCGATGTCTGAACAACTGGGTTATAAACTGTATCAGGTTCTGTATGTCCACTGGTTTTAGCCGAGCAGT
ACAAACACACAGCTCTAAATTTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAAATGTATGC
TTCATTACAAGAGGAATTTAAAGAGTATATGCAAAAAAGTGGAAGACAGTGAACAAGCAGTAGATAAACTAGTAAA
GGATGTAAACAGATTAAAACGAGAAATTGAGAAAAGGAGAGGAGCACAGATTGAGGACGCAAGAGAGAAGAACAT
CCAAAAAGACCTCAGGAGAACATTTTTCTTGTGAGGCATTACGGACCTTTTTTCCAAATTCTGAATTTCTTCA
TTCATGTGTTATGTCTTTAAAAAATAGACATGTTTCTAAAAGTAGCTGTAACACCAACCACATCTCGATGTAGT
AGACAATCTGACCTTAATGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCACAAATCATTAA
GCATAAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTCGGTTGTTAGATACACAAGACAAACGATC
TAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAATGAGCAGCCCAGAAACAGATGAAGAAATTGA
AAAGATGAAGGGTTTTGGTGAATATTCACGGTCTCCTACATTTTGATCCTTTTAACTTACAAGGAGATTTTTTT
ATTTGGCTGATGGGTAAAGCCAAACATTTCTATTGTTTTTACTATGTTGAGCTACTTGACAGTAAGTTCATTTGTT
TTTACTATGTTACCTGTTTGCAGTAATACACAGATAACTCTTAGTGCAATTTACTTCACAAAGTACTTTTTCAAA
CATCAGATGCTTTTTATTTCCAAACCTTTTTTTCACCTTTCACTAAGTTGTTGAGGGGAAGGCTTACACAGACACA
TTCTTTAGAATTGAAAAAGTGAGACCAGGCACAGTGGCTCACACCTGTAATCCCAGCACTTAGGGAAGACAAGTC
AGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCCTGGGCAACGTATTGAGACCATGTCTATTAAAAATAAA
ATGGAAAAGCAAGAATAGCCTTATTTTCAAAATATGAAAGAAATTTATATGAAATTTATCTGAGTCATTAAAA
TTCTCCTTAAGTGATACTTTTTTAGAAGTACATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCAAT
AAATTTGCAAAACATCATCTAAATTTAAAAA

135/615

FIGURE 134

MEGESTSAVLSGFVLGALAFQHLNTDSDEGFLGGEVKGEAKNSITDSQMDDVEVVYITIDIQKYIPCYQLFSFYN
SSGEVNEQALKKILSNVKKNVVGWYKERRHSDQIMTFRERLLHKNLQEHFSNODLVFLLLTPSIITESCSTHRL
HSLYKPQKGLFHRVPLVVANLGMSEQLGYKTVSGSCMSTGFSRAVQTHSSKFFEEEDGSLKEVHKINEMYASLQEE
LKSICKKVEDSEQAVDKLVKDVNRLKREIEKRRGAQIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMS
LKNRHVSKSSCNYNHLDVVDNLTLMEHTDIPEASPASTPQIIKHKALDLDDRWFKRSRLDQDKRSKANTG
SSNQDKASKMSSPETDEEIEKMKGFGEYSRSPTE

136/615

FIGURE 135

GGCACAGCCGCGCGGGCGGAGGGCAGAGTCAGCCGAGCCGAGTCCAGCCGGACGAGCGGACCAGCGCAGGGCAGCC
CAAGCAGCGCGCAGCGAACGCCGCCGCCGCCACACCTCTGCGGTCCCCGCGCGCCCTGCCACCTTCCCTCC
TTCCCCGCGTCCCCGCTCGCCGGCCAGTCAGCTTCCCGGGTTCGCTGCCCGCGAAACCCCGAGGTACACAGCC
CGCGCCTCTGCTTCCCTGGGCGCGCGCCGCTCCACGCCCTCCTTCTCCCTGGCCCGCGCCTGGCACCGGGG
ACCGTTGCTGACGCGAGGGCCAGCTCTACTTTTCGCCCCGCGTCTCCTCCGCTGCTCGCCTCTTCCACCAACT
CCAACTCCTTCTCCCTCCAGTCCACTCGCTAGTCCCCGACTCCGCCAGCCCTCGGCCCGCTGCCGTAGCGCCGC
TTCGCGTCCGGTCCCAAAGGTGGGAACGCGTCCGCCCGGCCCGCACCATGGCACGGTTCGGCTTGCCCGCGCTT
CTCTGCACCTTGGCAGTGCTCAGCGCCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAAGTTGCTCGGAAGTGCGA
CGTCTTTTACGTGTCCAAAGGCTTCAACAAGAACGATGCCCCCTCCACGAGATCAACGGTGATCATTGAAGATC
TGTCCCCAGGGTCTACCTGCTGCTCTCAAGAGATGGAGGAGAAGTACAGCCTGCAAAGTAAAGATGATTTCAA
AGTGTGGTCAGCGAACAGTGAATCATTGCAAGCTGTCTTTGCTTACGTTACAAGAAGTTGATGAATTCCTC
AAAGAACTACTTGAAAATGCAGAGAAATCCCTGAATGATATGTTGTGAAGACATATGGCATTATACATGC
AATTCTGAGCTATTTAAAGATCTCTCGTAGAGTTGAAACGTTACTACGTGGTGGGAAATGTGAACCTGGAAGAA
ATGCTAAATGACTTCTGGGCTCGCCTCCTGGAGCGGATGTTCCGCCCTGGTGAACCTCCAGTACCACTTTACAGAT
GAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAGCCCTTCGGAGATGTCCCTCGCAAATTGAAGCTC
CAGGTTACTCGTGCTTTTGTAGCAGCCCGTACTTTCGCTCAAGGCTTAGCGGTTGCGGGAGATGTCTGAGCAAG
GTCTCCGTGGTAAACCCACAGCCAGTGTACCCATGCCCTGTTGAAGATGATCTACTGCTCCCACTGCCGGGGT
CTCGTGAAGCTGTGAAGCCATGTTACAACACTGCTCAAAACATCATGAGAGGCTGTTTGGCCAACCAAGGGGATCTC
GATTTTGAATGGAACAATTTATAGATGCTATGCTGATGGTGGCAGAGAGGCTAGAGGGTCTTTCAACATTGAA
TCGGTCATGGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAGGATAATAGTGTTCAGTGTCT
CAGAAGGTTTTCCAGGGATGTGGACCCCCAAGCCCTCCCAGCTGGACGAATTTCTCGTTCCATCTCTGAAAGT
GCCTTCAGTGCTCGCTTCAGACCACATCACCCCGAGGAACGCCCAACCACAGCAGCTGGCACTAGTTTGGACCGA
CTGGTTACTGATGTCAAGGAGAACTGAAACAGGCCAAGAAATCTGGTCTCCTCCCTCCGAGCAACGTTTGAAC
GATGAGAGGATGGCTGCAGGAAACGGCAATGAGGATGACTGTTGGAATGGGAAAGGCAAAAGCAGGTACCTGTTT
GCAGTGACAGGAAATGGATTAGCCCAACCAGGGCAACAACCCAGAGGTCCAGGTTGACACCAGCAAACAGACATA
CTGATCCTTCGTCAAATCATGGCTCTTCGAGTGATGACCAGCAAGATGAAGAATGCATACAATGGGAACGACGTG
GACTTCTTTGATATCAGTGATGAAAGTAGTGGAGAAGGAAGTGGAAAGTGGCTGTGAGTATCAGCAGTGCCCTTCA
GAGTTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGCCATGAGAAAGCCGACAGTGCTGGTGTCCGTCTC
GGGGCACAGGCCTACCTCCTCACTGTCTTCTGCATCTTGTTCCTGGTTATGCAGAGAGAGTGGAGATTAATTCTCA
AACTCTGAGAAAAAGTGTTTCATCAAAAAGTTAAAAGGCACCAAGTTATCACTTTTCTACCATCCTAGTGACTTTGC
TTTTTAAATGAATGGACAACAATGTACAGTTTTTACTATGTGGCCACTGGTTTAAGAAGTGTGACTTTGTTTTTC
TCATTCAAGTTTTGGGAGGAAAAGGGACTGTGCATTGAGTTGGTTCTTGCTCCCCAAACCATGTTAAACGTGGCT
AACAGTGTAGGTACAGAACTATAGTTAGTTGTGATTTGTGATTTTATCACTCTATTATTTGTTTGTATGTTTTT
TTCTCATTTCGTTTGTGGGTTTTTTTTTCCAACGTGATCTCGCCTTGTTCCTTACAAGCAAACAGGGTCCCTT
CTTGGCACGTAAACATGTACGTATTTCTGAAATATTAAATAGCTGTACAGAAGCAGGTTTTATTTATCATGTTATC
TTATTAAAAAGAAAAGGCCAAAAAGC

137/615

FIGURE 136

MAREGLPALLCTLAVLSAALLAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQGSTCCSQEMEKEY
SLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMFVKTYGHLYMQNSSELFKDLFVELKRIY
VVGNNLEEMLNDFWARLLERMFLVNSQYHFTDEYLECVSKYTEQLKPFQDVPRKLKLQVTRAFVAARTFAQGL
AVAGDVVSKVSVVNPTAQCTHALLKMIYCSHCRGLVTVKPCYNYCSNIMRGCLANQGDLD FEWNNFIDAMLMVAE
RLEGPFNIESVMDPIDVKISDAIMNMQDNSVQVSQKVFQGCQPPKPLPAGRISRISSESASFARFRPHHPEERPT
TAAGTSLDRLVTDVKEKLKQAKKFWSSLPSNVCNDERMAAGNGNEDDCWNGKGSRYLFAVTGNGLANQGNNPEV
QVDTSPDILILRQIMALRVMTSKMKNAYNGNDVDFDISDESSGEGSGSGCEYQQCPSEFDYNATDHAGKSANE
KADSAGVRPGAQAYLLTVFCILFLVMQREWR

138/615

FIGURE 137

CGGGGCTGTTGACGGCGCTGCGATGGCTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTTCTCTCAGTCGGA
CTTCCTGACGCCGCCAGTGGGCGGGGCCCTTGGGCCGTCGCCACCACTGTAGTCATGTACCCACCGCCGCCGCC
GCCGCTCATCGGGACTTCATCTCGGTGACGCTGAGCTTTGGCGAGAGCTATGACACAGCAAGAGTTGGCGGGCG
GCGCTCGTGTGGAGGAAATGGAAGCAACTGTGAGATTGCAGCGGAATATGATTCTCTTCTCCTTGCCTTTCT
GCTTTTCTGTGGACTCCTCTTCTACATCAACTTGGCTGACCATTGGAAAGCTCTGGCTTTAGGCTAGAGGAAGA
GCAGAAGATGAGGCCAGAAATTGCTGGGTAAAACCAGCAAATCCACCCGCTTACCAGCTCCTCAGAAGGCGGA
CACCGACCTGAGAATTACCTGAGATTTCTGACAGAAAGACACAAAGACACATCCAGCGGGGACCACCTCACCT
GCAGATTAGACCCCCAAGCCAAGACCTGAAGGATGGGACCCAGGAGGAGGCCACAAAAGGCAAGAGCCCCCTGT
GGATCCCCGCCCGGAAGGAGATCCGCAGAGGACAGTCATCAGCTGGAGGGGAGCGGTGATCGAGCCTGAGCAGGG
CACCGAGCTCCCTTCAAGAAGAGCAGAAGTGCCCAACCAAGCCTCCCTGCCACCGGCCAGGACACAGGGCACACC
AGTGCATCTGAATATCGCCAGAAGGGCGTGATTGACGCTTCTCCTGCATGCATGGAAAGGATACCGCAAGTTTGC
ATGGGGCCATGACGAGCTGAAGCCTGTGTCCAGGTCTTTCAGTGAGTGGTTTGGCCTCGGTCTCACACTGATCGA
CGCGCTGGACACCATGTGGATCTTGGGTCTGAGGAAAGAATTTAGGAAAGCCAGGAAGTGGGTGTGAAGAAGTT
ACACTTTGAAAAGGACGTGGACGTCAACCTGTTTGGAGAGCAGATCCGCATCTTGGGGGGCTCCTGAGTGCCTA
CCACTGTCTGGGGACAGCCTCTTCTGAGGAAAGCTGAGGATTTTGGAAATCGGCTAATGCCTGCCTTCAGAAC
ACCATCCAAGATTCTTACTCGGATGTGAACATCGGTACTGGAGTTGCCACCCGCCACGGTGGACCTCCGACAG
CACTGTGGCCGAGGTGACCAGCATTGAGCTGGAGTTCCGGGAGCTCTCCCGTCTCACAGGGGATAAGAAGTTTCA
GGAGGCAGTGGAGAAGGTGACACAGCACATCCACGGCCTGTCTGGGAAGAAGGATGGGCTGGTGCCCATGTTTCAT
CAATACCCACAGTGGCCTCTTCAACCCACCTGGGCGTATTACGCTGGGCGCCAGGGCCGACAGCTACTATGAGTA
CCTGTGAAGCAGTGGATCCAGGGCGGGAAGCAGGAGACACAGCTGCTGGAAGACTACGTGGAAGCCATCGAGGG
TGTCAGAACGCACCTGCTGCGGCACTCCGAGCCCAAGTAACTCAGCTCACCCTTGTGGGGGAGCTTGCCACGGCCGCTT
CAGTGCCAAGATGGACCACCTGGTGTGCTTCTGCCAGGGACGCTGGCTCTGGGCGTCTACCACGGCCTGCCCGC
CAGCCACATGGAGCTGGCCAGGAGCTCATGGAGACTTGTACCAGATGAACCGGCAGATGGAGACGGGGCTGAG
TCCCGAGATCGTGCACCTTCAACCTTTACCCCCAGCCGGGCGCTCGGGACGTGGAGGTCAAGCCAGCAGACAGGCA
CAACCTGCTGCGGCCAGAGACCGTGGAGAGCCTGTTCTACCTGTACCGCGTCACAGGGGACCGCAAAATACCAGGA
CTGGGGCTGGGAGATTCTGCAGAGCTTCAGCCGATTACACGGGTCCCTCGGGTGGCTATTCTTCCATCAACAA
TGTCAGGATCCTCAGAAGCCCGAGCCTAGGGACAAGATGGAGAGCTTCTTCTGGGGGAGACGCTCAAGTATCT
GTTCTGTCTCTTCTCCGATGACCCAAACCTGCTCAGCCTGGACGCCTACGTGTTCAACACCGAAGCCACCCCTCT
GCCTATCTGGACCCCTGCCATAGGGTGGATGGCTGCTGGTGTGGGGACTTCGGGTGGGCAGAGGCACCTTGCTGGG
TCTGTGGCATTTCCTAAGGGGCCACGTAGCACCAGGCAACCGCCAAGTGGCCAGGCTCTGAATGGCTCTGGGCT
CCTCCTCGTCTCTGCTTTAATCAGGACACCGTGAGGACAAGTGAGGCCGTCAGTCTTGGTGTGATGCGGGGTGGG
CTGGGCGCTGGAGCCTCCGCCTGCTTCTCCAGAAGACACGAATCATGACTCACGATTGCTGAAGCCTGAGCAG
GTCTCTGTGGGCCGACCAGAGGGGGGCTTCGAGGTGGTCCCTGGTACTGGGTGACCGAGTGGACAGCCAGGGT
GCAGCTCTGCCCGGGCTCGTGAAGCCTCAGATGTCCCAATCCAAGGGTCTGGAGGGGCTGCCGTGACTCCAGAG
GCCTGAGGCTCCAGGGCTGGCTCTGGTGTTCACAAAGCTGGACTCAGGGATCCTCCTGGCCGCCCGCAGGGGGCT
TGGAGGGCTGGACGCAAGTCCGTCTAGCTCACGGGCCCTCCAGTGGAATGGGTCTTTTCGGTGGAGATAAAAG
TTGATTGCTCTAACCGCAA

139/615

FIGURE 138

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56529
><subunit 1 of 1, 699 aa, 1 stop
><MW: 79553, pI: 7.83, NX(S/T): 0
MAACEGRRSGALGSSQSDFLTPPVGGAPWAVATTVMYPPPPPPPHRDFISVTLSEGESYDNSKSWRRRSCWRKW
KQLSRLQRNMILFLLAFLLFCGLLFYINLADHWKALAFRLSEEQMRPEIAGLKPANPPVLPAPQKADTDPENLP
EISSQKTQRHIQRGPPHLQIRPPSQDLKDGTOEEATKRQEAPVDPRPEGDPQRTVISWRGAVIEPEQGTLPSSR
AEVPTKPPLPPARTQGTPVHLNRYQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSEWFGGLGLTLIDALDTMWI
LGLRKEFEEARKWVSKLHFEKDVDVNLFEISTIRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKIPYS
DVNIGTGVAPPRWTS DSTVAEVTSIQLEFRELRLTGDKKQEAQVEKVTQHIHGLSGKKDGLVPMFINTHSGLF
THLGVFTLGARADSYEYLLQWIQGGKQETQLLEDYVEAIEGVRTHLRLHSEPSKLTFFVGEAHGREFSKMDHL
VCFLEPGLALGVYHGLPASHMELAQELMETCYQMNQMETGLSPEIVHFNLYPQPGRRDVEVKPADRNLLRPET
VESLFYLYRVTGDRKYQDWGWEILQSFSTRVPSGGYSSINNVDQPKPEPRDKMESFFLGETLKYLFLLFSDD
PNLLSLDAYVFNTAEHPLPIWTPA
```

Important features of the protein:

Transmembrane domain:

amino acids 21-40 and 84-105 (type II)

140/615

FIGURE 139

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCTGACCTGAGTCATC
CCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAAGCAACTTACAGCTGCACCGACAGTTG
CGATGAAAGTTCTAATCTCTTCCCTCCTCCTGTTGCTGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGA
ATCCAGGGGTCGCCAGAGGCCACAGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCAAGAAT
GTGAGTGCAAAGATTGGTTCTGAGAGCCCCGAGAAGAAAATTCATGACAGTGTCTGGGCTGCCAAGAAGCAGT
GCCCCTGTGATCATTTCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGAAAGCCAAACAAGCATT
CCAGAGCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTTTGCTCTGCCTTTGTAGGAGCTCTGAGCGC
CCACTCTTCCAATTAAACATTCTCAGCCAAGAAGACAGTGAGCACACCTACCAGACACTCTTCTTCTCCACCTC
ACTCTCCCACTGTACCCACCCCTAAATCATTCCAGTGCTCTCAAAAAGCATGTTTTTCAAGATCATTTGTTTGT
TGCTCTCTAGTGTCTTCTTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCCTTACCCAGGCTTAGGCTTAATTAC
CTGAAAGATTCCAGGAACTGTAGCTTCCTAGCTAGTGTCAATTAACCTTAAATGCAATCAGGAAAGTAGCAAAC
AGAAGTCAATAAATATTTTTAAATGTCAAAAAAAAAAAAAAAAAA

141/615

FIGURE 140

MKVLISLLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRRKFMTVSGLPKKQC
PCDHEFGNVKKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL

142/615

FIGURE 141

AATGGCTGTCTTAGTACTTCGCCTGACAGTTGTCCTGGGACTGCTTGTCTTATTCCTGACCTGCTATGCAGACGA
CAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCAAAGCCAGACTTCCCCAAATTCCTAAG
CCTCCTGGGCACAGAGATCATTGAGAATGCAGTCGAGTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTTAT
GGAATTTGATGATAATGAAGGAAAACATTCATAAGTGAACATCCTCAGGACACACCCATGTGGCTCCTGGACAA
TCCAAGAGCAGCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAACTCC
CAACGAGTTCTCAGGATTCAGGCTCTGGCTTCAACCAAACAGAACTCATTTTGAACACCCTGACTGCATTTTGC
TTTGTAGAAAGTTAGAATAAATATGGCGCTTGGGATCACATAGTTGATGGAGAGGAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

143/615

FIGURE 142

MAVLVLRRLTVVLGLLVFLTCYADDKPKDPDDKPDGKDPKDFPKFLSLLGTEIIEENAVEFILRSMRSTGFM
EFDDNEGKHSSK

144/615

FIGURE 143

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCTCAGAGCTGGTCTG
CCATGGACATCCTGGTCCCCTCCTGCAGCTGCTGGTGCTGCTTCTTACCCTGCCCTGCACCTCATGGCTCTGC
TGGGCTGCTGGCAGCCCCCTGTGCAAAAGCTACTTCCCCTACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCA
AGATGGAGAGCAAGAAACGGGAGCTCTTCAGCCAGATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTAC
TGGAGCTGGGCTGCGGAACCGGAGCCAACCTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACCCAA
ATCCCCACTTTGAGAAGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATATGAGCGGTTTGTGGTGG
CTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGTGGTGGTCTGCACTCTGGTGTCTGTCTGTG
TGCAGAGCCCCAAGGAAGGTCTGCAAGAGGTCCGGAGAGTACTGAGACCGGGAGGTGTGCTCTTTTCTGGGAGC
ATGTGGCAGAACCATATGGAAGCTGGGCCTTCATGTGGCAGCAAGTTTTCGAGCCCACCTGGAACACATTGGGG
ATGGCTGCTGCCTCACCAGAGAGACCTGGAAGGATCTTGAGAACGCCAGTTCTCCGAAATCCAATGGAACGAC
AGCCCCCTCCCTTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTCAAACAATCTTTCCCAAGCT
CCAAGGCACTCATTTGCTCCTTCCCCAGCCTCCAATTAGAACAAGCCACCCACCAGCCTATCTATCTTCCACTGA
GAGGGACCTAGCAGAATGAGAGAAGACATTCATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGC
AATCTCTAACTTCAATCCCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGGAAACACTAGG
ACCTGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCTTCCCAATGTTGTCCCTTTCCTT
CGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACACCCATGCGTCTCTAGGAACTGGTCACAAAAG
TCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCCTCTCTCCCCACTACCACCTTCTTCTGAGCTGGGGGCA
CCAGGGAGAATCAGAGATGCTGGGGATGCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTTCTCAAATATTTTT
TAATAAATAGACGAAACCACG

145/615

FIGURE 144

MDILVPLLQLLVLLLTLPPLHLMALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSSQIKGLTGASGKVALL
ELGCGTGANFQFYPPGCRVTCCLDPNPHFEKFLTKSMAENRHLQYERFVVAPGEDMRQLADGSMDVVVCTLVLCVS
QSPRKVLQEVRRVLRPGGVLFWEHVAEPYGSWAFMWQQVFETWKHIGDGCCLTRETWKDLENAQFSEIQMERQ
PPPLKWLVPVGPHIMGKAVKQSFPSKALICSFPSLQLEQATHQPIYLPRLGT

146/615

FIGURE 145

GTGGGATTTATTTGAGTGCAAGATCGTTTTCTCAGTGGTGGTGGAAAGTTGCCTCATCGCAGGCAGATGTTGGGGC
TTTGTCCGAACAGCTCCCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAACTAATATTTATATGACAGAAGAAAA
AGATGTCATTCCGTAAAGTAAACATCATCATCTTGGTCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGCACCATA
ACTTCCTCAGCTTGAGCAGTTTGTTAAGGAATGAGGTTACAGATTGAGGAATTGTAGGGCCTCAACCTATAGACT
TTGTCCCAAATGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCCCTGTGGTCATCGCTGCATCTGAAG
ACAGGCTTGGGGGGGCCATTGCAGCTATAAACAGCATTGAGCACAACACTCGCTCCAATGTGATTTTCTACATTG
TTACTCTCAACAATACAGCAGACCATCTCCGGTCCTGGCTCAACAGTGATTCCCTGAAAAGCATCAGATACAAAA
TTGTCAATTTTGACCTAAACTTTTGGAAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGGAATCCATGAAACCTT
TAACCTTTGCAAGGTTCTACTTGCCAATCTGGTTCCCAGCGCAAAGAAGGCCATATACATGGATGATGATGTAA
TTGTGCAAGGTGATATTCTTGCCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATT
GTGATTGAGCCTCTACTAAAGTTGTCATCCGTGGAGCAGGAAACCAGTACAATTACATTGGCTATCTTGACTATA
AAAAGGAAAGAATTGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGCAAAACC
TGACGGAATGGAAACGACAGAATATAACTAACCAACTGGAAAAATGGATGAAACTCAATGTAGAAGAGGGACTGT
ATAGCAGAACCCTGGCTGGTAGCATCACAACCTCCTCTGCTTATCGTATTTTATCAACAGCACTCTACCATCG
ATCCTATGTGGAATGTCCGCCACCTTGGTTCCAGTGCTGGAAAACGATATTACCTCAGTTTGTAAGGCTGCCA
AGTTACTCCATTGGAATGGACATTTGAAGCCATGGGGAAGGACTGCTTCATATACTGATGTTTGGGAAAAATGGT
ATATTCCAGACCCAACAGGCAAATTCACCTAATCCGAAGATATACCGAGATCTCAAAACATAAAGTGAACAGAA
TTTGAAGTGTAAAGCAAGCATTTCTCAGGAAGTCTGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTC
AATGCCTATCGGTAGCAAGCCATGGAAAAAGATGTGTCAGCTAGGTAAAGATGACAAACTGCCCTGTCTGGCAGT
CAGCTTCCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTTCCTTACTACAATGCTG
AATGACTGGAAAGAAGAACTGATATGGCTAGTTCAGCTAGCTGGTACAGATAATTCAAAACTGCTGTTGGTTTTA
ATTTTGTAACCTGTGGCCTGATCTGTAAATAAACTTACATTTTTTC

147/615

FIGURE 146

MSFRKVNIIILVLAVALFLLVLHHNFLSLSSLLRNEVTDSGIVGQPIDFVPNALRHAVDGRQEEIPVVIAASED
RLGGAIAAINSIQHNTSRNVIFYIVTLNNTADHLRSWLNSDSLKSIRYKIVNFDPKLLEGKVKEDPDQGESMKPL
TFARFYLPILVPSAKKAIYMDDDVIVQGDILALYNTALKPGHAAAFSEDCDSASTKVIVIRGAGNQYNYIGYLDYK
KERIRKLSMKASTCSFNPGVFVANLTEWKRQNTNQLKWMKLNVEEGLYSRTLAGSITTPPLLIVFYQQHSTID
PMWNVRLGSSAGKRYSPQFVKAALKLHWNGHLKPWGRTASYTDVWEKWYIPDPTGKFNLIRRYTEISNIK

148/615

FIGURE 147

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCAGTTCCTCCAAGCA
AGTCATTTCCCTTATTTAACCAGATGTGTCCCTCAAACACCTGAGTGCTACTCCCTATTTGCATCTGTTTTGATAA
ATGATGTTGACACCCCTCCACCGAATTCCTAAGTGGGAATCATGTCGGGAAGAGATACAATCCTTGGCCTGTGTATCC
TCGCATTAGCCTTGTCTTTGGCCATGATGTTTACCTTCAGATTTCATCACCACCCTTCTGGTTCACATTTTCATTT
CATTGGTTATTTTGGGATTGTTGTTTGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACCTCA
GCATAGAATTGGACACAGAAAGGGAAAATATGAAGTGGCTGCTGGGGTTTGTCTATCGTATCCACAGGCATCACGG
CAGTGCTGCTCGTCTTGATTTTTGTTCTCAGAAAGAGAATAAAATTGACAGTTGAGCTTTTCCAAATCACAAATA
AAGCCATCAGCAGTGCTCCCTTCCTGCTGTCCAGCCACTGTGGACATTTGCCATCCTCATTTTCTTCTGGGTCC
TCTGGGTGGCTGTGCTGCTGAGCCTGGGAAGTGCAGGAGCTGCCAGGTTATGGAAGGCGGCCAAGTGGGAATATA
AGCCCCTTTCGGGCATTTCGGTACATGTGGTCGTACCATTTAATTGGCCTCATCTGGACTAGTGAATTCATCCTTG
CGTGCCAGCAAATGACTATAGCTGGGGCAGTGGTTACTTGTATTTCAACAGAAGTAAAAATGATCCTCCTGATC
ATCCCATCCTTTCTCTCTCTCTCCATTCTCTTCTTCTACCATCAAGGAACCGTTGTGAAAGGGTCATTTTAAATCT
CTGTGGTGAGGATTCGAGAAATCATTTGTCTGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCAATTGT
CCAGGTACCTGTTCCGATGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAATG
CATATACTACAACCTGCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAAATCTTGTCCAAGA
ACTCAAGTCACTTTACATCTATTAAGTCTTTGGAGACTTCATAATTTTTCTAGGAAAGGTGTTAGTGGTGTGTT
TCACTGTTTTTGGAGGACTCATGGCTTTTAACTACAATCGGGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGG
TAGCTTTTTTTGCCACTTAGTAGCCCATAGTTTTTTATCTGTGTTTGAAACTGTGCTGGATGCATTTTCCTGT
GTTTTGCTGTTGATCTGGAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTT
TCGTAAAAAGGAGCAACAAATTAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAAGGAATGAGGAGGGAA
CAGAACTCCAGGCCATTGTGAGATAGATACCCATTTAGGTATCTGTACCTGGAAAACATTTCTTCTAAGAGCCA
TTTACAGAATAGAAGATGAGACCACTAGAGAAAAGTTAGTGAATTTTTTTTTTAAAGACCTAATAAACCCCTATTCTCCTCAAAA

149/615

FIGURE 148

MSGRDTILGLCILALSLAMMFTFRFITLLVHIFISLVILGLLFVCGVLWWLYDYTNDSLIELDTERENMKC
VLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFLFQPLWTFAILIFFWVLWVAVLLSLGTAG
AAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFILACQQMTIAGAVVTCYFNRSKNDDPDHPILSSLSILFFY
HQGTVVKGSFLISVVRIPRIIVMYMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFC
TSAKDAFKILSKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAFOVWAVPLLLVAFFAYLVHSFL
SVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRNEEGTELQAIVR

FIGURE 149

[illegible]

151/615

FIGURE 150

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKCPAGCQDPKYHVYG
TDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSLSLPRWRESFIVLESKPKKGVITYPSAL
TYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMQLLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSQE
MDLWSTATYTTSSQNRPRADPGIQRQDPGSAAFQKPVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDG
STSIGKRRRFRIQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHTNRSRDLKTAIEKITQRGGLSNVGRA
ISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAENKQYVVEPNFANKAV
CRTNGFYSLHVQSWFGLHKTLOPLVKRVCDTDRLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQFVTNLTKF
EISDTDTRIGAVQYTYEQRLFEFGFDKYSSKPDILNAIKRVGYWSSGGTSTGAINFALQLFKKSKPNKRKLMILI
TDGRSYDDVRIPAMAAHLKGVITYAIGVAWAAQEELEVIATHPARDHSFFVDEFDNLHQYVPRIIQNICTEFNSQPRN

152/615

FIGURE 151

CAGGATGAACTGGTTGCAGTGGCTGCTGCTGCTGCGGGGGCGCTGAGAGGACACGAGCTCTATGCGCTTTCCGGCT
GCTCATCCCGCTCGGCCTCCTGTGCGCGCTGCTGCCTCAGCACCATGGTGCGCCAGGTCCCGACGGCTCCGCGCC
AGATCCCGCCCACTACAGTTTTTCTCTGACTCTAATTGATGCACTGGACACCTTGCTGATTTTGGGGAATGTCTC
AGAATTCCAAAGAGTGGTTGAAGTGCTCCAGGACAGCGTGGACTTTGATATTGATGTGAACGCCTCTGTGTTTGA
AACAAACATTTCGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGGTGGAAGTAGAGGC
TGGATGGCCCTGTTCCGGGCCCTCTCCTGAGAATGGCTGAGGAGGCGGCCCGAAAACCTCTCCAGCCTTTTCAGAC
CCCCACTGGCATGCCATATGGAACAGTGAACCTTACTTCATGGCGTGAACCCAGGAGAGACCCCTGTCACTGTAC
GGCAGGGATTGGGACCTTCATTGTTGAATTTGCCACCTGAGCAGCCTCACTGGTGACCCGGTGTTTGAAGATGT
GGCCAGAGTGGCTTTGATGCGCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTCCGCAACCACATTGATGTGCT
CACTGGCAAGTGGGTGGCCAGGACGCAGGCATCGGGGCTGGCGTGGACTCCTACTTTGAGTACTTGGTGAAAGG
AGCCATCCTGCTTCAGGATAAGAAGCTCATGGCCATGTTCTAGAGTATAACAAAGCCATCCGGAACCTACACCCG
CTTCGATGACTGGTACCTGTGGGTTTCAGATGTACAAGGGGACTGTGTCCATGCCAGTCTTCCAGTCCCTGGAGGC
CTACTGGCCTGGTCTTCAGAGCCTCATTGGAGACATTGACAATGCCATGAGGACCTTCTCAACTACTACACTGT
ATGGAAGCAGTTTGGGGGGCTCCCGGAATTCTACAACATTCCTCAGGGATACACAGTGGAGAAGCGAGAGGGCTA
CCCACTTCGCGCCAGAACTTATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGGATCCCAACCTCCTAGAACT
CGGAAGAGATGCTGTGGAATCCATTGAAAAAATCAGCAAGGTGGAGTGCGGATTTGCAACAATCAAAGATCTGCG
AGACCACAAGCTGGACAACCGCATGGAGTCGTTCTTCTGGCCGAGACTGTGAAATACCTCTACCTCCTGTTTGA
CCCAACCAACTTCATCCACAACAATGGGTCCACCTTCGACGCGGTGATCACCCCTATGGGGAGTGCATCCTGGG
GGCTGGGGGTACATCTTCAACACAGAAGCTCACCCATCGACCTTGCCGCCCTGCACTGCTGCCAGAGGCTGAA
GGAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGGAATTCTACTCTCTCAAACGGAGCAGGTGAAAATTTTCAGAA
AAACACTGTTAGTTCGGGGCCATGGGAACCTCCAGCAAGGCCAGGAACACTCTTCTCACCAGAAAACCATGACCA
GGCAAGGGAGAGGAAGCCTGCCAAACAGAAGGTCCCACTTCTCAGCTGCCCCAGTCAGCCCTTCACCTCCAAGTT
GGCATTACTGGGACAGGTTTTCTAGACTCCTCATAAACCACTGGATAATTTTTTTATTTTTTTTATTTTTTTGAGGCT
AAACTATAATAAATTGCTTTTGGCTATCATAAAA

153/615

FIGURE 152

MPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYFSLSLTLDALDTLLILGNVSEFQRVVEVLQDSVDFDIDVN
ASVFETNIRVVGGLLSAHLSSKKAGVEVEAGWPCSGPLLRMAEEAARKLLPAFQTPTGMPYGTVNLLHGVNPGET
PVTCTAGIGTFIVEFATLSSLTGDPVFEDVARVALMRLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFE
YLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDWYLWVQMYKGTVSMFVQSLEAYWPGLSLIGDIDNAMRTFL
NYTIVWKQFGGLPEFYNIPOGYTVEKREGYPLRPELIESAMYLYRATGDPDTLLELGRDAVESIEKISKVECGFAT
IKDLRDHKLDNRMESFFLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGYIFNTEAHPIDLAALHC
CQRLKEEQWEVEDLMREFYSLKRSRSKFQKNTVSSGPWEPPARPGTLFSPENHDQARERKPAKQKVPLLSQPSQP
FTSKLALLGQVFLDSS

154/615

FIGURE 153

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTGGGAGGGGGCAGGATGGGAGGGAAAGTGAAGAAAACA
GAAAAGGAGAGGGACAGAGGCCAGAGGACTTCTCATACTGGACAGAAACCGATCAGGCATGGAACTCCCCCTTCGT
CACTCACCTGTTCTTGCCCCCTGGTGTTCCTGACAGGTCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACG
CCTATTCCCAGGGCCACCAGAAGCTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGACAGCGATGGAT
GCTGGTGGGCGCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTTTATCGCTGCCCTGTAGGGGGGGC
CCACAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTACCAACTGGGAAATTCATCTCATCCTGCTGTGAATAT
GCACCTGGGGATGTCTCTGTTAGAGACAGATGGTGATGGGGGATTTCATGGTGAGCTAAGGAGAGGGTGGTGGCAG
TGCTCTGAAGGTCCATAAAAGAAAAAGAGAAGTGTGGTAAGGGAAAATGGTCTGTGTGGAGGGGTCAAGGAGT
TAAAAACCCTAGAAAGCAAAAGGTAGGTAATGTCAGGGAGTAGTCTTCATGCCTCCTTCAACTGGGAGCATGTTT
TGAGGGTGCCCTCCCAAGCCTGGGAGTAACATAATTTCCCCCATCCCCAGGCCTGTGCCCTCTCTGGTCTCGTGCT
TGTTGGCAGCTCTGTCTTCAGTTCTGGGATATGTGCCCGTGTGGATGCTTCATTCCAGCCTCAGGGAAGCCTGGCA
CCCCTGCCCCAAGTGTAGCCAGAGGAAGGCTGAGTACTTGGTTCCAGAGGAGATACTGGGTGGGAAAAAGATG
GGGCAAAGCGGTATGATGCCTGGCAAAGGGCCTGCATGGCTATCCTCATTGCTACCTAATGTGCTTGCAAAAGCT
CCATGTTTCCTAACAGATTTCAGACTCCTGGCCAGGTGTGGTGGCCACACCTGTAATTTCTAGCACTTTGGGAGGC
CAAGGTGGGCAGATCACTTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAACTCCATCTCTACTAA
AAAAAAAAAATAACAAAATTAGCTGGGTGCGCTAGTGCATGCCTGTAATCTCATCTACTCGGGAGGCTAAGACA
GGAGACTCTCACTTCAACCCAGGAGGTGGAGGTTGCGGTGAGCCAAGATTGTGCCTCTGCACTCTAGCGTGGGTG
ACAGAGTAAGCGAGACTCCATCTCAAAAATAATAATAATAATTTCAGACTCCTTATCAGGAGTCCATGATCTG
GCCTGGCACAGTAACATGCCTGTAATCCCAACATTTTGGGAGGCCAACGCAGGAGGATTGCTTGAGGTCTGGA
GGTTTGAGACCAGCCTGGGCAACATAGAAAGACCCATCTCTAAATAAATGTTTTAAAAAT

155/615

FIGURE 154

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57039
><subunit 1 of 1, 124 aa, 1 stop
><MW: 13352, pI: 5.99, NX(S/T): 1
MELPFVTHLFLPLVFLTGILCSPFNLDEHHPRLFPGPPEAEFGYSVLQHVGGGQRWMLVGAPWDGPSGDRRGDVYR
CPVGGAHNAPCAKGHLGDYQLGNSSHPAVNMHLGMSLLETGDGGGFMVS
```

Important features:**Signal peptide:**

amino acids 1-22

Cell attachment sequence.

amino acids 70-73

N-glycosylation site.

amino acids 98-101

Integrins alpha chain proteins

amino acids 67-81

156/615

FIGURE 155

CGGAGCTCCGGGTGCTGTGGCCCCGGCCTTGGCGGGGCGGCCTCCGGCTCAGGCTGGCTGAGAGGCTCCCAGCTGC
AGCGTCCCCGCCCCGCTCCTCGGGAGCTCTGATCTCAGCTGACAGTGCCCTCGGGGACCAACAGCCTGGCAGG
GTCTCACTTTTGTGCCCAGGCTGGAGTTCAGTGCCATGATCATGGTTTACTGCAGCCTTGACCTCCTGGGTTCAA
GCGATCCTGCTGAGTAGCTGGGACTACAGGACAAAATTAGAAGATCAAAATGGAAAATATGCTGCTTTGGTTGAT
ATTTTTACCCCTGGGTGGACCCCTCATTGATGGATCTGAAATGGAATGGGATTTTATGTGGCACTTGAGAAAGGT
ACCCCGGATTGTCAGTGAAAGGACTTTCCATCTCACCAGCCCCGATTTGAGGCAGATGCTAAGATGATGGTAAA
TACAGTGTGTGGCATCGAATGCCAGAAAGAACTCCCACTCCCAGCCTTTCTGAATTGGAGGATTATCTTTCTTA
TGAGACTGTCTTTGAGAATGGCACCCGAACCTTAACCAGGGTGAAAGTTCAGATTTGGTTCTTGAGCCGACTCA
AAATATCACCACAAAGGGAGTATCTGTAGGAGAAAGAGACAGGTGTATGGCACCGACAGCAGGTTGAGCATCTT
GGACAAAAGGTTCTTAACCAATTTCCCTTTGAGCAGCTGTGAAGCTTTCCACGGGCTGTAGTGGCATTCTCAT
TTCCCTCAGCATGTTCTAACTGCTGCCCCTGTGTTTATGATGGAAGGACTATGTCAAAGGGAGTAAAAAGCT
AAGGGTAGGGTTGTTGAAGATGAGGAATAAAAGTGGAGGCAAGAAACGTCGAGGTTCTAAGAGGAGCAGGAGAGA
AGCTAGTGGTGGTGACCAAAGAGAGGGTACCAGAGAGCATCTGCAGGAGAGAGCGAAGGGTGGGAGAAGAAGAAA
AAAATCTGGCCGGGGTTCAGAGGATTGCCGAAGGGAGGCCCTTCTTTGAGTGGACCCGGGTCAAGAATACCCACAT
TCCGAAGGGCTGGGCACGAGGAGGCATGGGGGACGCTACCTTGGACTATGACTATGCTCTTCTGGAGCTGAAGCG
TGCTCACAAAAAGAAATACATGGAACCTGGAATCAGCCCAACGATCAAGAAAATGCCTGGTGGAATGATCCACTT
CTCAGGATTGATAACGATAGGGCTGATCAGTTGGTCTATCGGTTTTGCAAGTGTGTCCGACGAATCCAATGATCT
CCTTTACCAATACTGCGATGCTGAGTCGGGCTCCACCGGTTCCGGGGTCTATCTGCGTCTGAAAGATCCAGACAA
AAAGAATTGGAAGCGCAAATCATTGCGGTCTACTCAGGGCACCAGTGGGTGGATGTCCACGGGGTTCAGAAGGA
CTACAACGTTGCTGTTGCGCATCACTCCCTAAAATACGCCAGATTGCTCTGGATTACAGGGGAACGATGCCAA
TTGTGCTTACGGCTTAACAGAGACCTGAAACAGGGCGGTGTATCATCTAAATCACAGAGAAAACAGCTCTGCTTA
CCGTAGTGAGATCACTTCATAGGTTATGCCTGGACTTGAAGTCTGTCAATAGCATTTCAACATTTTCAAAATCA
GGAGATTTTCGTCCATTTAAAAATGTATAGGTGCAGATATTGAACTAGGTGGGCACTTCAATGCCAAGTATAT
ACTCTTCTTTACATGGTGATGAGTTTCATTTGTAGAAAAATTTGTTGCCCTTCTTAAAAATTAGACACACTTTAA
ACCTTCAAACAGGTATTATAAATAACATGTGACTCCTTAATGGACTTATTCTCAGGGTCTACTCTAAGAAGAAT
CTAATAGGATGCTGGTTGTGTATTAAATGTGAAATGTCATAGATAAAGGTAGATGGTAAAGCAATTAGTATCAGA
ATAGAGACAGAAAGTTACAACAGTTTGTACTACTCTGAGATGGATCCATTGAGCTCATGCCCTCAATGTTTAT
ATTGTGTTATCTGTTGGGTCTGGGACATTTAGTTTAGTTTTTTGAAGAATTACAAATCAGAAGAAAAAGCAAGC
ATTATAAACAAAATAAATACTGTTTACTGCTTTAAGAAATAACAATTACAATGTGTATTATTTAAAAATGGGA
GAAATAGTTTGTCTATGAAATAAACCTAGTTTAGAAATAGGGAAGCTGAGACATTTTAAGATCTCAAGTTTTTA
TTTAATAATACTCAAAATATGGACTTTTCATGTATGCATAGGGAAGACACTTCACAAATTATGAATGATCATGT
GTTGAAAGCCACATTATTTTATGCTATACATTCTATGTATGAGGTGCTACATTTTATAGGACAAAGAATTCTGTAA
TCTTTTTCAAGAAAGAGTCTTTTCTCCTTGACAAAATCCAGCTTTTGTATGAGGACTATAGGGTGAATTCCTG
ATTAGTAATTTTAGATATGTCCTTTCCTAAAAATGAATAAAATTTATGAATATGA

157/615

FIGURE 156

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57253
<subunit 1 of 1, 413 aa, 1 stop
<MW: 47070, pI: 9.92, NX(S/T): 3
MENMLLWLIFFTPGWTLIDGSEMEWDFMWHLRKVPRIVSERTFHLTSPAFAEADAKMMVNTVCGIECQKELPTPSL
SELEDYLSYETVFEENGTRTLTRVKVQDLVLEPTQNITTKGVSVRRKRQVYGTDSRFSILDKRFLTNFPFSTAVKL
STGCSGILISPQHVLTAAHCVHDGKDYVKGSKKLRVGLLKMRNKSGGKKRRGSKRSRREASGGDQREGTREHLQE
RAKGGRRRKKSGRGQRIAEGRPSFQWTRVKNTHIPKGWARGGMDATLDYDYALLELKRAHKKKYMELGISPTIK
KMPGGMIHFSGFDNDRADQLVYRFCSVDESNDLLYQYCDAESGSTGSGVYLRLKDPDKKNWKRKI IAVYSGHQW
VDVHGVQKDYNVAVRITPLKYAQICLWIHGNDANCAYG
```

Important features:**Signal peptide:**

amino acids 1-16

N-glycosylation sites.

amino acids 90-93, 110-113 and 193-196

Glycosaminoglycan attachment site.

amino acids 236-239

Serine proteases, trypsin family, histidine active site.

amino acids 165-170

158/615

FIGURE 157

GGGACCCATGCGGCCGTGACCCCCGGCTCCCTAGAGGCCAGCGCAGCCGAGCGGACAAAGGAGCATGTCCGCG
CCGGGGAAGGCCCGCTCCTCCGGCCGCCATAAGGCTCCGGTCCGCGCTGGGCCCGCGCCGCTCCTGCCCCGCCG
GGCTCCGGGGCGGCCCGCTAGGCCAGTGCGCCGCGCTCGCCCCGAGGCCCGGCCCGCAGCATGGAGCCACCC
GGACGCCGGCGGGCCGCGCAGCCGCGCTGTTGCTGCCGCTCTCGCTGTTAGCGCTGCTCGCGCTGCTGGGA
GGCGGCGCGCGGCCGCGCGCGCTGCCCGCCGGCTGCAAGCACGATGGGCGGCCCGAGGGGCTGGCAGG
GCGGCGGGCGGCCGAGGGCAAGGTGGTGTGCAGCAGCCTGGAACTCGCGCAGGTCTGCCCCAGATACTCTG
CCCAACCGCACGGTCACCCTGATTCTGAGTAACAATAAGATATCCGAGCTGAAGAATGGCTCATTTTCTGGGTTA
AGTCTCCTTGAAAGATTGGACCTCCGAAACAATCTTATTAGTAGTATAGATCCAGGTGCCTTCTGGGGACTGTCA
TCTCTAAAAAGATTGGATCTGACAAACAATCGAATAGGATGTCTGAATGCAGACATATTTGAGGACTCACCAAT
CTGGTTCGGCTAAACCTTTTCGGGAATTTGTTTTCTTCATTATCTCAAGGAACTTTTGATTATCTTGCGTCATTA
CGGTCTTTGGAATTCCAGACTGAGTATCTTTGTGTGACTGTAACTACTGTGGATGCATCGCTGGGTAAAGGAG
AAGAACATCAGGTACGGGATACCAGGTGTGTTTATCCTAAGTCACTGCAGGCCCAACCAGTCACAGGCGTGAAG
CAGGAGCTGTGACATGCGACCCCTCCGCTTGAATTGCCGTCTTTCTACATGACTCCATCTCATCGCCAAGTTGTG
TTTGAAGGAGACAGCCTTCCTTTCCAGTGCATGGCTTCATATATTGATCAGGACATGCAAGTGTGTGGTATCAG
GATGGGAGAATAGTTGAAACCGATGAATCGCAAGGTATTTTGTGTTGAAAAGAACATGATTACAACCTGCTCCTT
ATTGCAAGTGCCCTAACCATTTCTAATATTACAGCTGGATCTACTGGAAATTGGGGCTGTCTATGTCAGACCAA
CGTGGGAATAATACGAGGACTGTGGATATTGTGGTATTAGAGAGTTCTGCACAGTACTGTCTCCAGAGAGGGTG
GTAAACAACAAGGTGACTTCAGATGGCCCAAGACATTTGGCAGGCATTACTGCATATCTGCAGTGTACGCGGAAC
ACCATGGCAGTGGGATATATCCCGGAAACCCACAGGATGAGAGAAAAGCTTGGCGCAGATGTGATAGAGGTGGC
TTTTGGGCAGATGATGATTATTTCTCGCTGTGATGCAATGATGTCACTAGAGTTCTTTATATGTTTAAATCAG
ATGCCCTCAATCTTACCAATGCCGTGGCAACAGCTCGACAGTTACTGGCTTACACTGTGGAAGCAGCCAACCTT
TCTGACAAAATGGATGTTATATTTGTGGCAGAAATGATTGAAAAATTTGGAAGATTTACCAAGGAGGAAAAATCA
AAAGAGCTAGGTGACGTGATGGTTGACATTGCAAGTAACATCATGTTGGCTGATGAACGTGTCTGTGGCTGGCG
CAGAGGGAAGCTAAAGCCTGCAGTAGGATTGTGCAGTGTCTCAGCGCATTGCTACCTACCGGCTAGCCGGTGGGA
GCTCACGTTTATTCAACATATTCACCAATATTGCTCTGGAAGCTTATGTCATCAAGTCTACTGGCTTCACGGGG
ATGACCTGTACCGTGTTCAGAAAAGTGGCAGCCTCTGATCGTACAGGACTTTCGGATTATGGGAGGCGGGATCCA
GAGGGAACCTGGATAAGCAGCTGAGCTTTAAGTGCAATGTTTCAAATACATTTTCGAGTCTGGCACTAAAGGTA
TGTTACATTCTGCAATCATTTTAAGACTATTTACAGTTAAATTAGAAATGCTCCAAATGTTCTGCTTCGCAAAATAA
CCTTATTAAGAGATTTTTTTTTTGCAGGAAGATAGGTATTATTGCTTTTGCTACTGTTTTAAAGAAAATAACCAG
GAAGAACTGCATTACGACTTTCAAGGGCCCTAGGCATTTTGCCTTTGATCCCTTTCTTCACATAAAAAATATCA
GAAATTACATTTTATAACTGCAGTGGTATAAATGCAATATACTATTGTTACATGTGAAAAAATTTTATTTGACT
TAAAGTTTATTTATTTGTTTTTTGCTCCTGATTTTAAGACAATAAGATGTTTTCATGGGCCCCATAAAGTATC
ATGAGCCTTTGGCACTGCGCCTGCCAAGCCTAGTGGAGAAGTCAACCCTGAGACCAGGTGTTTAAATCAAGCAAGC
TGATATCAAAAATTTTGGCAGAAAACACAAATATGTCATATATCTTTTTTAAAAAAGTATTTTCAATTGAAGCA
AGCAAAATGAAAGCATTTTACTGATTTTAAAAATGGTGCTTTAGATATATTTGACTACACTGTATTGAAGCAA
ATAGAGGAGGCACAACCTCCAGCACCTAATGGAAACCACATTTTTTCACTTAGCTTTCTGTGGGCATGTGTAATT
GTATTCTCTGCGGTTTTTAATCTCACAGTACTTTATTTCTGTCTGTCCCTCAATAATATCACAAACAATATTC
AGTCATTTTAAATGGCTGCATAATAACTGATCCACAGGTGTTAGGTGTTCTGGTTTAGTGTGAGCACTCAATAAA
TATTGAATGAATGAACGAAAAAAAAAAAAAAAAA

159/615

FIGURE 158

MEPPGRRRRGRAQPPLLLPLSLIALLALLGGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGKVVCSSLELAQVLP
PDTLPNRTVTILSNNKISELKNGSFSGLSLLERLDLRNNLISSIDPGAFFWGLSSLKRLDLTNNRIGCLNADIFR
GLTNLVRLNLSGNLFSSLSQGTFDYLASLRSLEFQTEYLLCDCNIIWMHRWVKEKNITVRDTRCVYPKSLQAQPV
TGVKQELLTCDPPELPSFYMTPSHRQVVFEGDSLFPQCMASYIDQDMQVLWYQDGRIVETDESQGI FVEKNMIH
NCSLIASALTISNIQAGSTGNWGC HVQTKRGNNTRTVDIVVLESSAQYCPPERVVNNKGDFRWPTLAGITAYLQ
CTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDDYSRCQYANDVTRVLYMFNQMPNLNLNAVATARQLLAYTVE
AANFSDKMDVIFVAEMIEKFGRFTKEEKSKELGDMVDIASNIMLADERVWLWLAQREAKACSRIVQCLQRIATYR
LAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCTVFQKVAASDRTGLSDYGRRDPEGNLDKQLSFKCNVSNTFSSL
ALKVCYILQSFKTIYS

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 13-40 (type II)

N-glycosylation site.amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336, 433-437,
453-457, 592-596**N-myristoylation site.**amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57, 57-63, 99-105,
123-129, 142-148, 162-168, 317-323, 320-326, 384-390, 403-409, 554-560

160/615

FIGURE 159

GGGGAATCTGCAGTAGGTCTGCCGGCGATGGAGTGGTGGGCTAGCTCGCCGCTTCGGCTCTGGCTGCTGTTGTTTCTCCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAAATGGAAAGTATTTATTGACCAAATTAACAGGTCCTTTGGAGAATTACGAACCATGTTCAAGTCAAACTGCAGCTGCTACCATGGTGTCTAGAGAAGAGGATCTAACTCCTTTCCGAGGAGGCATCTCCAGGAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCCTAAGAACAGACTGTACCGGGGAAAATGACTGCATGTTCCCTCAAGGTGTAGTGGTGTGAGCACTTTATTTTGAAGTGATCGGGCGTCTCCCTGACATGGAGATGGTGTATCAATGTACGAGATTATCCTCAGGTTCTAAATGGATGGAGCCTGCCATCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACCATGATATCATGTATCCTGCTTGGACATTTGGGAAGGGGGACCTGCTGTTTGGCCAAATTATCCTACAGGTCTTGGACGGTGGGACCTCTTCAGAGAAGATCTGTAAGGTGAGCAGCACAGTGGCCATGGAAAAAGAAAACTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCAGAACGAGATCCTCTCATTCTTCTGTCTCGGAAAAACCCAAAACCTTGTGATGCAGAATACACCAAAAACAGGCCGCGAAATCTATGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGTCCATCTTGTGGATCACTGCAAATACAAGTATCTGTTTAAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTTAAACACCTCTTCTGTGTGGCTCACTTGTTTTTCATGTTGGTGATGAGTGGCTAGAATCTTCTATCCACAGCTGAAGCCATGGGTTCACTATATCCAGTCAAAACAGATCTCTCCAATGTCCAAGAGCTGTTACAATTTGTAAAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGGGGAAGCCAGTTTATTAGGAACCATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCTCTTGAGTGAATACTCTAAATTCCTGTCTTATAATGTAACGAGAAGGAAAGGTTATGATCAAATTATTCCTAAAATGTTGAAAACCTGAACCTATAGTAGTCATCATAGGACCATAGTCCTCTTTGTGGCAACAGATCTCAGATATCCTACGGTGAGAAGCTTACATAAGCTTGGCTCCTATACCTTGAATATCTGCTATCAAGCCAAATACCTGGTTTTCTTATCATGCTGCACCCAGAGCAACTCTTGAGAAAGATTTAAATGTGTCTAATACTGATATGAAGCAGTTCAACTTTTTGGATGAATAAGGACCAGAAATCGTGAGATGTGGATTTTGAACCCAACTCTACCTTTCATTTTCTTAAGACCAATCACAGCTTGTGCCTCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCATGTGATGATGCCCTTTGTCCCATTATTTGGAGCAGAAAATTCGTCATTTGGAAGTAGTACAACCTCATTGCTGGAATTGTGAAATTATTCAAGGCGTGATCTGTCACTTTATTTTAAATGTAGGAAACCTATGGGGTTTATGAAAAATACTTGGGGATCATTCTCTGAATGGTCTAAGGAAGCGGTAGCCATGCCATGCAATGATGTAGGAGTTCTCTTTTGTAAAACCATAAACTCTGTACTCAGGAGGTTTCTATAATGCCACATAGAAAGAGGCCAATTGCATGAGTAATTATTGCAATTGGATTTTCAGTTCCCTTTTTGTGCCTTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAAA

161/615

FIGURE 160

MEWWASSPLRLWLLLFLLPSAQGRQKESGSKWKVFIDQINRSLENYEPCSSQNCSCYHGVI EEDLTPFRGGISRK
MMAEVVRRKLGTHYQITKNRLYREND CMFPSRCSGVEHFILEVIGRLPDMEMVINVRDYPQVPKWMEPAIPVFSF
SKTSEYHDIMYPAWTFWEGGPAVWPIYPTGLGRWDLFREDLVRSAQWPWKKKNSTAYFRGSRTSPERDPLILLS
RKNPKLVDAEYTKNQAWKSMKDTLGKPAAKDVHLVDHCKYKYLENFRGVAASFRFKHLFLCGSLVFHVGDWLEF
FYPQLKPVVHYIPVKTDLSNVQELLQFVKANDDVAQEIAERGSQFIRNHLQMD DITCYWENLLSEYSKFLSYNVT
RRKGYDQIIPKMLKTEL

162/615

FIGURE 161

CCGAGCACAGGAGATTGCCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGAAGAAATTGCCAAA
CCATGTCTTTTTTCTGTTTTTCAGAGTAGTTCCACAACAGATCTGAGTGTTTTAATTAAGCATGGAATACAGAAAA
CAACAAAAAACTTAAGCTTTAATTTTCATCTGGAATTCACAGTTTTCTTAGCTCCCTGGACCCGGTTGACCTGTT
GGCTCTTCCCGCTGGCTGCTCTATCACGTGGTGCTCTCCGACTACTACCCCGAGTGTAAGAACCCTTCGGCTCG
CGTGCTTCTGAGCTGCTGTGGATGGCCTCGGCTCTCTGGACTGTCCCTCCGAGTAGGATGTCACTGAGATCCCTC
AAATGGAGCCTCCTGCTGCTGTCACTCCTGAGTTTTCTTGTGATGTGGTACCTCAGCCTTCCCCACTACAATGTG
ATAGAACGCGTGAAC TGATGTACTTCTATGAGTATGAGCCGATTTACAGACAAGACTTTCACCTTCACACTTCGA
GAGCATTCAAACTGCTCTCATCAAATCCATTTCTGGTCATTCTGGTGACCTCCACCCCTTCAGATGTGAAAGCC
AGGCAGGCCATTAGAGTTACTTGGGGTGAAAAAAGTCTTGGTGGGGATATGAGGTTCTTACATTTTCTTATTA
GGCCAAGAGGCTGAAAAGGAAGACAAAATGTTGGCATTGTCCCTAGAGGATGAACACCTTCTTTATGGTGACATA
ATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAAACCATTATGGCATTCAGGTGGGTAAC TGAG
TTTTGCCCCAATGCCAAGTACGTAATGAAGACAGACACTGATGTTTTTCATCAATACTGGCAATTTAGTGAAGTAT
CTTTTAAACCTAAACCACTCAGAGAAGTTTTTCACAGGTTATCCTCTAATTGATAATTATTCTTATAGAGGATTT
TACCAAAAAACCCATATTTCTTACCAGGAGTATCCTTCAAGGTGTTCCCTCCATACTGCAGTGGGTTGGGTTAT
ATAATGTCCAGAGATTTGGTGCCAAGGATCTATGAAATGATGGGTCACGTAAAACCCATCAAGTTTGAAGATGTT
TATGTCGGGATCTGTTTGAATTTATTTAAAAGTGAACATTCATATTCAGAAGACACAAATCTTTCTTCTATAT
AGAATCCATTTGGATGTCTGTCAACTGAGACGTGTGATTGCAGCCCATGGCTTTTCTTCCAAGGAGATCATCACT
TTTTGGCAGGTCATGCTAAGGAACACCACATGCCATTATTAACCTTCACATTCTACAAAAAGCCTAGAAGGACAGG
ATACCTTGTGGAAAGTGTAAATAAAGTAGGTACTGTGGAAAATTCATGGGGAGGTCAGTGTGCTGGCTTACACT
GAACTGAAACTCATGAAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTATTAGTCAGGCCCTTCAA
GATGATATGTGGAGGAATTAAATATAAAGGAATTGGAGGTTTTTGTAAAGAAATTAATAGGACCAACAATTTG
GACATGTCACTTCTGTAGACTAGAATTTCTTAAAAGGGTGTACTGAGTTATAAGCTCACTAGGCTGTAAAAACAA
ACAATGTAGAGTTTTATTTATTGAACAATGTAGTCACTTGAAGGTTTTGTGTATATCTTATGTGGATTACCAAT
TTAAAAATATATGTAGTTCTGTGTCAAAAACTTCTTCACTGAAGTTATACTGAACAAAATTTTACCTGTTTTTG
GTCATTTATAAAGTACTTCAAGATGTTGCAGTATTTACAGTTATTATTATTTAAAATTACTTCACTTTGTGTT
TTTAAATGTTTTGACGATTTCAATACAAGATAAAAAGGATAGTGAATCATTCTTTACATGCAAAACATTTCCAGT
TACTTAACTGATCAGTTTATTATTGATACATCACTCCATTAAATGTAAAGTCATAGGTCATTATTGCATATCAGTA
ATCTCTTGGACTTTGTAAATATTTTACTGTGGTAATATAGAGAAGAATTAAAGCAAGAAAATCTGAAA

163/615

FIGURE 162

MASALWTVLPSRMSLRSLKWSILLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPYRQDFHFTLREHSNCSH
QNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEAEKEDKMLALSLEDEHLLYGDIIHQDFLD
TYNNLTCLKTIMAFRWVTEFCPNAKYVMKTDTDVFINTGNLVKYLNLNLHSEKFFTGYPLIDNYSYRGFYQKTHIS
YQEYPFKVFPYCSGLGYIMSRDLVPRIYEMMGHVKPIKFEDVYVGICLNLLKVNIIHPEDTNLFFLYRIHLDVC
QLRRVIAAHGFSSKEIITFWQVMLRNTTCHY

164/615

FIGURE 163

CATTTCTGAACTAATCGTGTGAGAATTGACTTTGAAAAGCATTGCTTTTTACAGAAGTATATTAACTTTTTAGG
AGTAATTTCTAGTTTGGATTGTAATATGAAATAATTTAAAAGGGCTTCGCTCATATATAGGAAAATCGCATATGG
TCCTAGTATTAAATTCCTATTGCTTACTGATTTTTTTGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGTG
AATATAAATAAGAGAAGAAAAAGAATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAAGTGGTT
TGTTTACATGCAAGCTTATAGTTGAAATATTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTTG
TTCGATTTCAACCAGAGACTATAGCATGTGCTTGCATCTACCTTGACAGCTAGAGCACTTCAGATTCGGTTGCCAA
CTCGTCCCCATTGGTTTCTCTTTTTGGTACTACAGAAGAGGAAATCCAGGAAATCTGCATAGAAACACTTAGGC
TTTATACCAGAAAAAGCCAACTATGAATTACTGGAAAAAGAGTAGAAAAAGAAAAGTAGCCTTACAAGAAG
CCAAATTTAAAGCAAAGGGATTGAATCCGGATGGAATCCAGCCCTTCAACCCTGGGTGGATTTTCTCCAGCCT
CCAAGCCATCATCACCAGAGAAGTAAAGCTGAAGAGAAATCACCATCTCCATTAATGTGAAGACAGTCAAAA
AAGAACCTGAGGATAGACAACAGGCTTCCAAAAGCCCTTACAATGGTGTAAAGAAAAGACAGCAAGAGAAGTAGAA
ATAGCAGAAGTGCAAGTCGATCGAGGTCAAGAACACGATCACGTTCTAGATCACATACTCCAAGAAGACACTATA
ATAATAGGCGGAGTCGATCTGGAACATACAGCTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAAGCCCTC
GAAGACATCATAATCATGGTTCTCCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAAGTTCAAACAGAC
ATGGTCATAAAAGGAAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAGCCAAGAAAC
ACAGGCATGAAAGGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCTTTGAGAGGTCCCATAAAAGCAAGC
ACCATGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCGCTGACTTTCTCTTCTTTGAGCCTGCATCAGTTCT
TGGTTTTGCCTATCTACAGTGTGATGTATGGACTCAATCAAAAACATTAAACGCAAACTGATTAGGATTTGATTT
CTTGAAACCCTCTAGGTCTCTAGAACACTGAGGACAGTTTCTTTTGAAGAAGTATGTTAATTTTTTGCACAT
TAAATGCCCTAGCAGTATCTAATTAAAAACCATGGTCAGGTTCAATTGTACTTTATTATAGTTGTGTATTGTTT
ATTGCTATAAGAAGTGGAGCGTGAATTCTGTAAAAATGTATCTTATTTTTATACAGATAAAATTCAGACACTGT
TCTATTTAAGTGGTTATTTGTTTAAATGATGGTGAATACTTTCTTAACACTGGTTTGTCTGCATGTGTAAGATT
TTTACAAGGAAATAAATAACAAATCTGTTTTTTCTAAAAAAGT

165/615

FIGURE 164

MNDSLRTNVFVRFQPETIACACIYLAARALQIPLPTRPHWFLFLFGTTEEEIQEICIETLRRLYTRKKPNYELLEKE
VEKRRKVALQEAKLKAKGLNPDGTPALSTLGGFSPASKPSSPREVKAEKSPISINVKTVMKEPEDRQQASKSPYN
GVRKDSKRSRNSRSASRSRSRSTRSRSRSHTPRRHYNNRRSRSGTYSSRSRSRSRSHSESPPRRHHNHGSPHLKAKH
TRDDLKSSNRHGHKRRKSRSRSQSKSRDHSDAAKKHRHERGHRDRRERSRSFERSHKSKHHGGSRSRSGHGRHRR

166/615

FIGURE 165

GGTTCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGCCCCGTGATTTATTAACGTGGCTTA
ATCTGAAGGTTCTCAGTCAAATTCCTTTGTGATCTACTGATTGTGGGGGCATGGCAAGGTTTGCTTAAAGGAGCTT
GGCTGGTTTGGGCCCCCTGTAGCTGACAGAAGGTGGCCAGGGAGAATGCAGCACACTGCTCGGAGAATGAAGGCGC
TTCTGTTGCTGGTCTTGCCCTTGGCTCAGTCCTGCTAACTACATTGACAATGTGGGCAACCTGCACTTCCTGTATT
CAGAACTCTGTAAAGGTGCCTCCCACTACGGCCTGACCAAAGATAGGAAGAGGCGCTCACAAGATGGCTGTCCAG
ACGGCTGTGCGAGCCTCACAGCCACGGCTCCCTCCCCAGAGGTTTCTGCAGCTGCCACCATCTCCTTAATGACAG
ACGAGCCTGGCCTAGACAACCCCTGCCTACGTGTCTCGGCAGAGGACGGGCAGCCAGCAATCAGCCCAGTGGACT
CTGGCCGGAGCAACCGAAGTAGGGCACGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTTAAAAAATAA
ATCGAGCTTTGAGTGTTCTTGAAGGACAAAGAGCGGGAGTGCAGTTGCCAACCATGCCGACCAGGGCAGGGAAA
ATTCTGAAAACACCACTGCCCCCTGAAGTCTTTCCAAGGTTGTACCACCTGATTCCAGATGGTGAATTACCAGCA
TCAAGATCAATCGAGTAGATCCCAGTGAAAGCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAACCCCACTGGTCC
ATATCATTATCCAACACATTTATCGTGATGGGGTGATCGCCAGAGACGGCCGGCTACTGCCAGGAGACATCATTC
TAAAGGTCAACGGGATGGACATCAGCAATGTCCTCACAACACGCTGTGCGTCTCTGCGGCAGCCCTGCCAGG
TGCTGTGGCTGACTGTGATGCGTGAACAGAAGTCCGAGCAGGAACAATGGACAGGCCCGGATGCCCTACAGAC
CCCAGATGACAGCTTTCATGTGATTTCTCAACAAAAGTAGCCCCGAGGAGCAGCTTGAATAAACTGGTGCGCA
AGGTGGATGAGCCTGGGGTTTTTCATCTCAATGTGCTGGATGGCGGTGTGGCATATCGACATGGTCAGCTTGAGG
AGAATGACCGTGTGTAGCCATCAATGGACATGATCTCGATATGGCAGCCCAGAAAGTGCGGCTCATCTGATTC
AGGCCAGTGAAAGACGTGTTACCTCGTGTGTCGCCAGGTTCCGCGAGCGGAGCCCTGACATCTTTCAGGAAG
CCGGCTGGAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGGAGAGGAGCAACACTCCCAAGCCCCCTCATCCTA
CAATTACTTGTGATGAGAAGGTGGTAAATATCCAAAAAGACCCCGTGAATCTCTCGGCATGACCGTCGCAGGGG
GAGCATCACATAGAGAATGGGATTTGCCTATCTATGTGATCAGTGTTGAGCCCGGAGGAGTCATAAGCAGAGATG
GAAGAATAAAACAGGTGACATTTTGTGTAATGTGGATGGGGTGAAGTACAGAGGTGAGCCGGAGTGAGGCAG
TGGCATTATTGAAAAGAACATCATCCTCGATAGTACTCAAAGCTTTGGAAGTCAAAGAGTATGAGCCCCAGGAAG
ACTGCAGCAGCCAGCAGCCCTGGACTCCAACCACAACATGGCCCCACCCAGTGAAGTGGTCCCCATCCTGGGTCA
TGTGGCTGGAATTACCACGGTGCTTGTATAACTGTAAAGATATTGTATTACGAAGAAACACAGCTGGAAGTCTGG
GCTTCTGCATTGTAGGAGGTTATGAAGAATACAATGGAAACAAACCTTTTTTCATCAAATCCATTGTTGAAGGAA
CACCAGCATACAATGATGGAAGAATTAGATGTGGTGATATCTTCTGTGCTGCAATGGTAGAAGTACATCAGGAA
TGATACATGCTTGCTTGGCAAGACTGCTGAAAGAAGCTTAAAGGAAGAATTACTCTAACTATTGTTTCTTGGCCTG
GCACTTTTTTATAGAATCAATGATGGGTCAGAGGAAAACAGAAAAATCACAAATAGGCTAAGAAGTTGAAACACT
ATATTTATCTTGTGCTGCTTTTATATTTAAAGAAAGAATACATTGTAAAAATGTGAGGAAAAGTATGATCATCTAA
TGAAAGCCAGTTACACCTCAGAAAATATGATTCCAAAAAATTAAGAACTACTAGTTTTTTTCAGTGTGGAGGAT
TTCTCATTACTCTACAACATTGTTTATATTTTTCTATTCAATAAAAAGCCCTAAAACAATAAATGATTGATT
TGATATACCCCACTGAATTCAGCTGATTAAATTTAAATTTGGTATATGCTGAAGTCTGCCAAGGGTACATTAT
GGCCATTTTTAATTTACAGCTAAAATATTTTTTAAATGCAATGCTGAGAAACGTTGCTTTTCATCAAACAAGAAT
AAATATTTTTTCAGAAAGTTAAA

167/615

FIGURE 166

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPCDGCASLTATAPSPEVSAAATIS
LMTDEPGLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFERSTIRSRSFKKINRALSVLRRTKSGSAVANHADQ
GRESENTTAPEVFPRLYHLIPDGEITSIKINRVDPSSELSIRLVGGSETPLVHIIIQHIYRDGVIARDGRLPG
DIILKVNMGMDISNPHNYAVRLLRQPCQVLWLTVMREQKFSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIK
LVRKVDEPGVFIFNVLDGGVAYRHGQLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVVSQRQVRQSPDI
FQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKVNIQKDPGESLGMTVAGGASHREWDLPIYVISVEPGGVI
SRDGRIKTGDILLNVGVELTEVSRSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNHNMAPPSDWSP
SWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIVGGYEEYNGNKPFIFIKSIVEGTPAYNDGRIRC GDILLAVNGRS
TSGMIHACLARLLKELKGRITLTIVSWPGTFL

168/615

FIGURE 167

GGGAAAGCCATTTGCGAAAACCCATCTATACAACTATATATTTTCATTTCTGCTGCTAGCTGCCTTGGGCCTCAC
AATTTTCATTCTGTTTTCTGACTTTCAAGTTATATACCGTGGAAATGGAGTTGATCCCACCATAACATCGTGGAG
GGTTTTAATTTTGGTGGTAGCCCTCACCCAATTCTGGTGTGGCTTTCTTTGCAGAGGATTCCACCTTCAAAATCA
TGAACCTCTGGCTGTTGATCAAAAGAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAAGAAGCT
AGCAGAAGACTCAACCTGGCCTCCCATAAACAGGACAGATTATTCAGGTGATGGCAAAAATGGATTCTACATCAA
CGGAGGCTATGAAAGCCATGAACAGATTCCAAAAGAAAAGTCAAATTGGGAGGCCAACCCACAGAACAGCATT
CTGGGCCAGGCTGTAATCAGAATTGTCGTCGTACATGCTCAACAGCATTGCTTTTTTCCCCAAAATTACACATT
GTGGAGAAGTGATGATACTCTCCCCTTACCTTTCCTCTCTCCATTCAAGCATTCAAAGTATATTTTCAATGAATT
AAACCTTGCAGCAAGGGACCTTAGATAGGCTTATTCTGACTGTATGCTTTACCAATGAGAGAAAAAATGCATT
CCTGTATCATCCTTTTCAATAAACTGTATTCATTTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

169/615

FIGURE 168

MELIPTITSWRVLILVVALTQFWCGFLCRGFHLQNHFWLLIKREFGFYSKSQYRTWQKKLAEDSTWPPINRTDY
SGDGKNGFYINGGYESHEQIPKRKLKLGQPTQHFWARL

FIGURE 169

FIGURE 169

[illegible]

171/615

FIGURE 170

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREVVGYTIPCCRNEENE
CDSCLIHPGCTIFENCKSCRNGSWGGLDDEFYVKGFYCAECRAGWYGGDCMRCGQVLRAPKGQILLESYPLNAHC
EWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDQIIKRVCGNERPAPIQSIGSSLHVLFHSDGSKN
FDGFHAIYEEITACSSSPCFHDGTCVLDKAGSYKACLAGYTGQRCEENLEERNCSDPGGFVNQYQKITGGPGLI
NGRHAKIGTVVSFFCNNSYVLSGNEKRTCQONGEWSGKQPICIKACREPKISDLVRRRVLPQVQSRETPLHQLY
SAAFSKQKLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPSCIPICGKIE
NITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLG
KFYRDDDRDEKTIQSLQISAILHPNYDPILLDADIAILKLLDKARISTRVQPICLAASRDLSTSFQESHITVAG
WNVLADVRS PGFKNDTLRSGVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDICTAETGGIAAVSFPG
RASPEPRWHLMGLVSWSYDKTCSHRLSTAFTKVLFPKDWIERNMK

172/615

FIGURE 171

CTGTCGTCTTTGCTTCAGCCGAGTCGCCACTGGCTGCCTGAGGTGCTCTTACAGCCTGTTCCAAGTGTGGCTTA
ATCCGTCTCCACCACCAGATCTTTCTCCGTGGATTCCCTCTGCTAAGACCGCTGCCATGCCAGTGACGGTAACCCG
CACCACCATCACAACCACCACGACGTATCTTCGGGCCTGGGGTCCCCCATGATCGTGGGGTCCCCCTCGGGCCCT
GACACAGCCCCTGGGTCTCCTTCGCCTGCTGCAGCTGGTGTCTACCTGCGTGGCCTTCTCGCTGGTGGCTAGCGT
GGGCGCCTGGACGGGGTCCATGGGCACTGGTCCATGTTCACTGGTGCTTCTGCTTCTCCGTGACCCTGATCAT
CCTCATCGTGGAGCTGTGCGGGCTCCAGGCCGCTTCCCCCTGTCTTGGCGCAACTTCCCCATCACCTTCGCCTG
CTATGCGGGCCCTCTTCTGCCTCTCGGCCTCCATCATCTACCCACACCTATGTCCAGTTCCTGTCCACGGCCG
TTCGCGGGACACGCCATCGCCGCCACCTTCTTCTCCTGCATCGCGTGTGTGGCTTACGCCACCGAAGTGGCCTG
GACCCGGGGCCCGCCCGGCGAGATCACTGGCTATATGGCCACCGTACCCGGGCTGCTGAAGGTGCTGGAGACCTT
CGTTGCCTGCATCATCTTCGCGTTTCATCAGCGACCCCAACCTGTACCAGCACCGCCGCCCTGGAGTGGTGCCT
GGCGGTGTACGCCATCTGCTTCATCCTAGCGGCCATCGCCATCCTGCTGAACCTGGGGGAGTGACCAACGTGCT
ACCCATCCCCCTTCCCCAGCTTCCCTGTGCGGGCTGGCCTTGTGTCTGTCTCCTCTATGCCACCGCCCTTGTTCCT
CTGGCCCTCTACCAGTTCGATGAGAAGTATGGCGGCCAGCCTCGGCGCTCGAGAGATGTAAGCTGCAGCCGCAG
CCATGCCTACTACGTGTGTGCCTGGGACCGCCGACTGGCTGTGGCCATCCTGACGGCCATCAACCTACTGGCGTA
TGTGGCTGACCTGGTGCATCTGCCCACCTGGTTTTTGTCAAGGCTCTAAGACTCTCCCAAGAGGCTCCCGTTCCC
TCTCCAACCTCTTTGTTCTTCTTGCCCGAGTTTTCTTTATGGAGTACTTCTTTCCTCCGCCTTTCTCTGTTTTC
CTCTCCTGTCTCCCTCCCTCCACCTTTTTCTTTCTTCCCAATTCCTTGCACTCTAACCAGTTCCTGGATGC
ATCTTCTTCCCTTCCCTTCCCTTCTGCTGTTTTCTTCTGTGTGTTTTGTTGCCACATCCTGTTTTACCCCTG
AGCTGTTTCTCTTTTCTTTCTTTCTTTTTTTTTTTTTTTTAAAGACGGATTCTCACTCTGTGGCCAGGCTG
GAGTGCAGTGGTGCGATCTCAGCTCACTGCAACCCCGCCTCCTGGGTTCAAGCGATTCTCCTCCCCAGCCTCC
CAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGACCCAGCCTGTTTCTCTTTTCCACTCTTCTTTTTTCTCATC
TCTTTTCTGGGTTGCCGTGTGCGCTTTCTATCTGCCTGTTTGGCAAGCACCTTCTCCTGTGTCTTGGGAGCCCT
GAGACTTCTTTCTCTCCTTGCCTCCACCCACCTCCAAAGGTGCTGAGCTCACATCCACACCCCTTGACGCCGTCC
ATGCCACAGCCCCCAAGGGGCCCCATTGCCAAAGCATGCCTGCCACCCCTCGCTGTGCCTTAGTCAGTGTGTAC
GTGTGTGTGTGTGTGTTTTGGGGGGTGGGGGGTGGGTAGCTGGGGATTGGGCCCTCTTCTCCAGTGGAGGAA
GGTGTGAGTGTACTTCCCCTTTAAATTAAAAACATATATATATATATTTGGAGGTCAATAATTCCAATGG
GCGGGAGGCATTAAAGCACCGACCTGGGTCCCTAGGCCCCGCTGGCACTCAGCCTTGCCAGAGATTGGCTCCAG
AATTTTTGCCAGGCTTACAGAACCCCACTGCCTAGAGGCCATCTTAAAGGAAGCAGGGGGCTGGATGCCTTTTCAT
CCCACTATTCTCTGTGGTATGAAAAAG

173/615

FIGURE 172

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727
<subunit 1 of 1, 322 aa, 1 stop
<MW: 35274, pI: 8.57, NX(S/T): 1
MPVTVTRTTITTTTTSSSGLGSPMIVGSPRALTQPLGLLRLLQLVSTCVAFSLVASVGAWTGSMGNWSMFTWCFC
FSVTLLIILIVELCGLQARFPLSWRNFPITFACYAALFCLSASIIYPTTYVQFLSHGRSRDHAIATFFSCIACVA
YATEVAWTRARPGEITGYMATVPGLLKVLETFVACIIFAFISDPNLYQHQPALWCVAVYAICFILAAIAILLNL
GECTNVLPPIPPSFLSGLALLSVLLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRRLAVAILT
AINLLAYVADLVHSAHLVFVKV
```

Important features:**Transmembrane domains:**

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192, 205-226, 235-255 and 294-312

N-glycosylation site.

amino acids 66-69

Glycosaminoglycan attachment site.

amino acids 18-21

174/615

FIGURE 173

GAACGTGCCACCATGCCAGCTAATTTTTGTATTTTTAGTAGAGACGGGGTTTCACCATGTTGGCCAGGCTGGTCTTGAACTCGTGACCTCATGATCCGCTCACTCTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGACGCCTGGCCAGCCTATGCACTTTTAAAGAAATTTCTGTATTAGGTGCTGTGCTAAACATTTGGGCATACAGTGACCAAAACAGACTGAATTTCCCAAAGACCAAGACCACTGAGGGAGACCAACAAAGAAACAGGAATGCAAAAGACCAATTATTACTCACTATGACTAAGGGTCACAAATGGGGTACGGTGTGATGGAGAGTATTTGTTAAGAGACTACAGAGGGAGGACAGACTACCAAGAGGGGGGCCAGGAAAGCTCCTCTGACGAGGTGGTATTTAGCCCAAACCTGGAAGAATGAGAAAGAGCTAGCCAGCCATCAGAATAGTCCAGAAGAGATGGGGAGCATTACACTCACTACACTTTGGCCTGAGAAATAGCATGGGATTTGGAGGAGGCTGGGGGAACACCACTTCTGCCGACCTGGGCAGGAGGCATTGAGGGCTTGAGAAGGGCAATGGCAGTAGCATAGAAGGACAGGGTAGGACGAGGACTTTGCAGGTGGAATCATTAGGCTTATTAACAGATATGGGCAGCAAGCCAGGGGAGAAATTGATGTAATGCTGAGGTTTGAGCCAGGCTAGATGGGACAGTGGTGGGTGATGCAAAGGAAGAGGTCAGGAAGCAGGGCCAGACGTGGGGAGAAGGTGTGGGGGTTTGGTTTCCCATCTTGCCGAGTCTGCCGAATGTGGATGGGAAGCAAGAGGAGGACAGGGGCAGAGGGGAAGGGAATCTTAAAGAAGTCTGGATGCCCACACTTGTCTCTCTTCCCTCTCCCTCTCCCTCAGAGGCTCACTCGTGGTTCTTTCATTCTGCCCTGCCCTCCATCTCCTCTGGGTGCTGGGAAAGTGGAGGATTAGCTGAAGTTTGCTTCTCGGGGCTGTGTAATCTCCATTGCTTTCTGGGAGGACATAATTCACCTGTCCTAGCTTCTTATCATCTTACATTCCCTGTAGCCACTGGGACATATGTGGTGTCTCTCTAGCTCCTGTCTCCTCCTCATGCCTTTGCTGGGTATGGGCATGTTAGGGGAAGGTCAATTGCTGTGAGAGGGGCACTGACTTTCTAATGGTGTTACCAAGGTGAATGTTGAGACACAGTCGCCATGCTGCCAAAGTCCCGGGCAGCCCTAACTATCCAGGAGATCGCTGCGCTGGCCAGGCTCCTCCTGTCATGGTATGCAAGCCCCCTCCCATTTCTTGCCCACTTTGTCTCTTCTCCCTGGTATGTCACATCCCTTTGGAATCTTTCTGTGAGTACATGCTGGGGTCTCCCCCTTCTCCCTTGCTCAGTGAATCTCAGCCCTTCTCCCAACCAAGGTTTACATGGATCCTAACTACTGCCACCCTTCCACCTCCCTGCACCTGTGCTCCCTGGCCTGGTCTTTACCAGGCTTCTCCACCCTCCCTTATCTCCAGGTATTTCCAGGTGGTGAAGGACCACGTGACCAAGCCTACCGCCATGGCCAGGGCCGAGTGGCTCACCTCATTGAGTGGAAAGGGCTGGAGCAAGCCGAGTGACTCACCTGCTGCCCTGGAATCAGCCTTTCTCTCTTATTCAGACCTCAGCGAGGGCGAACAAGAGGCTCGCTTTGACAGCAGGAGTGGCTGAGCAGTTTGCCATCGCGGAAGCCAAAGCTCCGAGCATGCTTCTCGGTGGATGGCGAGGACTCCACTGATGACTCCTATGATGAGGACTTTGCTGGGGGAATGGACACAGACATGGCTGGGCAGCTGCCCTGGGGCCGCACCTCCAGGACCTGTTACCGGGCCACCGTTTCTCCCGCCTGTGCGCCAGGGCTCCGTGGAGCCTGAGAGCGACTGCTCACAGACCTGTCCCCAGACACCTGTGCTCTAGTCTGTGCAGCCTGGAGGATGGGTGTGTTGGGCTCCCGGGCCGGCTGGCCTCCAGCTGTCTGGCGATGAGCTGCTTCTGCCAACTGCCCCCCAGCCCGGAGGTCCTTCCCGCGGAGGAGGAGCAGCCCTGCAAGACTGCCAGCCACTCTGCCACCCTAACGGGCAGCTGGGAACGGCAGCGGCAAGCCTCTGACCTGGCCTCTTCTGGGTGGTGTCTTAGATGAGGATGAGGCAGAGCCAGAGGAACAGTGAACCAATCATGCCTGGCAGTGGCATGCAATCCCCGGCTGCTGCCAGGGGCAGAGCCTCTGTGCCCAAGTGTGGGCTCAAGGCTCCCAGCAGAGCTCCACAGCCTAGAGGGCTCTGGGAGCGCTCGCTTCTCGGTGTGTTTGCATGAAGTGTGGAGAGGAGGCAGGGGCTGGCTGGGGGCGCATGTCTGCCCCACTCCGGGGTGTGCCGGGGTGTGCCGGGGCTCTGGGCATGGCTACAGCTGTGGCAGACAGTGATGTTCTATGTTCTTAAATGCCACACACATTTCTCTCCTCGGATAATGTGAACCACTAGGGGTTGTGACTGGGCTGTGTAGGGTGGGGTGGGAGGGGGCCAGCAACCCCCACCCTCCCATGCCTCTCTCTCTCTGCTTTTCTTCTCACTTCCGAGTCCATGTGCAGTGCTTGATAGAATCACCCCCACCTGGAGGGGGCTGGCTCTGCTGCCCGAGCCTATGGGTGAGCCGTCCCTCAAGGGCCCCCTGCCAGCTGGGCTCGTGTGCTGCTTATTCACCTCTCCATCGTCTCTAAATCTTCTCTTTTCTTAAAGACAGAAGGTTTTTGGTCTGTTTTTTCAGTGGATCTTCTCTCTCTGAGGCTTTGGAATGATGAAAGCATGTACCCTCCACCCTTTTCTGGCCCCCTAATGGGCCTGGGGCTTTTCCCAACCCCTCCTAGGATGTGCGGGCAGTGTGCTGGCGCCTCACAGCCAGCCGGGCTGCCATTCACGCAGAGCTCTCTGAGCGGGAGGTGGAAGAAAGGATGGCTCTGGTTGCCACAGAGCTGGGACTTCATGTTCTTCTAGAGAGGGCCACAAGAGGCCACAGGGGTGGCGGGAGTTGTACGTGATGCTGAGAGGCAAGGAATGTCGACAGTAGTGACAGTGCAGTGCATGAGGAGTGTGCTTCTTCTGGGAGGAAAGAAAGGTAGAGCTTTCTGTCTGAATGAAAGGCCAAGGCTACAGTACAGGGCCCCGCCAGCCAGGGTGTTAATGCCACGTAGTGGAGGCTCTGGCAGATCCTGCAATTCCAAGGTCACTGGAAGTGTACGTTTTTATGTTTGTGGGAAGGGTGGGTGGCTTTAGAATTAAGGGCTGTGTAGGCTTTGGCAGGTAAGAGGGCCCAAGGTAAGAACGAGAGCCAACGGGCACAAGCATTCATATATATAAGTCTGCTCATTAGGTGTTTATTTTGTCTATTTAAGAATTTGTTTTATTAAATTAATATAAAAACTTTGTAATCTCTAAAA

175/615

FIGURE 174

MFLATLSFLLPFAHPFGTVSCEYMLGSPSSLAQVNLSPFSPKPVHMDPNYCHPSTSLHLCSLAWSFTRLLHPPL
SPGISQVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPAALESFSSYSDLSEGEQEARFAAGVAEQFAIAEAK
LRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLGPHLQDLFTGHRFSRPVRQGSVEPESDCSQTVPDTLCSS
LCSLEDGLLGSPARLASQLLGDELLAKLPPSRESAFRSLGPLEAQDSLNSPLTESCLSPAEEEEPAPCKDCQPL
CPPLTGSWERQRQASDLASSGVVSLDEDEAEPEEQ

Signal peptide:
amino acids 1-15

Casein kinase II phosphorylation site.
amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232, 285-289,
324-328

Tyrosine kinase phosphorylation site.
amino acids 44-52

N-myristoylation site.
amino acids 17-23, 26-32, 173-179

Prokaryotic membrane lipoprotein lipid attachment site.
amino acids 11-22

176/615

FIGURE 175

GGTTCCTGGGCGCTCTGTTACACAAGCAAGATACAGCCAGCCCCACCTAATTTGTTTCCCTGGCACCCTCCTGC
TCAGTGGGACATTGTCACACTTAACCCATCTGTTTTCTCTAATGCACGACAGATTCCTTTCAGACAGGACAACCTG
TGATATTTTCAGTTCCTGATTGTAAATACCTCCTAAGCCTGAAGCTTCTGTTACTAGCCATTGTGAGCTTCAGTTT
CTTCATCTGCAAAATGGGCATAATAACAATCTATTCTTGCCACATCAAGGGATTGTTATTCCTTTAAAAAAAACC
AATACCAAAGAAGCCTACAATGTGTTGGCCTTAGCCAAAATTCTGTTGATTTCAACGTTGTTTTATTCACTTCTATC
GGGGAGCCATGGAAGAAAATCAAGACATAAACACAACACAGAACATTGCAGAAGTTTTTAAACAATGGAAAA
TAAACCTATTTCTTTGGAAAGTGAAGCAAACCTTAAACTCAGATAAAGAAAATATAACCACCTCAAATCTCAAGGC
GAGTCATTCCCCCTCTTTGAATCTACCCAACAACAGCCACGGAATAACAGATTTCTCCAGTAACCTCATCAGCAGA
GCATTCTTTGGGCAGTCTAAAACCCACATCTACCATTTCACACAAGCCCTCCCTTGATCCATAGCTTTGTTCTAA
AGTGCCCTTGGAATGCACCTATAGCAGATGAAGATCTTTTGCCCATCTCAGCACATCCCAATGCTACACCTGCTCT
GTCTTCAGAAAACCTCACTTGGTCTTTGGTCAATGACACCGTGAAAACCTCCTGATAACAGTTCCATTACAGTTAG
CATCCTCTCTTCAGAACCAACTTCTCCATCTGTGACCCCTTGATAGTGGAACCAAGTGGATGGCTTACCACAAA
CAGTGATAGCTTCACCTGGGTTTACCCCTTATCAAGAAAAAACAACCTTACAGCCTACCTTAAATTCACCAATAA
TTCAAAACTCTTTCCAAATACGTGAGATCCCCAAAAGAAAATAGAAATACAGGAATAGTATTCGGGGCCATTTT
AGGTGCTATTCTGGGTGTCTCATTGCTTACTCTTGTGGGCTACTTGTGTGTGGAAAAAGGAAAACGGATTCATT
TTCCCATCGGCGACTTTATGACGACAGAAATGAACAGTTCTGCGATTAGACAATGCACCGGAACCTTATGATGT
GAGTTTTGGGAATTCTAGCTACTACAATCCAACCTTTGAATGATTTCAGCCATGCCAGAAAGTGAAGAAAATGCACG
TGATGGCATTCTATGGATGACATACCTCCACTTCGTACTTCTGTATAGAACTAACAGCAAAAAGGCGTTAAACA
GCAAGTGTCATCTACATCCTAGCCTTTTGACAAATTCATCTTTCAAAGGTTACACAAAATTACTGTCACGTGGA
TTTTGTCAAGGAGAATCATAAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCATCAAAGGTTTTCT
TTTCTTACAATTTTTGGCCATCTGAGGCATTTACTAAGTAGCCTTAATTTGTATTTTAGTAGTATTTCTTAGT
AGAAAATATTTGTGGAATCAGATAAAACTAAAAGATTTACCATTACAGCCCTGCCTCATAACTAAATAATAAAA
ATTATTCACCAAAAAATCTAAAACAATGAAGATGACTCTTACTGCTCTGCCTGAAGCCCTAGTACCATAATT
CAAGATTGCATTTTCTTAAATGAAAATTGAAAGGGTGCTTTTTAAAGAAAATTTGACTTAAAGCTAAAAAGAGGA
CATAGCCCAGAGTTTCTGTTATTGGGAAATTGAGGCAATAGAAATGACAGACCTGTATTCTAGTACGTTATAATT
TTCTAGATCAGCACACACATGATCAGCCCACTGAGTTATGAAGCTGACAATGACTGCATTCAACGGGGCCATGGC
AGGAAAGCTGACCCTACCCAGGAAAGTAATAGCTTCTTTAAAAGTCTTCAAAGGTTTTGGGAATTTTAACTTGTC
TTAATATATCTTAGGCTTCAATTATTTGGGTGCCTTAAAACTCAATGAGAATCATGGT

177/615

FIGURE 176

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732
><subunit 1 of 1, 334 aa, 1 stop
><MW: 36294, pI: 4.98, NX(S/T): 13
MLALAKILLISTLFYSLLSGSHGKENQDINTTQNI AEVFKTMENKPISESEANLNSDKENITTSNLKASHSPPL
NLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHSFVSKVPWNAPIADEDLLPISAHPNATPALSSSENF
WSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVEPSGWLTTNSDSFTGFTPYQEKTTLQPTLKFTNNSKLFPN
TSDPQKENRNTGIVFGAILGAILGVSLTLVGYLLCGKRKTD SFSHRRLYDDRNEPVLRLDNAPEPYDV SFGNSS
YYNPTLND SAMP ESEENARDGIPMDDIPPLRTSV
```

Signal peptide:
amino acids 1-23

Transmembrane domain:
amino acids 235-262

N-glycosylation site.
amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159, 163-167, 218-222,
225-229, 298-302, 307-311

178/615

FIGURE 177

ACCAGGCATTGTATCTTCAGTTGTCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGAAGCTTCTTGCCCT
GCAGTGAAGCAGAGAGATAGATATTATTACGTAATAAAAAACATGGGGCTTCAACCTGACTTTCCACCTTTCCCTA
CAAATTCGGATTACTGTTGCTGTTGACTTTGTGCCCTGACAGTGGTTGGGTGGGCCACCAGTAACCTCTCGTGGG
TGCCATTCAAGAGATTCCCTAAAGCAAAGGAGTTCATGGCTAATTTCCATAAGACCCTCATTGTTGGGGAAGGGAAA
AACTCTGACTAATGAAGCATCCACGAAGAAGGTAGAACTTGACAACCTGTCTTCTGTGTCTCCTTACCTCAGAGG
CCAGAGCAAGCTCATTTTCAAACCAGATCTCACTTTGGAAGAGGTACAGGCAGAAAATCCCAAAGTGTCCAGAGG
CCGGTATCGCCCTCAGGAATGTAAAGCTTTACAGAGGGTCCCATCCTCGTTCCCCACCGGAACAGAGAGAAAACA
CCTGATGTACCTGCTGGAACATCTGCATCCCTTCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCA
CCAGGCTGAAGGTAAAAAGTTAATCGAGCCAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAA
TTGGGACTGCTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGAGGAGCA
TCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTGGATATTTTGGGGGTGTTAC
TGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCTAACAACTACTGGGGATGGGGAGGCGAAGACGA
TGACCTCAGACTCAGGGTTGAGCTCCAAAGAATGAAAATTTCCCGCCCCCTGCCTGAAGTGGGTAAATATACAAT
GGTCTTCCACACTAGAGACAAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTCTTACACCAAGTGTACAGAGT
CTGGAGAACAGATGGGTTGAGTAGTTGTTCTTATAAATTAGTATCTGTGGAACACAATCCTTTATATATCAACAT
CACAGTGGATTTCTGGTTTGGTGCA~~TG~~ACCCTGGATCTTTTGGTGATGTTTGGGAAGAACTGATTCTTTGTTTGCA
ATAATTTTGGCCTAGAGACTTCAAATAGTAGCACACATTAAGAACCTGTTACAGCTCATTGTTGAGCTGAATTTT
TCCTTTTGTATTTTCTTAGCAGAGCTCCTGGTGATGTAGAGTATAAAACAGTTGTAACAAGACAGCTTTCTTAG
TCATTTTGATCATGAGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGA
TAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATATTATGGGATAAAA
GGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCTCGTCCAAGGTAGAAAGGTACGAAGA
TACAATACTGTTATTCATTTATCCTGTACAATCATCTGTGAAGTGGTGGTGTGAGGTGAGAAGGCGTCCACAAAA
GAGGGGAGAAAAGGCGACGAATCAGGACACAGTGAACCTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTGCGC
TGCAAAGGCAGCAGTAGCTGAGCTGGTTGCAGGTGCTGATAGCCTTCAGGGGAGGACCTGCCAGGTATGCCTTC
CAGTGATGCCCCACCAGAGAATACATTCTCTATTAGTTTTTAAAGAGTTTTTGTAATAATGATTTTGTACAAGTAGG
ATATGAATTAGCAGTTTACAAGTTTACATATTAATAATAATAATATGTCTATCAAATACCTCTGTAGTAAAAAT
GTGAAAAAGCAAAA

179/615

FIGURE 178

MGFNLTFHLSYKFRLLLLLTLCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLLILGKGKTLTNEASTKKVELD
NCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYPQECKALQRVAILVPHRNREKHLMYLLEHLHPFLQR
QQLDYGIIYVIHQAEKGKFNRAKLLNVGYLEALKEENWDCFIHFDVLDVPENDFNLYKCEEHPKHLVVGRNSTGYR
LRYSGYFGGVLTALSREQFFKVNGFSNNYWGWGGEDDLRLRLVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAE
RMKLLHQVSRVWRDGLSSCSYKLVSVEHNPLYINITVDFWFGA

Important features:**Signal peptide:**

amino acids 1-27

N-glycosylation sites.

amino acids 4-8, 220-224, 335-339

Xylose isomerase proteins.

amino acids 191-202

180/615

FIGURE 179

CGTGGGCCGGGGTCGCGCAGCGGGCTGTGGGCGCGCCCGGAGGAGCGACCGCCGAGTTCTCGAGCTCCAGCTGC
ATTCCTCCGCGTCCGCCCCACGCTTCTCCGCTCCGGGCCCCGCAATGGCCCCAGGCAGTGTGGTCGCGCCTCGG
CCGCATCCTCTGGCTTGCCCTGCCTCCTGCCCTGGGCCCCGGCAGGGGTGGCCGCAGGCCTGTATGAACCTCAATCT
CACCACCGATAGCCCTGCCACCACGGGAGCGGTGGTGACCATCTCGGCCAGCCTGGTGGCCAAGGACAACGGCAG
CCTGGCCCTGCCCGTGACGCCCACCTCTACCGCTTCCACTGGATCCACACCCCGCTGGTGCTTACTGGCAAGAT
GGAGAAGGGTCTCAGCTCCACCATCCGTGTGGTCGGCCACGTGCCCGGGGAATCCCGGTCTCTGTCTGGGTAC
TGCCGCTGACTGCTGGATGTGCCAGCCTGTGGCCAGGGGCTTTGTGGTCCTCCCATCACAGAGTTCTCGTGGG
GGACCTTGTGTCACCCAGAACACTTCCCTACCCTGGCCAGCTCCTATCTCACTAAGACCGTCTGAAAGTCTC
CTTCCTCCTCCACGACCCGAGCAACTTCTCAAGACCGCCTTGTTCCTCTACAGCTGGGACTTCGGGGACGGGAC
CCAGATGGTGACTGAAGACTCCGTGGTCTATTATAACTATTCCATCATCGGGACCTTACCCTGAAGCTCAAAGT
GGTGGCGGAGTGGGAAGAGGTGGAGCCGGATGCCACGAGGGCTGTGAAGCAGAAGACCGGGGACTTCTCCGCCCTC
GCTGAAGCTGCAGGAAACCTTTCGAGGCATCCAAGTGTGGGGCCACCCCTAATTCAGACCTTCCAAAGATGAC
CGTGACCTTGAACCTTCCGGGGAGCCCTCCTCTGACTGTGTCTGGCGTCTCAAGCCTGAGTGCCTCCCGCTGGA
GGAAGGGGAGTGCCACCTGTGTCCGTGGCCAGCACAGCGTACAACCTGACCCACACCTTCAGGGACCTGGGGA
CTACTGCTTCAGCATCCGGGCCGAGAATATCATCAGCAAGACACATCAGTACCACAAGATCCAGGTGTGGCCCTC
CAGAATCCAGCCGGCTGTCTTTGCTTTCCCATGTGCTACACTTATCACTGTGATGTTGGCCTTCATCATGTACAT
GACCTGCGGAATGCCACTCAGCAAAAGGACATGGTGGAGAACCCGGAGCCACCTCTGGGGTCAGGTGCTGCTG
CCAGATGTGCTGTGGGCCCTTCTTGCTGGAGACTCCATCTGAGTACCTGGAAATTTGTTGCTGAGAACCACGGGCT
GCTCCCGCCCCTCTATAAGTCTGTCAAACTTACACCGTGTGAGCACTCCCCCTCCCCACCCCATCTCAGTGTTA
ACTGACTGCTGACTTGGAGTTTCCAGCAGGGTGGTGTGCACCACTGACCAGGAGGGGTTCAATTTGCGTGGGGCTG
TTGGCCTGGATCATCCATCCATCTGTACAGTTCAGCCACTGCCACAAGCCCCCTCCCTCTCTGTACCCCTGACCC
CAGCCATTACCCATCTGTACAGTCCAGCCACTGACATAAGCCCCACTCGGTTACCACCCCTTGACCCCTACC
TTTGAAGAGGCTTCGTGCAGGACTTTGATGCTTGGGGTGTTCGTTGACTCCTAGGTGGGCCTGGCTGCCCAC
TGCCCATTCCTCTCATATTGGCACATCTGCTGCCATTGGGGTCTCAGTTTCTCCCCAGACAGCCCTACCT
GTGCCAGAGAGCTAGAAAGAAGGTCTATAAAGGTTAAAAATCCATAACTAAAGTTGTACACATAGATGGGCACA
CTCAGAGAGAAGTGTGCATGTACACACACACACACACACACACACACAGAAATATAAACACATG
CGTCACATGGGCATTTAGATGATCAGCTCTGTATCTGGTTAAGTCGGTTGCTGGGATGCACCTGCACTAGAGC
TGAAAGGAAATTTGACCTCCAAGCAGCCCTGACAGGTTCTGGGCCCCGGGCCCTCCCTTTGTGCTTTGTCTGCA
GTTCTTGCGCCCTTTATAAGGCCATCCTAGTCCCTGCTGGCTGGCAGGGGCCCTGGATGGGGGGCAGGACTAATAC
TGAGTGATTGCAGAGTGCTTTATAAATATCACCTTATTTTATCGAAACCCATCTGTGAAACTTTCACTGAGGAAA
AGGCCTTGACGGGTAGAAGAGGTTGAGTCAAGGCCGGGCGCGGTGGCTCACGCCTGTAATCCAGCACTTTGGG
AGGCCGAGGCGGGTGGATCACGAGATCAGGAGATCGAGACCACCTGGCTAACACGGTGAAACCCCGTCTCTACT
AAAAAATACAAAAGTTAGCCGGGCGTGGTGGTGGGTGCTGTAGTCCAGCTACTCGGGAGGCTGAGGCAGGA
GAATGGTGCGAACCCGGGAGGCGGAGCTTGCAGTGAGCCAGATGGCGCCACTGCACTCCAGCCTGAGTGACAGA
GCGAGACTCTGTCTCA

181/615

FIGURE 180

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLALPADAHLYRFHWI
HTPLVLTGKMEKGLSSTIRVVGHVPGEFPVSVVWTAADCWMCQPVARGFVVLPITEFLVGDVVTQNTSLPWSS
YLTKTVLKVSFLLHDPNFKLTALFLYSWDFGDTQMVTEDSVVYYNYSIIIGTFTVKLKVVAEWEEVEPDATRAV
KQKTGDFSASLKLQETLRGIQVLGPTLIQTFOKMTVTNLNGLSPPLTVCWRLKPECLPLEEGECHPVSVASTAYN
LHTFRDPGDYCFSSIRAENIISKTHQYHKIQVWPSRIQPAVFAFPATLITVMLAFIMYMTLRNATQQKDMVENP
EPPSGVRCCCQMCQGFLLLETPSEYLEIVRENHGLLPPLYKSVKTYTV

Important features of the protein:

Signal peptide:
amino acids 1-24

Transmembrane domain:
amino acids 339-362

N-glycosylation sites.
amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

182/615

FIGURE 181

CGGACGCGTGCGGCGCGGCTGCGGAACTCCCGTGAGGGGCCGGTGGGCCCTCGGGCCTGACAGATGGCAGTGGC
CACTGCGGCGGCAGTACTGGCCGCTCTGGGCGGGGCGCTGTGGCTGGCGGCCCGCCGGTTTCGTGGGGCCAGGGT
CCAGCGGCTGCGCAGAGGCGGGGACCCCGGCTCATGCACGGGAAGACTGTGCTGATCACCGGGCGAACAGCGG
CCTGGGCGCGCCACGGCCCGGAGCTACTGCGCCTGGGAGCGCGGGTGATCATGGGCTGCCGGGACCGCGCGG
CGCCGAGGAGGCGGGCGGGTCAGCTCCGCCGCGAGCTCCGCCAGGCCGCGGAGTGCGGCCAGAGCCTGGCGTCAG
CGGGGTGGGCGAGCTCATAGTCCGGGAGCTGGACCTCGCCTCGCTGCGCTCGGTGCGCGCCTTCTGCCAGGAAAT
GCTCCAGGAAGAGCCTAGGCTGGATGTCTTGATCAATAACGCAGGGATCTTCCAGTGCCCTTACATGAAGACTGA
AGATGGGTTTGAGATGCAGTTCGGAGTGAACCATCTGGGGCACTTTCTACTCACCAATCTTCTCCTTGGACTCCT
CAAAAGTTCAGCTCCCAGCAGGATTGTGGTAGTTTCTTCCAACTTTATAAATACGGAGACATCAATTTTGATGA
CTTGAACAGTGAACAAAGCTATAATAAAAGCTTTTGTTATAGCCGGAGCAAAGTGGCTAACATTCTTTTACCAG
GGAAGTACCCCGCGCTTAGAAGGCACAAATGTCACCGTCAATGTGTTGCATCCTGGTATTGTACGGACAAATCT
GGGAGGCGACATACATTTCCACTGTTGGTCAAACCACTCTTCAATTTGGTGTGATGGGCTTTTTTCAAACTCC
AGTAGAAGGTGCCAGACTTCCATTTATTTGGCCTCTTACCTGAGGTAGAAGGAGTGTGAGGAAGATACTTTGG
GGATTGTAAGAGGAAGAACTGTTGCCCAAAGCTATGGATGAATCTGTTGCAAGAAAAGTCTGGGATATCAGTGA
AGTGATGGTTGGCCTGCTAAAAATAGGAACAAGGAGTAAAGAGCTGTTTATAAAAGTGCATATCAGTTATATCTG
TGATCAGGAATGGTGTGGATTGAGAACTTGTTACTTGAAGAAAAAGAATTTTGATATTGGAATAGCCTGCTAAGA
GGTACATGTGGGTATTTTGGAGTTACTGAAAAATTATTTTGGGATAAGAGAATTTGAGCAAGATGTTTTAAAT
ATATATAGTAAGTATAATGAATAATAAGTACAATGAAAAATACAATTATTTGTAATAATTATACTGGGCAAGCA
TGGATGACATATTAATATTTGTCAGAATTAAGTGAAGTCAAGTGTATCGAGAGGTTTTTCAAGTATCTTTGAGT
TTCATGGCCAAAGTGTAACTAGTTTTACTACAATGTTTGGTGTGTTGTGGAATTTATCTGCCTGGTGTGTGCA
CACAAGTCTTACTTGAATAAATTTACTGGTAC

183/615

FIGURE 182

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58747

<subunit 1 of 1, 336 aa, 1 stop

<MW: 36865, pI: 9.15, NX(S/T): 2

MAVATAAAVLAALGGALWLAARRFVGPRVQRLRRGGDPGLMHGKTVLITGANSGLGRATAAELLRLGARVIMGCR
DRARAEAAAGQLRRELQAAECGPEPGVSGVVELIVRELDLASLRSVRAFCQEMLQEEPRLDVLINNAGIFQCPY
MKTEDGFEMQFGVNHGHLNLLNLLGLLKSSAPSRIVVVSSKLYKYGDINFDDLNSEQSYNKSFCYSRSLANI
LFTRELARRLEGTNVTNVNLHPGIVRTNLGRHIHPLLVKPLENLVSWAFFKTPVEGAQTISIYLASSPEVEGVSG
RYFGDCKEEELLPKAMDESVARKLWDISEVMVGLLK

Important features:**Signal peptide:**

amino acids 1-21

Short-chain alcohol dehydrogenase family protein

amino acids 134-144, 44-56 and 239-248

N-glycosylation site.

amino acids 212-215 and 239-242

184/615

FIGURE 183

AACAGGATCTCCTCTTGCACTCTGCAGCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGCAGCCGAAGATTCT
ACTATGGTGAAAATCGCCTTCAATACCCCTACCGCCGTGCAAAAGGAGGAGGCGCGGCAAGACGTGGAGGCCCTC
CTGAGCCGCACGGTCAGAACTCAGATACTGACCGGCAAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCC
TCTGGGAGATGTATGCTTACTCTCTTAGGCCTTTCATTCATCTTGGCAGGACTTATTGTTGGTGGAGCCTGCATT
TACAAGTACTTCATGCCCAAGAGCACCATTACCGTGGAGAGATGTGCTTTTTTGATTCTGAGGATCCTGCAAAT
TCCCTTCGTGGAGGAGAGCCTAACTTCCTGCCTGTGACTGAGGAGGCTGACATTCGTGAGGATGACAACATTGCA
ATCATTGATGTGCCTGTCCCAAGTTTCTCTGATAGTGACCCTGCAGCAATTATTCATGACTTTGAAAAGGGAATG
ACTGCTTACCTGGACTTGTTGCTGGGGAACCTGCTATCTGATGCCCTCAATACTTCTATTGTTATGCCTCCAAAA
AATCTGGTAGAGCTCTTGGCAAACCTGGCGAGTGGCAGATATCTGCCTCAAACCTTATGTGGTTCGAGAAGACCTA
GTTGCTGTGGAGGAAATTCGTGATGTTAGTAACCTTGGCATCTTTATTTACCAACTTTGCAATAACAGAAAGTCC
TTCCGCCTTCGTGCGAGAGACCTCTTGTGGGTTTCAACAAACGTGCCATTGATAAATGCTGGAAGATTAGACAC
TTCCCAACGAATTTATTGTTGAGACCAAGATCTGTCAAGAGTAAGAGGCAACAGATAGAGTGTCTTGGTAATA
AGAAGTCAGAGATTTACAATATGACTTTAACATTAAGGTTTATGGGATACTCAAGATATTTACTCATGCATTTAC
TCTATTGCTTATGCTTTAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGG
TAATTGGCATTGCTTGTGTTTGGAACTGAAATTACATGAGTTTCATTTTTTCTTGCATTTATAGGGTTTAGAT
TTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATTCCATCCGTTGTTTTTTTTGTTGTTTGT
TTTTTCTTTTCTTTAAGTAAGCTCTTTATTCATCTTATGGTGGAGCAATTTAAAATTTGAAATATTTAAATT
GTTTTTGAACCTTTTTGTGTAATAATATATCAGATCTCAACATTGTTGGTTTCTTTGTTTTTCATTTTGTACAAC
TTCTTGAATTTAGAAATFACATCTTTGCAGTTCTGTTAGGTGCTCTGTAATTAACCTGACTTATATGTGAACAAT
TTTCATGAGACAGTCATTTTAACTAATGCAGTGATTCTTCTCACTACTATCTGTATTGTGGAATGCACAAAAT
TGTGTAGGTGCTGAATGCTGTAAGGAGTTTAGGTTGTATGAATTCTACAACCTATAATAAATTTACTCTATAC
AAAAAAAAAAAAAAAAAAAA

185/615

FIGURE 184

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828
<subunit 1 of 1, 263 aa, 1 stop
<MW: 29741, pI: 5.74, NX(S/T): 1
MVKIAFNTPTAVQKEEARQDVEALLSRTVVRTQILTGKELRVATQEKEGSSGRCMLTLLGLSFIAGLIVGGACIY
KYFMPKSTIYRGEMCFFDSEDPANSLRGGEPNFLPVTEEADIREDDNIAIIDVPVPSFSDSDPAAIHDFEKGMT
AYLDLLGNLCYLMPLNTSIVMPPKNLVELFGKLASGRYLPQTYVVREDLVAVEEIRDVSNLGIFIYQLCNNRKSF
RLRRRDLLGFGNKRAIDKCWKIRHFPNEFIVETKICQE

Type II transmembrane domain:
amino acids 53-75

N-glycosylation site.
amino acids 166-170

Casein kinase II phosphorylation site.
amino acids 35-39, 132-136, 134-138

N-myristoylation site.
amino acids 66-72, 103-109

Prokaryotic membrane lipoprotein lipid attachment site.
amino acids 63-74

186/615

FIGURE 185

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACGATGGCACTGAGCTCCCAGATCTGGGCCGCTTGCCT
CCTGCTCCTCCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTTTCCACAAACAGACGGGACAACCTTGCAGAGCT
GCAACCCAGGACAGAGCTGGAGCCAGGGCCAGCTGGATGCCCATGTTCCAGAGGCGAAGGAGGCGAGACACCCA
CTTCCCCATCTGCATTTTCTGCTGCGGCTGCTGTCATCGATCAAAGTGTGGGATGTGCTGCAAGACGTAGAACCT
ACCTGCCCTGCCCCCGTCCCCTCCCTTATTTATTCCTGCTGCCCCAGAACATAGGTCTTGGAATAAAATGG
CTGGTCTTTTGTTCCTCAA
AAA

187/615

FIGURE 186

MALSSQIWAACLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTHFPICIFCCGCCHR
SKCGMCCKT

188/615

FIGURE 187

CTGTCAGGAAGGACCATCTGAAGGCTGCAATTTGTTCTTAGGGAGGCAGGTGCTGGCCTGGCCTGGATCTTCCAC
CAIGTTCTCTGTTGCTGCGCTTTTGATAGCCTGATTGTCAACCTTCTGGGCATCTCCCTGACTGTCTCTTCAACCT
CCTTCTCGTTTTTCATCATAGTGCCAGCCATTTTGGAGTCTCCTTTGGTATCCGCAAACCTCTACATGAAAAGTCT
GTTAAAAATCTTTGCGTGGGCTACCTTGAGAAATGGAGCGAGGAGCCAAGGAGAAGAACCACCAGCTTTACAAGCC
CTACACCAACGGAATCATTGCAAAGGATCCCACTTCACTAGAAGAAGAGATCAAAGAGATTTCGTCGAAGTGGTAG
TAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTCTGACATTTTCTACTTTTGCCGGAAGGAATGGAGAC
CATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAACTGGAGTCTTGGAACTGCTGAGCAGAACC
TTATAACTTCCAGTACATCAGCCTTCGGCTCACGGTCTGTGGGGGTAGGAGTGCTGATTCCGGTACTGCTTTCT
GCTGCCGCTCAGGATAGCACTGGCTTTACAGGGATTAGCCTTCTGGTGGTGGGCACAACCTGTGGTGGGATACTT
GCCAAATGGGAGGTTTAAGGAATTATGAGTAAACATGTTCACTTAATGTGTTACCGGATCTGCGTGCAGCGCT
GACAGCCATCATCACCTACCATGACAGGGAAAACAGACCAAGAAATGGTGGCATCTGTGTGGCCAATCATACCTC
ACCGATCGATGTGATCATCTTGGCCAGCGATGGCTATTATGCCATGGTGGGTCAAGTGCACGGGGGACTCATGGG
TGTGATTGAGAGGCCATGGTGAAGGCTGCCACACGTCTGGTTGAGCGCTCGGAAGTGAAGGATCGCCACCT
GGTGGCTAAGAGACTGACTGAACATGTGCAAGATAAAGCAAGCTGCCTATCCTCATCTTCCAGAAAGGAACCTG
CATCAATAATACATCGGTGATGATGTTCAAAAAGGGAAGTTTTGAAATTGGAGCCACAGTTTACCCTGTTGCTAT
CAAGTATGACCCTCAATTTGGCGATGCCTTCTGGAACAGCAGCAAATACGGGATGGTGACGTACCTGCTGCGAAT
GATGACCAGCTGGGCCATTGTCTGCAGCGTGTGGTACCTGCCTCCCATGACTAGAGAGGCAGATGAAGATGCTGT
CCAGTTTGCGAATAGGGTGAAATCTGCCATTGCCAGGCAGGGAGGACTTGTGGACCTGCTGTGGGATGGGGGCCT
GAAGAGGGGAGAAGGTGAAGGACAGCTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGAACCA
CAAGGACAGGAGCCGCTCCTGAGCCTGCCTCCAGCTGGCTGGGGCCACCGTGCGGGGTGCCAACGGGCTCAGAGC
TGGAGTTGCCGCCGCCGCCCTGCTGTGTCTTTCCAGACTCCAGGGCTCCCCGGGCTGCTCTGGATCCCAG
GACTCCGGCTTTGCGCGAGCCGAGCGGGATCCCTGTGACCCGGCGCAGCTACCTTGGTGGTCTAAACGGAT
GCTGCTGGGTGTTGCGACCCAGGACGAGATGCCTTGTCTTTTACAATAAGTCGTTGGAGGAATGCCATTAAAG
TGAATCCCCACCTTTGCACGCTGTGCGGGCTGAGTGGTTGGGGAGATGTGGCCATGGTCTTGTGCTAGAGATGG
CGGTACAAGAGTCTGTTATGCAAGCCCGTGTGCCAGGGATGTGCTGGGGGCGGCCACCCGCTCTCCAGGAAAGGC
ACAGCTGAGGCACTGTGGCTGGCTTCGGCTCAACATCGCCCCAGCCTTGGAGCTCTGCAGACATGATAGGAAG
GAACTGTCTATCTGCAGGGGCTTTTACGAAAATGAAGGGTTAGATTTTTATGCTGCTGCTGATGGGGTTACTAAA
GGGAGGGGAAGAGGCCAGGTGGGCCGCTGACTGGGCCATGGGGAGAACGTGTGTTTCGTACTCCAGGCTAACCTTG
AACTCCCCATGTGATGCGCGCTTTGTTGAATGTGTCTCGGTTTCCCCATCTGTAATATGAGTCGGGGGGAATG
GTGGTGATTCTTACCTCACAGGGCTGTTGTGGGGATTAAAGTGCTGCGGGTGAGTGAAGGACACATCACGTTTCA
TGTTTCAAGTACAGGCCACAAAACGGGGCAGGCGAGGCTGAGCTCAGAGCTGCTGCACTGGGCTTTGGATTTG
TTCTTGTGAGTAAATAAACTGGCTGGTGAATGA

189/615

FIGURE 188

MFLLLPFD SLIVNLLGISLTVLFTLLLVFII VPAIFGV SFGIRKLYMKSLLKIFAWATLRMERGAKEKNHQLYKP
YTNGIIAKDPTSLEEEIKEIRRS GSSKALDNTPEFELSDIFYFCRKG METIMDDEVTKRFS AEELESWNLLSRTN
YNFYI SLRLTVLWGLGV LIRYCFLLPLRIALFTGISLLVVGTTVVGYLPNGRFKEFMSKHVHLMCYRICVRL
TAITYHDRENRP RGGICVANHTSPIDV IILASDGY YAMVGQVHGGLMGVIQRAMVKACPHVWFERSEVKDRHL
VAKRLTEHVQDKSKLPILIFPEGTCINNTSVMMFKKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMVTYLLRM
MTSWAIVCSVWYLP PMTREADED AVQFANRVKSAIARQGGLVDLLWDGGLKREKVKDTFKEEQQKLYSKMIVGNH
KDRSRS

190/615

FIGURE 189

GCCCCTCGAAACCAGGACTCCAGCACCTCTGGTCCCGCCCTCACCCGGACCCCTGGCCCTCACGTCTCCTCCAGG
GATGGCGCTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGGCCTCCACACCTGGCAGGCCAGGCTGTTCCCAC
CATCCTGCCCCCTGGCCCTGGCTCCAGACACCTTTGACGATACCTATGTGGGTTGTGCAGAGGAGATGGAGGAGAA
GGCAGCCCCCCTGCTAAAGGAGGAAATGGCCCCACCATGCCCTGCTGCGGGAATCCTGGGAGGCAGCCCAGGAGAC
CTGGGAGGACAAGCGTCGAGGGCTTACCTTGCCCCCTGGCTTCAAAGCCCAGAATGGAATAGCCATTATGGTCTA
CACCAACTCATCGAACACCTTGTACTGGGAGTTGAATCAGGCCGTGCGGACGGGCGGAGGCTCCCGGGAGCTCTA
CATGAGGCACTTTCCCTTCAAGGCCCTGCATTTCTACCTGATCCGGGCCCTGCAGCTGCTGCGAGGCAGTGGGGG
CTGCAGCAGGGGACCTGGGGAGGTGGTGTTCGAGGTGTGGGCAGCCTTCGCTTTGAACCCAAGAGGCTGGGGGA
CTCTGTCCGCTTGGGCCAGTTTGCCTCCAGCTCCCTGGATAAGGCAGTGGCCACAGATTGGGGAGAAGAGGCG
GGGCTGTGTGTCTGCGCCAGGGGTGCAGCTAGGGTCACAATCTGAGGGGGCCTCCTCTCTGCCCCCTGGAAGAC
TCTGCTCTTGGCCCCCTGGAGAGTTCCAGCTCTCAGGGGTGGGGCCCTTGAAAGTCCAACATCTGCCACTTAGGAGC
CCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAGCAGCCTTGAGAAGCAAGAACATGGTTCCGGAC
CCAGCCCTAGCAGCCTTCTCCCCAACAGGATGTTGGCCTGGGGAGGCCACAGCAGGGCTGAGGGAACTCTGCTA
TGTGATGGGGACTTCCTGGGACAAGCAAGGAAAGTACTGAGGCAGCCACTTGATTGAACGGTGTGCAATGTGGA
GACATGGAGTTTTATTGAGGTAGCTACGTGATTAATGGTATTGCAGTGTGGA

191/615

FIGURE 190

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGCAEEMEKAAPLLKEEMAHHALLRESWEAAQET
WEDKRRGLTLPPGFKAQNGIAIMVYTNSSNTLYWELNQAVRTGGGSRELYMRHFPFKALHFYLIRALQLLRGSGG
CSRGPGEVVFRGVGSLRFEPKRLGDSVRLGQFASSSLDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPWK
LLLAPGEFQLSGVGP

192/615

FIGURE 191

GTGGCTTCATTTAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCTCAACATGCCTCACCTCATCTATAT
CCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTGGTCGGTTCCGTTGGTGGGGCCGTGAC
TTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTCAACAT
ACAGCCAGAAGGGGGCACTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTA
CTCCCTGAAGCTCAGCAAACTGAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACTCCA
GCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCA
GAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATTTATAC
CTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTCCCATATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAGA
AAGTGATATGACCTTCATCTGCGTTGCCAGGAACCTGTGAGCAGAACTTCTCAAGCCCCATCCTTGCCAGGAA
GCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCCTCCTGTGTCTCCTGTTGGTGCCCTCCTGCT
CAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAA
GAGAGTGGACATTTGTGCGGAACTCCTAACATATGCCCCATTCTGGAGAGAACACAGAGTACGACACAATCCC
TCACACTAATAGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAAAGAT
GGAAAATCCCCACTCACTGCTCACGATGCCAGACACACCAAGGCTATTTGCCTATGAGAATGTTATCTAGACAGC
AGTGCACCTCCCTAAGTCTCTGCTCA

193/615

FIGURE 192

MAGSPTCLTLIYILWQLTGSAAAGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVTIQPEGGTIIIVTON
RNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHVYEHLSKPKVTMGLQSNKNGTCVTNLT
CCMEHGEEDVIYTWKALGQAANESHNGSILPISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSS
MVLCLLLVPLLLSLFVLGLFLWFLKRERQEEYIEKKRVDICRETPNICPHSGENTYDTPHTNRTILKEDPA
NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI

FIGURE 193

[illegible]

195/615

FIGURE 194

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852

><subunit 1 of 1, 283 aa, 1 stop

><MW: 29191, pI: 4.52, NX(S/T): 0

MVSAAAPSLILLILLLLGSPATDARSVPLKATFLEDVAGSGEAGSSASSPSLPPPWTTPALSPTSMGPQPTTLG
GPSPTNFDGIVDFFRQYVMLIAVVGSLAFLLMFIVCAAVITRQKQKASAYYPSSFPPKKKYVDQSDRAGGPRAF
SEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSPTRAALGGGDGARMVEGRGAEEEEKGSQEGDQEVQGHGVP
VETPEAQEEPCSGVLEGAVVAGEGQGELEGSLLLAQEAQGPVGPPEPCACSSVHPSV

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 94-118

N-myristoylation site.amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199, 211-217, 238-244,
242-248

196/615

FIGURE 195

GAAAGACGTGGTCTCTGACAGACAGACAATCCTATTCCCTACCAAAATGAAGATGCTGCTGCTGCTGTGTTTGGGA
CTGACCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGAACTTTAATGTAGAAAAGATTAATGGG
GAATGGCATACTATTATCCTGGCCTCTGACAAAAGAGAAAAGATAGAAGAACATGGCAACTTTAGACTTTTTCTG
GAGCAAATCCATGTCTTGGAGAATTCCTTAGTTCTTAAAGTCCATACTGTAAGAGATGAAGAGTGTCCGAATTA
TCTATGGTTGCTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACTATA
CCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAAACGAAAAGGATGGGGAAACCTTCCAGCTGATG
GGGCTCTATGGCCGAGAACCAGATTTGAGTTCAGACATCAAGGAAAGGTTGCACAACTATGTGAGGAGCATGGA
ATCCTTAGAGAAAATATCATTGACCTATCCAATGCCAATCGCTGCCTCCAGGCCCGAGAATGAAGAATGGCCTGA
GCCTCCAGTGTGAGTGGACACTTCTCACCAGGACTCCACCATCATCCCTTCCTATCCATACAGCATCCCCAGTA
TAAATTCTGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATTCCAGTCTATCAACATGTTACCTAGGAT
ACCTCATCAAGAATCAAAGACTTCTTAAATTTCTCTTGATACACCCTTGACAATTTTTTCATGAAATTATTCCT
CTTCCTGTTCAATAAATGATTACCCTTGCACTTAA

197/615

FIGURE 196

MKMLLLLCGLTLVCVHAAEEASSTGRNFNVEKINGEWHTIILASDKREKIEEHGNFRLFLEQIHVLENSLVLVKH
TVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLINEKDGETFQLMGLYGREPDLSSEDIKE
RFAQLCEEHGILRENIIDLSNANRCLQARE

198/615

FIGURE 197

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAATGGATTGAGCCTG
CTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTGTCAGCTTAGTTGAGGAAGACCAATTT
TCTCAAAACCCCATCTCTTGCTTTGAGTGGTGGTCCCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCA
ACAACAATGTCCTTGACAGCAAGAAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTC
AGTGTGATCACAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTCATG
TGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGACATTTCATCCAGAATCC
TTCAACTTGCAAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTGGTTTTCAATAAACCACAGTAACGACACC
ATGGCGAGTGGCTGGAGAGCATCTAGTTTCCACTTCGATTCTGAAGAAAACAAACATAGGCTTATCCACTTCTCA
GTATTTTATAGTCTATTGCTTGTGGAATTCGGAGGTCCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCCTT
GGCTGTCTGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTGTAGTTTAAATGGAATAAAATGTAAGTATCAGTA
GTTTGAAAAA

199/615

FIGURE 198

MTCCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMAIPATTMSLTARKR
ACCNNRTGMFLSSFFSVITVIGALYCM LISIQALLKGPLMCNSPSNSNANCEFSLKNISDIHPESFNLQWFFNDS
CAPPTGFNKPTSNDTMASGWRASSFHF DSEENKHRLIHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGVSKRR
SQIV

200/615

FIGURE 199

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGGTGAAGGAGCAGTG
AGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTGGAGCAGATCCGTGGGCTGCAGACCCC
CGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCCCTCGAACTGTGACATGGAGAGAGTGACCCTGGCCCTTCTCCT
ACTGGCAGGCCTGACTGCCTTGAAGCCAATGACCCATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAA
AAACCTGCAGCTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGGCAA
ATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCACTCATCACTCCAGGCTC
TGCCACTACTTGCTGAGCACAGGACTGGCCTCCAGGGATGGCCTGAAGCCTAACACTGGCCCCCAGCACCTCCTC
CCCTGGGAGGCCTTATCCTCAAGGAAGGACTTCTCTCCAAGGGCAGGCTGTTAGGCCCTTTCTGATCAGGAGGC
TTCTTTATGAATTAACTCGCCCCACCACCCCTCA

201/615

FIGURE 200

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCKYKSSQKQHSPVPE
KAIPLITPGSATTC

FIGURE 201

[illegible]

203/615

FIGURE 202

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212
><subunit 1 of 1, 440 aa, 1 stop
><MW: 42208, pI: 6.36, NX(S/T): 1
MKFQGFLACLLALCLGSGEAGFLQSGEESTGTNIGEALGHGIGDALSEGVGKAIGKEAGGAAGSKVSEALGQGT
REAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHGADAVRGSWQGVPGHSGAWETSGGHGI
FGSQGGLGGQGGQGNPGGLGTPWVHGYPGNSAGSFGMNPQGAPWQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQ
NEGCTNPPPSGSGGGSSNSGGGSGSQSGSSGSGSNGDNNNGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSS
RGDSGSESSWGSSTGSSSGNHGGSGGGNGHKPGCEKPGNEARGSGESGIQGRGQGVSSNMREISKEGNRLLGGS
GDNYRGQGSWSGSGGDAVGGVNTVNSETPGMFNFDTFWKNFKSKLGFINWDAINKDQRSSRIP
```

Signal peptide:
amino acids 1-21

N-glycosylation site.
amino acids 265-269

Glycosaminoglycan attachment site.
amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.
amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.
amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70, 74-80, 90-96,
96-102, 130-136, 140-146, 149-155, 152-158, 155-161, 159-165, 163-169,
178-184, 190-196, 194-200, 199-205, 218-224, 236-242, 238-244, 239-245,
240-246, 245-251, 246-252, 249-252, 253-259, 256-262, 266-272, 270-276,
271-277, 275-281, 279-285, 283-289, 284-290, 287-293, 288-294, 291-297,
292-298, 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,
323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387, 383-389,
387-393, 389-395, 395-401

Cell attachment sequence.
amino acids 301-304

204/615

FIGURE 203

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGGATGTCGCTGCTGAGCCTGCCCTGGCTGGGCCTCA
GACCGGTGGCAATGTCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTCCTGGCTACTCGCCCGCATCCTGGCTT
GGACCTATGCTTCTATAACAAGTCCCGCCGGCTCCAGTGTTTCCACAGCCCCAAAACGGAAGTGGTTTTGGG
GTCACCTGGGCTGATCACTCCTACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTGCGCCACCTATTCCCAGG
GCTTTACGGTATGGCTGGGTCCCATCATCCCCTTCATCGTTTTATGCCACCCTGACACCATCCGGTCTATACCA
ATGCCTCAGCTGCCATTGCACCAAGGATAATCTCTTCATCAGGTTCCCTGAAGCCCTGGCTGGGAGAAGGGATAC
TGCTGAGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGACGCCCGCCTTCCATTTCAACATCCTGAAGT
CCTATATAACGATCTTCAACAAGAGTGCAAACATCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCA
GTCGTCTGGACATGTTTGAGCACATCAGCCTCATGACCTTGAGACAGTCTACAGAAATGCATCTTCAGCTTTGACA
GCCATTGTCAGGAGAGGCCAGTGAATATATTGCCACCATCTTGGAGCTCAGTGCCCTTGTAGAGAAAAGAAGCC
AGCATATCCTCCAGCACATGGACTTTCTGTATTACCTCTCCCATGACGGGCGGCGCTTCCACAGGGCCTGCCGCC
TGGTGTCATGACTTCACAGACGCTGTCATCCGGGAGCGGCGTCGCACCTCCCCACTCAGGTATTGATGATTTTT
TCAAAGACAAAGCCAAGTCCAAGACTTTGGATTTCATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGG
CATTGTGAGATGAGGATATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACGGCCAGTGGCC
TCTCCTGGGTCTGTACAACCTTGCGAGGCACCCAGAATACCAGGAGCGCTGCCGACAGGAGGTGCAAGAGCTTC
TGAAGGACCGCGATCCTAAAGAGATTGAATGGGACGACCTGGCCCAGCTGCCCTTCTGACCATGTGCGTGAAGG
AGAGCCTGAGGTTACATCCCCAGCTCCCTTCATCTCCCGATGCTGCACCCAGGACATTGTTCTCCAGATGGCC
GAGTCATCCCCAAAGGCATTACCTGCCTCATCGATATTATAGGGGTCCATCACAACCAACTGTGTGGCCGGATC
CTGAGGTCTACGACCCCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTACCTCTGGCTTTTATTCTTTCT
CCGACGGGCCCAGGAAGTGCATCGGGCAGGCGTTTCGCCATGGCGGAGATGAAAGTGGTCCTGGCGTTGATGCTGC
TGCATTCCGGTTCCTGCCAGACCACACTGAGCCCCGCAGGAAGCTGGAATTGATCATGCGCGCCGAGGGCGGGC
TTTGGCTGCGGTGGAGCCCCTGAATGTAGGCTTGAGTGACTTTCTGACCCATCCACCTGTTTTTTTGCAGATT
GTCATGAATAAAACGGTGCTGTCAA

205/615

FIGURE 204

MSLLSLPWLGLRPVAMSPWLLLLLVGSWLLARILAWTYAFYNNCRRLQCFPQPPKRNWFWGHLGLITPTEGLK
DSTQMSATYSQGFTVWLGPPIPFIVLCHPDTIRSITNASAAIAPKDNLFIRFLKPWLGEIGILLSGGDKWSRHRM
LTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGSSRLDMFEHISLMTLDSLQKCFSDSHCQERPSEYIATI
LELSALVEKRSQHILQHMDFLYYLSHDGRRFHRACRLVHDFTDVIRERRRTLPTQGIDDFKDKAKSKTLD FID
VLLSKDEDGKALSDEDIRAEADTFMFGGHD TTASGLSWVLYNLARHPEYQERCQEVQELLKDRDPKEIEWDDL
AQLPFLTMCVKESLRLHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVWPDPEVYDPFRFDPENS
KGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHTEPRRKLELIMRAEGGLWLRVEPLNVGLQ

206/615

FIGURE 205

TCCCTTGACAGGTCTGGTGGCTGGTTCGGGGTCTACTGAAGGCTGTCTTGATCAGGAACTGAAGACTCTCTGCT
TTTGCCACAGCAGTTCCCTGCAGCTTCCTTGAGGTGTGAACCCACATCCCTGCCCCAGGGCCACCTGCAGGACGC
CGACACCTACCCCTCAGCAGACGCCGGAGAGAAATGAGTAGCAACAAAGAGCAGCGGTGAGCAGTGTTCGTGATC
CTCTTTGCCCTCATCACCATCCTCATCCTCTACAGCTCCAACAGTGCCAATGAGGTCTTCCATTACGGCTCCCTG
CGGGGCCGTAGCCGCCGACCTGTCAACCTCAAGAAGTGGAGCATCACTGACGGCTATGTCCCCATTCTCGGCAAC
AAGACACTGCCCTCTCGGTGCCACCAGTGTGTGATTGTGACGAGCTCCAGCCACCTGCTGGGCACCAAGCTGGGC
CCTGAGATCGAGCGGGCTGAGTGTACAATCCGCATGAATGATGACCCACCCTGGCTACTCAGCTGATGTGGGC
AACAGACCACCTACCGCGTCGTGGCCCATTCAGTGTGTTCCGCGTGCTGAGGAGGCCCCAGGAGTTTGTCAAC
CGGACCCCTGAAACCGTGTTTCATCTTCTGGGGGCCCCGAGCAAGATGCAGAAGCCCCAGGGCAGCCTCGTGCGT
GTGATCCAGCGAGCGGGCCTGGTGTTCCTCAACATGGAAGCATATGCCGTCTCTCCGGCCGCATGCGGCAATTT
GACGACCTCTTCCGGGGTGAGACGGGCAAGGACAGGGAGAAGTCTCATTCGTGGTTGAGCACAGGCTGGTTTACC
ATGGTGATCGCGGTGGAGTTGTGTGACCAGTGCATGTCTATGGCATGGTCCCCCACTACTGCAGCCAGCGG
CCCCGCTCCAGCGCATGCCCTACCACTACTACGAGCCCAAGGGGCCGACGAATGTGTACCTACATCCAGAAT
GAGCAGTGCAGGGCAACCACCACCGCTTCATCACCAGAAAAAGGGTCTTCTCATCGTGGGCCAGCTGTAT
GGCATCACCTTCTCCACCCCTCCTGGACCTAGGCCACCCAGCCTGTGGGACCTCAGGAGGGTCAGAGGAGAAGC
AGCCTCCGCCCAGCGCTAGGCCAGGGACCATCTTCTGGCCAATCAAGGCTTGCTGGAGTGTCTCCAGCCAATC
AGGGCCTTGAGGAGGATGTATCCTCCAGCCAATCAGGGCCTGGGGAATCTGTTGGCGAATCAGGGATTTGGGAGT
CTATGTGGTTAATCAGGGGTGTCTTTCTTGTGAGTCAAGGCTGTGCGCACAGTCAATCAGGGTAGAGGGGGTATT
TCTGAGTCAATCTGAGGCTAAGGACATGTCTTTCCCATGAGGCTTGTTTCAGAGCCCCAGGAATGGACCCCC
AATCACTCCCCACTCTGCTGGGATAATGGGGTCTGTCCAAGGAGCTGGGAATTTGGTGTGCCCCCTCAATTT
CCAGCACCAGAAAGAGAGATTGTGTGGGGGTAGAAGCTGTCTGGAGGCCCGGCCAGAGAATTTGTGGGGTTGTGG
AGGTTGTGGGGGCGGTGGGGAGGTCCCAGAGGTGGGAGGCTGGCATCCAGGTCTTGGCTCTGCCCTGAGACCTTG
GACAAACCCTTCCCCCTCTCTGGGCACCCCTTCTGCCCACACAGTTTCCAGTGCGGAGTCTGAGACCCCTTTCCAC
CTCCCCACAAGTGCCCTCGGGTCTGTCTCCCGCTCTGGACCTCCAGCCACTATCCCTTGCTGGAAGGCTCA
GCTCTTTGGGGGGTCTGGGGTGACCTCCCCACCTCCTGGAAACTTTAGGGTATTTTTCGCAAACTCCTTCAGG
GTTGGGGGACTCTGAAGGAAACGGGACAAAACCTTAAGCTGTTTTCTTAGCCCCCTCAGCCAGCTGCCATTAGCTT
GGCTCTTAAAGGGCCAGGCCTCCTTTCTGCCCTCTAGCAGGGAGGTTTTCCAATGTTGGAGGCGCCTTTGGGG
CTGCCCCCTTTGTCTGGAGTCACTGGGGGCTTCCGAGGGTCTCCCTCGACCTCTGTCTGCTCCTGGGATGGCTGTCTG
GGAGCTGTATCACCTGGGTTCTGTCCCCCTGGCTCTGTATCAGGCACTTTATTAAAGCTGGGCCTCAGTGGGGTGT
GTTTGTCTCCTGCTCTTCTGGAGCCTGGAAGGAAAGGGCTTCAGGAGGAGGCTGTGAGGCTGGAGGGACCATG
GAGGAGGCCAGCAGTAGCCATTGCACACTGGGGTGATGGGTGGGGGCGGTGACTGCCCCAGACTTGGTTTTGTA
ATGATTTGTACAGGAATAAACACACCTACGCTCCGGAAAAA

207/615

FIGURE 206

MSSNKEQRSADFVILFALITILILYSSNSANEVFHYGSLRGRSRPVLKKWSITDGYVPILGNKTLPSRCHQCV
IVSSSSHLIGTKLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAHSSVFRVLRRPQEFVNRTPETVFIFWG
PPSKMQKPPQGSLLRVVIQRAGLVFPNMEAYAVSPGRMRQFDDLFRGETGKDREKSHSWLSTGWFTMVIAVELCDHV
HVGMPVPPNYCSQRRLQRMPIHYEYPKGPDECVTYIQNEHSRKGNNHRRFITEKRVFSSWAQLYGITFSHPST

Signal peptide:
amino acids 1-29

Transmembrane domain:
amino acids 9-31 (type II)

N-glycosylation site.
amino acids 64-68, 115-119

cAMP- and cGMP-dependent protein kinase phosphorylation site.
amino acids 50-54

Casein kinase II phosphorylation site.
amino acids 3-7, 29-33, 53-57, 197-201

Tyrosine kinase phosphorylation site.
amino acids 253-262

N-myristoylation site.
amino acids 37-43, 114-120, 290-294

208/615

FIGURE 207

GTAGCGCGTCTTGGGTCTCCCGGCTGCCGCTGCTGCCGCCGCCGCTCGGGTCTGGAGCCAGGAGCGACGTCAC
CGCCATGGCAGGCATCAAAGCTTTGATTAGTTTGTCTTTGGAGGAGCAATCGGACTGATGTTTTGATGCTTGG
ATGTGCCCTTCCAATATACAACAAATACTGGCCCTCTTTGTTCTATTTTTTTACATCCTTTCACCTATTCCATA
CTGCATAGCAAGAAGATTAGTGGATGATACAGATGCTATGAGTAACGCTTGTAAGGAAGTTGCCATCTTTCTTAC
AACGGGCATTGTCGTGTGAGCTTTTGGACTCCCTATTGTATTTGCCAGAGCACATCTGATTGAGTGGGGAGCTTG
TGCATTGTTCTCACAGGAAACACAGTCATCTTTGCAACTATACTAGGCTTTTCTTGGTCTTTGGAAGCAATGA
CGACTTCAGCTGGCAGCAGTGGTGAAGAAATTACTGAAGTATTGTCAAATGGACTTCCTGTCAATTTGTTGGCC
ATTCACGCACACAGGAGATGGGGCAGTTAATGCTGAATGGTATAGCAAGCCTCTTGGGGTATTTAGGTGCTCC
CTTCTCACTTTTATTGTAAGCATACTATTTTACAGAGACTTGCTGAAGGATTAAAGGATTTTCTCTTTGGAA
AAGCTTGACTGATTTACACTTATCTATAGTATGCTTTTGTGGTGTCTGCTGAATTTAAATATTTATGTGTTT
TTCTGTTAGGTTGATTTTTTTTGGAAATCAATATGCAATGTTAAACACTTTTTTAATGTAATCATTTGCATTGGT
TAGGAATTCAGAATTCGCCCGGCTCTATTACTGGTCAAGTACATCTTTTCTTAAATATTTAGCCTCCATTA
TTACAAAAAATTATAAAAAAAGTTTTCAGTCAGTCAGGATGACATCACTCCCAATGTTATGCAGACATACAGAC
GGTTGGCATACTGTTATAGACTGTATACTCAGTGCATAATAGCTGCATTTATACCTCAGAGGGCCAAAGTGTTAA
TGCCCATGCCCTCCGTTAAGGGTTGTTGGTTTACTGGTAGACAGATGTTTTGTGGATTGAAATTTATTTATGG
AATTGCTACAGAGGAGTGTCTTTCTCTCAATTGTTAGAAGAATTTATGTTAACTTTAAGGTAAGGGTGTA
ACATTTTGTAGATAAGGTTTTTATTTATGTTTATTATGTTAGAGTGAGTTGCAATGTGGGAAGAAATGACATTG
AAATCCAGTTTTTGAATCCTGTTTCTATTATAAGTGAATTTGTGATCTCCTATCAACCTTTCATGTTTTACC
CTGTTAAATGGACATACATGGAACCACTACTGATGAGGACAGTTGTATGTTTGCATCATATATGCCAGAAAAC
CTTCTCTGCTTCTCTCTTTTGACTTATTTGGTATGTTGTATATATTACATAAAATAAATTTTCAATATAGTTT
AATAACACTTAGAAGTGTTTACTTACCTGGAAAATAATTGCTATGCCGTACATTCAGAGTGCCCCCTCCCCTGCA
AGGCCTTGCCATGATTAACAAGTAACCTGTTAGTCTTACAGATAATTCATGCATTAACAGTTTAAAGATTTAGACC
ATGGTAATAGTAGTCTTATTTCTCTAAGGTTATATCATATGTAATTTAAAGTATTTTTAAGACAAGTTTCTGT
ATACCTCTGAAGTGTGTTTGTATTTTGTGTTTCAATCATGATAGATCTGCTGTTTCTTATAAAAGGCATTGTTGTGT
GAGTTAATGCAAAGTAGCCAAGTCCAGCTATATAGCAGCTTCAGAAACATACCTGACCAAAAAATTTCCAGTAAC
CAGGCATGATCAATTTATAGTGGTCTGTTTACATCTAATAATATCAGGACTTTTTTCAGGAGTGGGTATAAAAA
CATTCAAGTTGGTCTGACAGTATTTTGTAAAGGATATTGTTTGTATGTTTATTCAGTATACTTACATAAAAAAT
ATTTGCCATCAGCCAAAACCTCAGTAATCATGACAGCTGTCTGTTGTTTTATGAAGTTTATTTCTCAAGAAAATG
GGAATAAATTTGGGATTTGTTTCTAGCTTTTTTACTAAAGATGCCTAAAGCCACAGGTTTTATTGCTAACTTAAGC
CATGACTTTTAGATATGAGATGACGGGAAGCAGGACGAAATATCGGCGTGTGGCTGGAGCCTTCCCACTGGAGGC
TGAAAGTGGCTTGTGGTATTATAATGTTTACAGTTTCAAGAGGAAGGTGCAGGTACACATGAGTTAGAGAGCTGGT
GAGACAGTTGGGAACCTTTTGTGCTTGTGATCTACTGGACTTTTTTTTTTGCAGGAAGTGCATTCTGCTGCTTC
CCTATTTTCTGTTCTGGATGTGAGTGCAGTGCAGTGCCTACTGTTTTATCCACTTGGCCACAGACTTTTTCTAACA
GCTGCGTATTATTTCTATATACTAATTGCATTGGCAGCATTGTGTCTTTGACCTTGTATACTAGCTTGACATAGT
GCTGTCTCTGATTTCTAGGCTAGTTACTTGAGATATGAATTTCCATAGAATATGCACTGATACAAACATTACCAT
TCTTCTATGGAAGAAAACCTTTTGATGATGAACAATAAAGATTTTAAATATCTATTTTAAAAA

209/615

FIGURE 208

MAGIKALISLSFGGAIGLMFLMLGICALPIYNKYWPLFVLFFYILSPIPYCIARRLVDDTDAMSNACKELAIFLT
T
GIVVSAFGLPIVFARAHLEWGACALVLTGNTVIFATILGFFLVFGSNDDFSWQQW

210/615

FIGURE 209

CTTGCAGAGAAAGAGTCTTTTGTGCAGCACCCCTTTAAAGGGTGACTCGTCCCCTTGTGTTCTCTCTCTCTGGTGC
AGAGTTGCAAGCAAGTTTATCAGAGTATCGCCATGAAGTTTCGTCCCCTGCCTCCTGCTGGTGACCTTGTCTCTGCC
TGGGGACTTTGGGTGAGGCCCCGAGGCAAAAGCAAGGAAGCACTGGGGAGGAATTCATTTCCAGACTGGAGGGA
GAGATTCTGCACTATGCGTCCCAGCAGCTTGGGGCAAGGTGCTGGAGAAGTCTGGCTTCGCGTGCAGTGGCGCA
ACACAGACCAGACCTACTGGTGTGAGTACAGGGGGCAGCCAGCATGTGCCAGGCTTTTGCTGCTGACCCCAAAC
CTTACTGGAATCAAGCCCTGCAGGAGCTGAGGCGCCTTCACCATGCGTGCCAGGGGGCCCCGGTGCTTAGGCCAT
CCGTGTGCAGGGAGGCTGGACCCAGGCCCATATGCAGCAGGTGACTTCCAGCCTCAAGGGCAGCCAGAGCCCA
ACCAGCAGCCTGAGGCTGGGACGCCATCTCTGAGGCCAAGGCCACAGTGAAACTCACAGAAGCAACACAGCTGG
GAAAGGACTCGATGGAAGAGCTGGGAAAAGCCAAACCCACCACCCGACCCACAGCCAAACCTACCCAGCCTGGAC
CCAGGCCCCGGAGGGAATGAGGAAGCAAAGAAGAAGGCCTGGGAACATTGTTGGAAACCCCTCCAGGCCCTGTGCG
CCTTTCTCATCAGCTTCTTCCGAGGGTGACAGGTGAAAGACCCCTACAGATCTGACCTCTCCCTGACAGACAACC
ATCTCTTTTTATATTATGCGCTTCAATCCAACGTTCTCACACTGGAAGAAGAGAGTTTCTAATCAGATGCAAC
GGCCCAAATTCTTGATCTGCAGCTTCTCTGAAGTTTGAAAAGAAACCTTCCTTTCTGGAGTTTCAGAGTTTCAG
CAATATGATAGGGAACAGGTGCTGATGGGCCCAAGAGTGACAAGCATACACAATACTATTATCTGTAGAAGTT
TTGCTTTGTTGATCTGAGCCTTCTATGAAAGTTTAAATATGTAACGCATTTCATGAATTTCCAGTGTTCAGTAAAT
AGCAGCTATGTGTGTGCAAAATAAAAGAATGATTCAGAAAAA

211/615

FIGURE 210

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59602

<subunit 1 of 1, 223 aa, 1 stop

<MW: 24581, pI: 9.28, NX(S/T): 0

MKFVPCILLVTLSCILGQAPRQKQGSGTGEFFHFQTGGRDCTMRPSSLGQGAGEVWLR
VDCRNTDQTYWCEYRGQPSMCQAFADPKPYWNQALQELRRLHHACQGAPVLRPSVCREA
GPQAHMQQVTSSLKGSPEPNQQPEAGTPSLRPKATVKLTEATQLGKDSMEELGKAKPTTR
PTAKPTQPGPRPGGNEEAKKKAWEHCWKPFQALCAFLISFFRG

Important features:**Signal peptide:**

Amino acids: 1-19

N-myristoylation sites:

Amino acids: 38-44;51-57;194-200

DNA photolyases class 1 proteins:

Amino acids: 58-69

Tyrosine kinase phosphorylation site:

Amino acids: 64-71

N-myristoylation sites:

Amino acids: 38-44;51-57;194-200

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids: 4-15

212/615

FIGURE 211

GTGCAAGGAGCCGAGGCGAGATGGGCGTCCTGGGCCGGGTCTGCTGTGGCTGCAGCTCTGCGCACTGACCCAGGCG
GTCTCCAAACTCTGGGTCCCCAACACGGACTTCGACGTCGCAGCCAACTGGAGCCAGAACCGGACCCCGTGCGCC
GGCGGCGCCGTTGAGTTCCCGGCGGACAAGATGGTGTCACTCCTGGTGCAAGAAGGTACAGCCGTCTCAGACATG
CTCCTGCCGCTGGATGGGGAACTCGTCCTGGCTTCAGGAGCCGGATTTCGGCGTCTCAGACGTGGGCTCGCACCTG
GACTGTGGCGCGGGCGAACCTGCCGTCTTCCGCGACTCTGACCGCTTCTCCTGGCATGACCGCACCTGTGGCGCT
CTGGGGACGAGGCACCTGGCCTCTTCTTCGTGGACGCCGAGCGCGTGCCCTGCCGCCACGACGACGTCTTCTTTC
CGCCTAGTGCCTCCTTCGCGTGGGGCTCGGCCCTGGCGCTAGCCCCGTGCGTGTCCGCAGCATCTCGGCTCTGG
GCCGACGTTACGCGCGACGAGGACCTGGCTGTTTTCTGGCGTCCCGCGGGGCCCTACGCTTCCACGGGC
CGGGCGCGCTGAGCGTGGGCCCCGAGGACTGCGCGGACCCGTGGGCTGCGTCTGCGGCAACGCGGAGGCGCAGC
CGTGGATCTGCGCGGCCCTGCTCCAGCCCCT

213/615

FIGURE 212

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59603

<subunit 1 of 1, 197 aa, 1 stop

<MW: 20832, pI: 8.74, NX(S/T): 2

MGVLGRVLLWLQLCALTQAVSKLWVPNTDFDVAANWSQNRTPCAGGAVEFPADKMVSVLV
QEGHAVSDMLLPDGEIVLASGAGFGVSDVGSHLDCGAGEPAVFRDSDRFSWHDRTCGAL
GTRHLASSSWTPSACPAATTTSSFRIVPPSAWGSALALAPCVSAASRLWAGRSRATRTWL
FSWRPARAAYASTGRAR

Important features:**Signal peptide:**

Amino acids 1-19

N-glycosylation site:

Amino acids 35-39

Glycosaminoglycan attachment site:

Amino acids 81-85

N-myristoylation sites:

Amino acids 82-88;118-124;153-159

C-type lectin domain proteins:

Amino acids 108-118

214/615

FIGURE 213

[illegible]

215/615

FIGURE 214

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSFIPFARDAVKKCFVCLA

216/615

FIGURE 215

GGATTTTTGTGATCCGCGATTTCGCTCCACGGGCGGGACCTTTGTAAGTGCAGGGAGGCCAGGACAGGCCCACCC
TGCGGGGGCGGGAGGCAGCCGGGGTGAGGGAGGTGAAGAAACCAAGACGCAGAGAGGCCAAGCCCCCTGCCTTGGG
TCACACAGCCAAAGGAGGCAGAGCCAGAACTCACAACCAGATCCAGAGGCAACAGGGACATGGCCACCTGGGACG
AAAAGGCAGTCACCCGCAGGGCCAAGGTGGCTCCCGCTGAGAGGATGAGCAAGTTCTTAAGGCACTTCACGGTCG
TGGGAGACGACTACCATGCCTGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGGAGC
AGCCACCACCCACACCAGTCTCAGGCGAGGAAGGCAGAGCTGCAGCCCCCTGACGTTGCCCCCTGCCCCCTGGCCCCG
CACCAGGGCCCCCCTTGACTTCAGGGGCATGTTGAGGAACTGTTTCAGCTCCACAGGTTTCAGGTCATCATCA
TCTGCTTGGTGGTCTGGATGCCCTCCTGGTGCTTGCTGAGCTCATCCTGGACCTGAAGATCATCCAGCCGACA
AGAATAACTATGCTGCCATGGTATTCCACTACATGAGCATCACCATCTTGGTCTTTTTTATGATGGAGATCATCT
TTAAATTATTTGTCTTCCGCCTGAGTTCTTTCACCACAAGTTTGAGATCCTGGATGCCCGTCGTGGTGGTGGTCT
CATTTCATCCTGGACATTGTCTCCTGTTCCAGGAGCACCAGTTTGAGGCTCTGGGCCTGCTGATTCTGCTCCGGC
TGTGGCGGGTGGCCCGATCATCAATGGGATTATCATCTCAGTTAAGACACGTTTCAAGACGGCAACTCTTAAGGT
TAAACAGATGAATGTACAATTGGCCGCCAAGATTCAACACCTTGAGTTTCAGCTGCTCTGAGAAGCCCTGGACT
GATGAGTTTGCTGTATCAACCTGTAAGGAGAAGCTCTCTCCGGATGGCTATGGGAATGAAAGAATCCGACTTCTA
CTCTCACACAGCCACCGTGAAAGTCCTGGAGTAAATGTGCTGTGTACAGAAGAGAGAGAAGGAAGCAGGCTGGC
ATGTTCACTGGGCTGGTGTACGACAGAGAACCTGACAGTCACTGGCCAGTTATCACTTCAGATTACAAATCACA
CAGAGCATCTGCCTGTTTTCAATCACAAGAGAACAAAACCAAAATCTATAAAGATATTCTGAAAATATGACAGAA
TTTGACAAATAAAAGCATAAACGTGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

217/615

FIGURE 216

MATWDEKAVTRRAKVAPAERM SKFLRHFTVVGDDYHAWNINYKKWENEEEEEEEEQPPPTPVS GEEGRAAAPDVA
PAPGPAPRAPLDFRGMLRKLFS SHRFQVIIICLVVLDALLVLAELIDLKIIQPDKN NYAAMVFHYMSITILVFF
MMEIIFKLFVFR LSSFTTSLRSWMPVVVVVSFILDIVLLFQEHQFEALG LLLRLWRVARIINGIIISVKTRSE
RQLRLKQMN VQLAAKIQHLEFSCSEKPLD

FIGURE 217

GGAAGGCGACGGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGGCCATGGCTTCCCTGGGG
CAGATCCTCTTCTGGAGCATAATTAGCATCATATTATTCTGGCTGGAGCAATTGCACTCATCATTTGGCTTTGGT
ATTTCAAGGAGACACTCCATCAGCTCATCTGTGCGCTCAGCTGGGAACATTTGGGGAGGATGGAATCCTTGAGC
TGCACTTTTGAACCTGACATCAAACTTTCTGATATCGTGATACAATGGCTGAAGGAAGGTGTTTGGCTTTGGCT
CATGAGTTCAAAGAGGCCAAGATGAGCTGTGCGAGCAGGATGAAATGTTTCAGAGGCCGGACAGCAGTGTGTTGCT
GATCAAGTGATAGTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGCTGGCACCTACAAATGT
TATATCATCACTTCTAAAGGCAAGGGGATGCTAACCTTGAGTATAAACTGGAGCCTTCAGCATGCCGGAAGTG
AATGTGGACTATAATGCCAGCTCAGAGACCTTTCGGGTGTGAGGCTCCCCGATGGTTCCCCCGACCCACAGTGGTC
TGGGCATCCCAAGTTGACCAAGGGAGCCAACTTCTCGGAAGTCTCCAATACCACTTTGAGCTGAACCTTGAGAAT
GTGACCATGAAGGTTGTGTCTGTGCTCTACAATGTTACGATCAACAACACATACTCCTGTATGATTGAAAATGAC
ATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAATCGGAGATCAAAGGCGGAGTCACCTACAGCTGCTAAAC
TCAAAGGCTTCTCTGTGTGCTCTCTCTTTCTTTGCCATCAGCTGGGCCTTCTGCCTCTCAGCCCTTACCTGATG
CTAAAATTAATGTGCTTTGGCCACAAAAGCATGCAAGTCATTGTTACAACAGGATCTACAGAACTATTTTAC
CCACAGATATGACCTAGTTGTTTATATTTCTGGGAGGAATAATTCATATCTAGAACTCTGGAGTGAGCAAAACAG
AGCAAGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATCTTCAAAGACATATTA
GAAGTTGGGAAAAATATTCATGTGAACTAGACAAGTGTGTTAAGAGTGATAAGTAAAATGCACGTGGAGACAAGT
GCATCCCCAGATCTCAGGGGACCTCCCCCTGCTGTCACCTGGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTG
TCTGTGAATTTTTTAGTTATATGTGCTGTAAGTTGTCTCTGAGGAAGCCCTGGAAGTCTATCCCAACATATCCA
CATCTTATATTTCCACAAATTAAGCTGTAGTATGTACCTTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAG
GGGCGGCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAAGGTGCCTTGGCTTCTCTTC
CCAACGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAAACAGAGCAGTGGGGACACCGATTT
TATAAATAAATGAGCACCTTCTTTTAAACAAAAA
AAAAAAAAA

219/615

FIGURE 218

MASLGQILFWSIIISIIILAGAIALIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLSDIVIQWLKEG
VLGLVHEFPKEGKDELSEQDEMFRGRTAVFADQVIVGNASRLKNVQLTDAGTYKCYIITSKGKGNANLEYKTGAF
SMPEVNVDYNASSETLRCEAPRWFPPQPTVVWASQVDQGANFSEVSNTSFELNSENVTMKVVSVLNVNTINNTYSC
MIENDIAKATGDIKVTSEIKRRSHLQLLNSKASLCVSSFFAISWALLPLSPYMLK

FIGURE 219

[illegible]

221/615

FIGURE 220

MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLQEMKTLFLNTEYLMFPFLNQCGSILYYLTL
ASTDLTLAVPICNSLAIIFTLIVGKALGEDIGGKRKLDYCECGTQLCGSRHTCVSSFPEPISPEWVRTRPFPILP
FPLQLFCFLVAIRVPFPWTVWRKTEAGVWD

222/615

FIGURE 221

CTTCTGTAGGACAGTCAACCAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTGGAAGATGACAGCA
ATTATAGCAGGACCCTGCCAGGCTGTCGAAAAGATTCCGCAATAAACTTTGCCAGTGGGAAGTACCTAGTGAAA
CGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCTTGAGGCCCTGTGGTCCCCTATCCTTGGGAGAAGTCAGCTC
CAGCACCATGAAGGGCATCCTCGTTGCTGGTATCACTGCAGTGTGTTGTCAGCTGTAGAATCTCTGAGCTGCGT
GCAGTGTAATTCATGGGAAAAATCCTGTGTCAACAGCATTGCCTCTGAATGTCCCTCACATGCCAACACCAGCTG
TATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGTTCTGCTCAGCGGAGAA
CTGCAGTGAGGAGACACACATTACAGCCTTCACTGTCCACGTGTCTGCTGAAGAACACTTTCATTTTGTAAAGCCA
GTGCTGCCAAGGAAAGGAATGCAGCAACACCAGCGATGCCCTGGACCCTCCCCTGAAGAACGTGTCCAGCAACGC
AGAGTGCCCTGCTTGTATGAATCTAATGGAACTTCCTGTCTGGGAAGCCCTGGAAATGCTATGAAGAAGAACA
GTGTGTCTTTCTAGTTGCAGAACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGTGAAAGGCTGTTCCAACGT
CAGTAACGCCACCTGTCAGTTCCTGTCTGGTGAAAACAAGACTCTTGGAGGAGTCATCTTTCGAAAGTTTGAGTG
TGCAAATGTAAACAGCTTAACCCCCACGTCTGCACCAACCACTTCCCACAACGTGGGCTCCAAAGCTTCCCTCTA
CCTCTTGGCCCTTGCCAGCCTCCTTCTTCGGGGACTGCTGCCCTGAGGTCTGGGGCTGCACFTTGCCCAGCACC
CCATTTCTGCTTCTCTGAGGTCCAGAGCACCCCTGCGGTGCTGACACCCTCTTCCCTGCTCTGCCCCGTTTAA
CTGCCCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCGACAGCTGCCTTGTTCTTCATTATTAAGCACTGG
TTCATTCACTGCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

223/615

FIGURE 222

MKGILVAGITAVLVAAVESLSCVQCNSWEKSCVNSIASECPSHANTSCISSSASSSLET
PVRLYQNMFCSAENCS
EETHITAFTVHVSAEEHFHFVSQCCQGKECSNTSDALDPPLKNVSSNAECPACYESNGT
SCRGKPKWCYEEEQCV
FLVAELKNDIESKSLVLKGCNSVSNATCQFLSGENKTLGGVIFRKFEKANVNSLTPTS
APTTSHNVGSKASLYLL
ALASLLLRGLLP

224/615

FIGURE 223

GGCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGGAGCGAAGGTAGGAGGCAGGGCTTGCCTCAC
TGGCCACCCTCCCAACCCCAAGAGCCCAGCCCCATGGTCCCCGCCGCCGGCGCGCTGCTGTGGGTCTGCTGCTG
AATCTGGGTCCCCGGGCGGCGGGGGCCCAAGGCTGACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTTACGC
TTTGGGGGCCCCATGACCCGCAGCTACCGGAGCACCGCCCGGACTGGTCTTCCCCGGAAGACAAGGATAATCCTA
GAGGACGAGAATGATGCCATGGCCGACGCGGACCGCCTGGCTGGACCAAGCGGCTGCCGAGCTCTTGGCCGCCACG
GTGTCCACCGGCTTTAGCCGGTCTGTCCGCCATTAACGAGGAGGATGGGTCTTCAGAAGAGGGGGTTGTGATTAAT
GCCGGAAGGATAGCACCAGCAGAGAGCTTCCAGTGCGACTCCCAATACAGCGGGGAGTTCCAGCACGAGGTTT
ATAGCCAATAGTCAGGAGCCTGAAATCAGGCTGACTTCAAGCCTGCCGCGCTCCCCGGGAGGTCTACTGAGGAC
CTGCCAGGCTCGCAGGCCACCCTGAGCCAGTGGTCCACACCTGGGTCTACCCGAGCCGGTGGCCGTCACCCTCA
CCCACAGCCATGCCATCTCCTGAGGATCTGCGGCTGGTGTGATGCCCTGGGGCCCGTGGCACTGCCACTGCAAG
TCGGGCACCATGAGCCGGAGCCGGTCTGGGAAGCTGCACGGCCTTTCGGGGCGCCTTCGAGTTGGGGCGCTGAGC
CAGTCCGCACGGAGCACAAGCCTTGACCTATCAACAATGTCCCTGCAACCGACTTCGGGAAGAGTGCCCCCTG
GACACAAGTCTCTGTACTGACACCAACTGTGCCTCTCAGAGCACCAACAGTACCAGGACCACCCTACCCCCCTTC
CCCACCATCCACCTCAGAAGCAGTCCCAGCCTGCCACCCGCCAGCCCCTGCCAGCCCTGGCTTTTTGGAAACGG
GTCAGGATTGGCCTGGAGGATATTTGGAATAGCCTCTCTTCAGTGTTCACAGAGATGCAACCAATAGACAGAAAC
CAGAGGTAATGGCCACTTCATCCACATGAGGAGATGTGAGTATCTCAACCTCTCTTGCCCTTTCAATCCTAGCAC
CCTAGATATTTTTAGTACAGAAAAACAAAACCTGGAAAAACAAA

225/615

FIGURE 224

MVPAAGALLWVLLNLGPRAAGAOGLTQTPTEMQRVSLRFGGPMTRSYRSTARTGLPRKTRIILEDENDAMADAD
RLAGPAAAELLAATVSTGFSSAINEEDGSSEEGVINAGKDSTSRELPSATPNTAGSSSTRFIANSQEPEIRL
TSSLPRSPGRSTEDLPGSQATLSQWSTPGSTPSRWSPSPPTAMPSPEDLRLVLMWPWGPWHCHCKSGTMSRSRSGK
LHGLSGRLRVGALSQRLTEHKPCTYQQPCNRLREECPLDTSLCDTNCASQSTTSTRTTTTTFFPTIHLRSSPSL
PPASPCPALAFWKVRIGLEDIWNSLSSVFTEMQPIDRNQR

226/615

FIGURE 225

CCCCGGGTCGACCCACGCGTCCGGGGAGAAAGGATGGCCGGCCTGGCGGCGCGGTTGGTCCTGCTAGCTGGGGCAG
CGGCGCTGGCGAGCGGCTCCCAGGGCGACCGTGAGCCGGTGTACCGCGACTGCGTACTGCAGTGCAGAGAGCAGA
ACTGCTCTGGGGGCGCTCTGAATCACTTCCGCTCCCGCCAGCCAATCTACATGAGTCTAGCAGGCTGGACCTGTC
GGGACGACTGTAAGTATGAGTGTATGTGGGTACCGTTGGGCTCTACCTCCAGGAAGGTCACAAAGTGCCTCAGT
TCCATGGCAAGTGGCCCTTCTCCCGTTCTGTCTTTCAAGAGCCGGCATCGGCCGTGGCCTCGTTTCTCAATG
GCCTGGCCAGCCTGGTGATGCTCTGCCGCTACCGCACCTTCGTGCCAGCCTCCTCCCCATGTACCACACCTGTG
TGGCCTTCGCCTGGGTGCCCTCAATGCATGGTTCTGGTCCACAGTCTTCCACACCAGGGACACTGACCTCACAG
AGAAAATGGACTACTTCTGTGCCTCCACTGTCATCTACCTCAATCTACCTGTGCTGCGTCAGGACCGTGGGGC
TGCAGCACCCAGCTGTGGTCAGTGCCTTCCGGGCTCTCCTGCTGCTCATGCTGACCGTGCACGTCTCCTACCTGA
GCCTCATCCGCTTCGACTATGGCTACAACCTGGTGGCCAACGTGGCTATTGGCCTGGTCAACGTGGTGTGGTGGC
TGGCCTGGTGCCTGTGGAACAGCGGGCGCTGCCTCACGTGCGCAAGTGCCTGGTGGTGGTCTTGCTGCTGCAGG
GGCTGTCCCTGCTCGAGCTGCTTGACTTCCACCGCTCTTCTGGGTCTGGATGCCCATGCCATCTGGCACATCA
GCACCATCCCTGTCCACGTCTCTTTTTCAGCTTTCTGGAAGATGACAGCCTGTACCTGCTGAAGGAATCAGAGG
ACAAGTCAAGCTGGACTGAAGACCTTGGAGCGAGTCTGCCCCAGTGGGGATCCTGCCCCGCGCTGCTGGCCTC
CCTTCTCCCCCTCAACCTTGAGATGATTTTCTCTTTTCAACTTCTTGAACCTTGGACATGAAGGATGTGGGCCAG
AATCATGTGGCCAGCCACCCCTGTTGGCCCTCACCAGCCTTGGAGTCTGTTCTAGGGAAGGCCTCCAGCATC
TGGGACTCGAGAGTGGGCAGCCCTCTACCTCCTGGAGCTGAACCTGGGGTGGAACTGAGTGTGTTCTTAGCTCTA
CCGGGAGGACAGCTGCCGTGTTTCTCCTCCCCACAGCCTCCTCCCCACATCCCAGCTGCCTGGCTGGGTCTGAAG
CCCTCTGTCTACCTGGGAGACCAGGGACCACAGGCCTTAGGGATACAGGGGGTCCCCTTCTGTTACCACCCCCCA
CCCTCCTCCAGGACACCACTAGGTGGTGTCTGGATGCTTGTCTTTGGCCAGCCAAGGTTACGGCGATTTCTCCCC
ATGGGATCTTGAGGGACCAAGCTGCTGGGATTGGGAAGGAGTTTACCCTGACCGTTGCCCTAGCCAGGTTCCCA
GGAGCCTCACCATACTCCCTTTTCAAGGCCAGGGCTCCAGCAAGCCCAGGGCAAGGATCCTGTGCTGCTGTCTGG
TTGAGAGCCTGCCACCGTGTGTGCGGAGTGTGGGCCAGGCTGAGTGCATAGGTGACAGGGCCGTGAGCATGGGCC
TGGGTGTGTGTGAGCTCAGGCCTAGGTGCCAGTGTGGAGACGGGTGTTGTGCGGGAAGAGGTGTGGCTTCAAAG
TGTGTGTGTGCAGGGGGTGGGTGTGTTAGCGTGGGTAGGGGAACGTGTGTGCGCGTGTGCTGGTGGGCATGTGAGA
TGAGTGAAGTGCCTGGAATGTGTCCACAGTTGAGAGGTTGGAGCAGGATGAGGGAATCCTGTACCATCAATAAT
CACTTGTGGAGCGCCAGCTCTGCCCAAGACGCCACCTGGGCGGACAGCCAGGAGCTCTCCATGGCCAGGCTGCCT
GTGTGCATGTTCCCTGTCTGGTGGCCCTTTGCCCGCCTCCTGCAAACCTCACAGGGTCCCCACACAACAGTGGCC
TCCAGAAGCAGCCCCCTCGGAGGCAGAGGAAGGAAATGGGGATGGCTGGGGCTCTCTCCATCCTCTTTCTCCT
TGCTTTCGCATGGCTGGCCTTCCCCCTCCAAAACCTCCATTCCCCTGCTGCCAGCCCTTTGCCATAGCTGATTT
TGGGGAGGAGGAAGGGGCGATTTGAGGGAGAAGGGGAGAAAGCTTATGGCTGGGTCTGGTTTCTTCCCTTCCCAG
AGGTCTTACTGTTCAGGGTGGCCCCAGGGCAGGCAGGGGCCACACTATGCCTGTGCCCTGGTAAAGGTGACCC
CTGCCATTTACCAGCAGCCCTGGCATGTTTCTGCCCCACAGGAATAGAATGGAGGGAGCTCCAGAACTTTCCAT
CCCAAAGGCAGTCTCCGTGGTTGAAGCAGACTGGATTTTGTCTCTGCCCTGACCCCTTGTCCCTCTTTGAGGGA
GGGAGCTATGCTAGGACTCCAACCTCAGGGACTCGGGTGGCCTGCGCTAGCTTCTTTTGATACTGAAAACCTTT
AAGGTGGGAGGGTGGCAAGGGATGTGCTTAATAAATCAATTCCAAGCCTCAAAAAAAAAAAAAAAAAA

227/615

FIGURE 226

MAGLAARLVLLAGAAALASGSQGDREPVRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGWTCRDDCKYECMWV
TVGLYLQEGHKVPQFHGKWPFSSRFLFFQEPASAVASFLNGLASLVMLCRYRTFVPASSPMYHTCVAFWVSLNAW
FWSTVFHTRDTDLTEKMDYFCASTVILHSIYLCCVRTVGLQHPAVVSAFRALLLLMLTVHVSYSLSLIRFDYGYNL
VANVAIGLVNVVWWLAWCLWNQRRLPVVRKCVVVVLLQLGLSLELLDFPPLFWVLDAAHAIWHISTIPVHVLFSS
FLEDDSLYLLKESEDKFKLD

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domains:

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

N-glycosylation site.

amino acids 40-44

N-myristoylation site.

amino acids 43-49

CUB domain proteins profile.

amino acids 285-302

Amiloride-sensitive sodium channels proteins.

amino acids 162-186

FIGURE 227

TTCGGCTTCCGTTAGAGGAAGTGGCGCGGACCTTCATTGGGGTTTTCGGTTCCCCCCTTCCCCTTCCCCGGGGTCTGGGGGTGACATTGACCGCGCCCCCTCGTGGGGTTCGGTTGCCACCCACGCGGACTCCCCAGCTGGCGCGCCCCTCCCATTGCGCTGTCTTGGTTCAGGCCCCCCACCCCCCTTCCCACCTGACCAGCCATGGGGGCTGCGGTGTTTTTCGCTGCACCTTTCGTCGCGTTTCGGCCGGCCTTCGCGCTTTTCTTGATCACTGTGGCTGGGACCCGCTTCGCGTTATCATCTGGTTCGACGGGCATTTTTCTTGCTGGTCTCCTGCTCCTGCGCCTCTGTGCTGTTTATCTTGGTCTATGTGACCGACCGGTTCAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTGTCTGTCTTCTAAGGAGGTGTTCCGCTTTCGCTACTACAAGCTGCTTAAGAAGGCAGATGAAGGGTTAGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTGGTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTTTGGCTGATGCACTTGGGCCAGGTGTGGTTGGGATCCATGGAGACTCACCTTATTACTTCCTGACTTTCAGCCTTCTGACAGCAGCCATTATCTGCTCCATACCTTTGGGGAGTTGTGTTCTTTGATGCGCTGAGGAGGAGGACCGTATGGGCTTTGGGCTTGGTGGTGGGAGTCACTTATGACATCGGAGACTGACATTCCTGAACCCTGGTATGAGGCCAGCCTGCTGCCCATCTATGCAGTCACTGTTTCCATGGGGCTCTGGGCCCTTCATCACAGCTGGAGGGTCCCTCCGAAGTATTAGCGCGAGCCTCTTGTTGAAGGACTGCACTACCTGGACTGATCGCCTGACAGATCCCACTGCGCTGTCCACTGCCCATGACTGAGCCAGCCCCAGCCCGGGTCCATTGCCACATTCTCTGTCTCCTTCTCGTCGGTCTACCCCACTACCTCCAGGGTTTTGCTTTGTCTCTTTGTGACCGTTAGTCTCTAAGCTTACCAGGAGCAGCCTGGGTTTCAGCCAGTCACTGTTGGGTTTTGAATCTGCACCTATCCCCACCACCTGGGAGCCCCCTTGTGTGTCCAGGACTCCCCCTGTGTCACTGCTGTCTGCTCACTGCCCCAAGACTCACTCCCTTCCCCCTGTCAGGCCGACCGGACGAGGACAGTTCGGGTGATGGTGTATTCTGCCCTGCGCATCCACCCGAGGACTGAGGGAACCTAGGGGGACCCCTGGGCCCTGGGGTGCCCTCCTGATGTCTCGCCCTGTATTTCTCCATCTCCAGTTCTGGACAGTGCAAGTTGCCAAGAAAAGGGACCTAGTTTAGCCATTGCCCTGGAGATGAAATTAATGAGGCTCAAGGATAGATGAGCTCTGAGTTTCTCAGTACTCCCTCAAGACTGGACATCTTGGTCTTTTTCTCAGGCCTGAGGGGAACCACTTTTGGTGTGATAAATAACCTAAGCTGCCTTTTTTTTCTTTTTCGAGGTGGGGGAGGAGGAGGTATATTGGAACCTTTCTAACCTCCTTGGGCTATATTTTCTCTCCTCGAGTTGCTGCTCATGGCTGGGCTCATTTTCGGTCCCTTTCTCCTTGGTCCCAGACCTTGGGGGAAGGAAGGAAGTGCATGTTTGGGAAGTGGCATTACTGGAACATAATGGTTTTAACCTCTTAACCACCGCATCCCTCCTCTCCCCAAGGTGAAGTGGAGGGTGTCTGTGGTGAAGTGGCCACTCCAGAGCTGCACTGCCACTGGAGGAGTTCAGACTACCATGACATCGTAGGGAAGGAGGGGAGATTTTTTTGTAGTTTTTAATTGGGGTGTGGGAGGGCGGGGAGGTTTTCTATAAAGTATCACTTTTCTGCTGAGGGTGGAGTGTCCCATCCTTTTAATCAAGGTGATTGTGATTTTACTAATAAAAAAGAAATTTGTAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

229/615

FIGURE 228

MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIIILVAGAFFWLVSLLLASVVWFILVHVTDRSDARLQYGLLIFG
AAVSVLLQEVFRFAYYKLLKKADEGLASLSEDRSPISIRQMAYVSGLSFGIISGVFSVINILADALGPGVVGIH
GDSPYYFLTSAFLTAAILLHTFWGVVFFDACERRRYWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMG
LWAFITAGGSLRSIQRSLCKD

230/615

FIGURE 229

CGGGAGGCTGGGTCGTCATGATCCGGACCCCATTTGTCGGCCTCTGCCCATCGCCTGCTCCTCCCAGGCTCCCGCG
GCCGACCCCCCGCAACATGTCAGCCACGGGCCGCGAGGGTTCCCGCGCGCTCAGCCGGCGGTATCTGCGGCGTC
TGCTGCTCCTGCTACTGCTGCTGCTGCTGCGGCAGCCCGTAACCCGCGCGGAGACCAGCCGGGCGCCCCAGAG
CCCTCTCCACGCTGGGCTCCCCAGCCTCTTACCACGCGGGGTGTCCCAGCGCCCTCACTACCCAGGCCTCA
CTACGCCAGGCACCCCCAAAACCTGGACCTTCGGGGTTCGCGCGCAGGCCCTGATGCGGAGTTTCCCACTCGTGG
ACGGCCACAATGACCTGCCCCAGGTCCTGAGACAGCGTTACAAGAATGTGCTTCAGGATGTTAACCTGCGAAATT
TCAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGTGGGTGCCAGTTCTGGTCAGCCTCCGTCT
CATGCCAGTCCCAGGACCAGACTGCCGTGCGCCTCGCCCTGGAGCAGATTGACCTCATTACCGCATGTGTGCCT
CCTACTCTGAACCTCGAGCTTGTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAGCTGGCCTGCCTCATTGGCG
TGNAGGGTGGTCACTCACTGGACAGCAGCCTCTCTGTGCTGCGCAGTTTCTATGTGCTGGGGGTGCGCTACCTGA
CACTTACCTTCACCTGCAGTACACCATGGGCAGAGAGTTCCACCAAGTTCAGACACCACATGTACACCAACGTCA
GCGGATTGACAAGCTTTGGTGAGAAAGTAGTAGAGGAGTTGAACCGCCTGGGCATGATGATAGATTTGTCCATG
CATCGGACACCTTGATAAGAAGGGTCCTGGAAGTGTCTCAGGCTCCTGTGATCTTCTCCCACTCAGCTGCCAGAG
CTGTGTGTGACAATTTGTTGAATGTTCCCGATGATATCCTGCAGCTTCTGAAGAACGGTGGCATCGTGATGGTGA
CACTGTCCATGGGGGTGCTGCAGTGCAACCTGCTTGCTAACGTGTCCACTGTGGCAGATCACTTTGACCACATCA
GGGCAGTCATTGGATCTGAGTTCATCGGGATTGGTGAAATTATGACGGGACTGGCCGTTCCCTCAGGGGCTGG
AGGATGTGTCCACATACCCAGTCTGATAGAGGAGTTGCTGAGTCGTASCTGGAGCGAGGAAGAGCTTCAAGGTG
TCCTTCGTGGAACCTGCTGCGGGTCTTCAGACAAGTGGAAAAGGTGAGAGAGGAGAGCAGGGCGCAGAGCCCCG
TGGAGGCTGAGTTTCCATATGGGCAACTGAGCACATCCTGCCACTCCACCTCGTGCCTCAGAATGGACACCAGG
CTACTCATCTGGAGGTGACCAAGCAGCCAACCAATCGGGTCCCCCTGGAGGTCTCAAATGCCTCCCATACCTTG
TTCCAGGCCTTGTGGCTGCTGCCACCATCCCAACCTTACCCAGTGGCTCTGCTGACACAGTCGGTCCCCGAGA
GGTCACTGTGGCAAAGCCTCACAAAGCCCCCTCTCCTAGTTCATTACACAAGCATATGCTGAGAATAAACATGTTA
CACATGGAAAA

231/615

FIGURE 230

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817
><subunit 1 of 1, 487 aa, 1 stop, 2 unknown
><MW: 53569.32, pI: 7.68, NX(S/T): 5
MQPTGREGSRALSRRYLRRLLLLLLLLLLLLLRQPVTRAETTPGAPRALSTLGSPSLFTTPGVPSALTTPGLTTPGTP
KTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLNFSHGQTSLDRLRDGLVGAQFWSASVSCQSQD
QTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSSQKLACLIGVXGGHSLDSSLSVLRSFYVLGVRYLTTLFTC
STPWAESSTKFRHHMYTNVSGLTSGEKEVVEELNRLGMMIDLSYASDTLIRRVLEVSQAPVIFSHSAARAVCDNL
LNVDDILQLLKNGGIVMTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGGNYDGTGRFPQGLEDVSTY
PVLIEELLSRWSEELQGVLRGNLLRVFRQVEKVRRESRAQSPVEAEFFPYGQLSTSCHSHLVPQNGHQATHLEV
TKOPTNRVPWRSSNASPYLVPGLVAAATIPFTQWLC
```

Important features of the protein:**Signal peptide:**

amino acids 1-36

Transmembrane domain:

amino acids 313-331

N-glycosylation sites.

amino acids 119-122, 184-187, 243-246 and 333-336

N-myristoylation sites.amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359,
357-362, 394-399, 427-432 and 472-477.**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 136-146

232/615

FIGURE 231

GCTCTGGCCGGCCCCGGCGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGATTGGCAAGCGCTGG
CCACCTCCCCACACCCCTTGCGAACGCTCCCCCTAGTGGAGAAAAGGAGTAGCTATTAGCCAATTTCGGCAGGGCCC
GCTTTTATAGAAGCTTGATTTCTTTGAAGATGAAAGACTAGCGGAAGCTCTGCCTCTTTCCCCAGTGGGCGAGGG
AACTCGGGGCGATTGGCTGGGAACGTATCCACCCAAATGTCACCGATTCTTCCTATGCAGGAAATGAGCAGAC
CCATCAATAAGAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAACCTGGAGGCAAAGAGG
GTTGCTCAACGCCCCGCCTCATTGGAAAACCAAATCAGATCTGGGACCTATATAGCGTGGCGGAGGCGGGGCGAT
GATTGTCGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTTCTTTCCCCGCCCCCTGAGACCCTGCAGCACCA
TCTGTCATGGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGTCTTTTGGCGGCAGCGGCGACGCGAGGGCTCCCC
GCGCCCCGCTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCTGTGGCGGGAAGCGGCCC
CCAGAACCAGACACCCGTGGCAAGAGGACCCAGAACCAGGACGAAAACCTGTATGAGAAGAACCAGACTCC
CATGGTTATGACAAGGACCCCGTTTGGACGCTCTGGAACATGCGACTTGTCTTCTTTGGCGTCTCCATCATC
CTGGTCCTTGGCAGCACCTTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGGAAGCTGAG
AGGCTTGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAACCTGCTTCGACCCCAGCAAGATCCAG
CTGCCAGAGGATGAGTGACCAAGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTTCCCCACCCCTGCCTGCCATTC
TGACCTCTTCTCAGAGCACCTAATTAAAGGGGCTGAAAGTCTGAA

233/615

FIGURE 232

MAAGLFGLSARRLLAAAATRGLPAARVRWESSFSRTVVAPSAVAGKRPPEPTTPWQEDPEPEDENLYEKNPDSHG .
YDKDPVLDVWNMRLVFFFGVSIILVLGSTFVAYLPDYRMKEWSRREAERLVKYREANGLPIMESNCFDPSKIQLPEDE

234/615

FIGURE 233

GC GCGCGGCTATGCGGCTTGCTCTGCTCGTCTGTTGCTCCTGGGGCCCGGCGGCTGGTGCCTTG CAGAACCCCCA
CGCGACAGCCTGCGGGAGGAACCTTGTCATCACCCCGCTGCCTTCCGGGGACGTAGCCGCCACATTCCAGTTCCGC
ACGCGCTGGGATTCCGAGCTTCAGCGGGAAGGAGTGTCCCATTACAGGCTCTTTCCCAAAGCCCTGGGGCAGCTG
ATCTCCAAGTATTCTCTACGGGAGCTGCACCTGTCATTACACAAAGGCTTTTGGAGGACCCGATACTGGGGGCCA
CCCTTCCTGCAGGCCCCATCAGGTGCAGAGCTGTGGGTCTGGTTCCAAGACACTGTCACTGATGTGGATAAATCT
TGGAAGGAGCTCAGTAATGTCCTCTCAGGGATCTTCTGCGCCTCTCTCAACTTCATCGACTCCACCAACACAGTC
ACTCCCACTGCCTCCTCAAACCCCTGGGTCTGGCCAATGACACTGACCACTACTTTCTGCGCTATGCTGTGCTG
CCGCGGGAGGTGGTCTGCACCGAAAACCTCACCCCTGGAAGAAGCTCTTGCCCTGTAGTTCCAAGGCAGGCCTC
TCTGTGCTGCTGAAGGCAGATCGCTTGTTCCACACAGCTACCACTCCCAGGCAGTGCATATCCGCCCTGTTTGC
AGAAATGCACGCTGTACTAGCATCTCCTGGGAGCTGAGGCAGACCCTGTCAGTTGTATTTGATGCCCTTCATCACG
GGGCAGGGAAGAAAGACTGGTCCCTCTTCCGGATGTTCTCCGAACCCCTCACGGAGCCCTGCCCCCTGGCTTCA
GAGAGCCGAGTCTATGTGGACATCACCACTACAACAGGACAACGAGACATTAGAGGTGCACCCACCCCGACC
ACTACATATCAGGACGTCTATCCTAGGCACTCGGAAGACCTATGCCATCTATGACTTGCTTGACACCGCCATGATC
AACAACTCTCGAAACCTCAACATCCAGCTCAAGTGGAAGAGACCCCAAGAGAATGAGGCCCCCAGTGCCTTC
CTGCATGCCAGCGGTACGTGAGTGGCTATGGGCTGCAGAAGGGGGAGCTGAGCACACTGCTGTACAAACCCAC
CCATACCGGGCCTTCCCGGTGCTGCTGCTGGACACCGTACCCTGGTATCTGCGGCTGTATGTGCACACCCCTCACC
ATCACTCCAAGGGCAAGGAGAACAAACCAAGTTACATCCACTACCAGCCTGCCAGGACCGGTGCAACCCAC
CTCCTGGAGATGCTGATTGAGCTGCCGGCCAACTCAGTCACCAAGGTTTCCATCCAGTTTGAGCGGGCGCTGCTG
AAGTGGACCGAGTACACGCCAGATCCTAACCATGGCTTCTATGTGAGCCATCTGTCCTCAGCGCCCTTGTGCCC
AGCATGGTAGCAGCCAAAGCCAGTGGACTGGGAAGAGAGTCCCCTCTTCAACAGCCTGTTCCAGTCTCTGATGGC
TCTAACTACTTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAACCTGCCGACACCGGACTTCAGCATGCCCTAC
AACGTGATCTGCCTCAGTGCCTGTGGTGGCCGTGTGTACGGCTCCTTCTACAATCTCCTCACCCGAACCTTC
CACATCGAGGAGCCCCGCACAGGTGGCCTGGCCAAGCGCTGGCCAACCTTATCCGGCGCGCCCCGAGGTGTCCCC
CCACTCTGATTCTTGCCCTTTCAGCAGCTGCAGCTGCCGTTTCTCTCTGGGGAGGGGAGCCCAAGGGCTGTTTC
TGCCACTTGCTCTCCTCAGAGTTGGCTTTTGAACCAAAAGTGCCCTGGACCAGGTCAGGGCCTACAGCTGTGTTGT
CCAGTACAGGAGCCACGAGCCAAATGTGGCATTGAAATTTGAATTAACCTAGAAATTCATTTCTCACCTGTAGT
GGCCACCTCTATATTGAGGTGCTCAATAAGCAAAAGTGGTGGTGGCTGCTGATTGGACAGCACAGAAAAAGAT
TTCCATCACACAGAAAGGTGGGCTGGCAGCACTGGCCAAGGTGATGGGGTGTGCTACACAGTGTATGTCACTGT
GTAGTGGATGGAGTTTACTGTTTGTGGAATAAAAAACGGCTGTTTCCGTGGAAAAA

235/615

FIGURE 234

MPLALLVLLLLGPGGWCLAEPDRSLREELVITPLPSGDVAATFQFRTRWDSELQREGVSHYRLF PKALGQLISK
YSLRELHLSFTQGFWRTRYWGPPFLQAPSGAELWVWFQDTVTDVDSWKELSNVLSGIFCASLNFIDSTNTVTPT
ASFKPLGLANDTDHYFLRYAVLPREVVCTENLTPWKKLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCRNA
RCTSISWELRQTLSSVFDAFITGQGKKDWSLFRMFSRTLTEPCPLASESRVYVDITTYNQDNETLEVHPPPTTTY
QDVILGTRKTYAIYDLLDTAMINNSRNLNIQLKWKRPPENEAPPVPFLHAQRYVSGYGLQKGELSTLLYNTHPYR
AFPVLLLDTPWYLRLYVHTLTITSKGKENKPSYIHYQPAQDRLQPHLLEMLIQLPANSVTKVSIQFERALLKWT
EYTPDPNHGFYVSPSVLSALVPSMVAAPVDWEESPLFNSLFPVSDGSNYFVRLYTEPLLVLNLTPTDFSMYPYNI
CLTCTVVAVCYGSFYNNLLTRTFHIEEPRTGGLAKRLANLIRRARGVPPL

236/615

FIGURE 235

TGACGTCAGAATCACCAATGGCCAGCTATCCTTACCGGCAGGGCTGCCCAGGAGCTGCAGGACAAGCACCCAGGAGC
CCCTCCGGGTAGCTACTACCCTGGACCCCCCAATAGTGGAGGGCAGTATGGTAGTGGGGCTACCCCTGGTGGTGG
TTATGGGGGTCTGCCCTGGAGGGCCTTATGGACCACCAGCTGGTGGAGGGCCCTATGGACACCCCAATCCTGG
GATGTTCCCTCTGGAACCTCCAGGAGGACCATATGGCGGTGCAGCTCCCGGGGGCCCTATGGTCAGCCACCTCC
AAGTTCTACGGTGCCAGCAGCCTGGGCTTTATGGACAGGGTGGCGCCCTCCCAATGTGGATCCTGAGGCCTA
CTCCTGGTTCCAGTCGGTGGACTCAGATCACAGTGGCTATATCTCCATGAAGGAGCTAAAGCAGGCCCTGGTCAA
CTGCAATTGGTCTTCATTCAATGATGAGACCTGCCTCATGATGATAAACATGTTTGACAAGACCAAGTCAGGCCG
CATCGATGTCTACGGCTTCTCAGCCCTGTGGAAATTCATCCAGCAGTGGAAGAACCTCTTCCAGCAGTATGACCG
GGACCGCTCGGGCTCCATTAGCTACACAGAGCTGCAGCAAGCTCTGTCCCAATGGGCTACAACCTGAGCCCCCA
GTTCAACCCAGCTTCTGGTCTCCCGCTACTGCCACGCTCTGCCAATCCTGCCATGCAGCTTGACCGCTTCATCCA
GGTGTGCACCCAGCTGCAGGTGCTGACAGAGGCCTTCCGGGAGAAGGACACAGCTGTACAAGGCAACATCCGGCT
CAGCTTCGAGGACTTCGTACCATGACAGCTTCTCGGATGCTATTGACCCCAACCATCTGTGGAGAGTGGAGTGCAC
CAGGGACCTTTCTGGCTTCTTAGAGTGAGAGAAGTATGTGGACATCTCTTCTTTCTGTCCCTCTAGAAGAAC
ATTCTCCCTTGCTTGATGCAACACTGTTCAAAAGAGGGTGGAGAGTCTGCATCATAGCCACCAATAGTGAGG
ACCGGGGCTGAGGCCACACAGATAGGGGCCTGATGGAGGAGAGGATAGAAGTTGAATGTCCTGATGGCCATGAGC
AGTTGAGTGGCACAGCCTGGCACCAGGAGCAGGTCTTGTAAATGGAGTTAGTGTCCAGTCAGCTGAGCTCCACCC
TGATGCCAGTGGTGAGTGTTTCATCGGCCTGTTACCGTTAGTACCTGTGTTCCTCACCAGGCCATCCTGTCAAAC
GAGCCCATTTTCTCCAAAGTGAATCTGACCAAGCATGAGAGAGATCTGTCTATGGGACCAGTGGCTTGGATTCT
GCCACACCCATAAATCCTTGTGTGTTAACTTCTAGCTGCCTGGGGCTGGCCCTGCTCAGACAAATCTGCTCCCTG
GGCATCTTTGGCCAGGCTTCTGCCCCCTGCAGCTGGGAECCTCACTTGCCTGCCATGCTCTGCTCGGCTTCAGT
CTCCAGGAGACAGTGGTCACCTCTCCCTGCCAATACTTTTTTTAATTTGCATTTTTTTTCATTTGGGGCCAAAAG
TCCAGTGAAATTGTAAGCTTCAATAAAAGGATGAAACTCTGA

237/615

FIGURE 236

MASYPYRQGCPGAAGQAPGAPPGSYYPGPPNSGGQYGSGLPPGGGYGGPAPGGPYGPPAGGGPYGHPNPGMFPSG
TPGGPYGGAAPGGPYGQPPSSYGAQQPGLYGQGGAPPNVDPEAYSWFQSVSDHSGYISMKELKQALVNCNWSS
FNDETCLMMINMFDKTKSGRIDVYGFSALWKFIQQWKNLFQQYDRDRSGSISYTELQQALSQMGYNLSPQFTQLL
VSRYCPRSANPAMQLDRFIQVCTQLQVLTEAFREKDTAVQGNIRLSFEDFVTMTASRML

Important features of the protein:**Signal peptide:**

amino acids 1-19

N-glycosylation site.

amino acids 147-150

Casein kinase II phosphorylation sites.

amino acids 135-138, 150-153, 202-205, 271-274

N-myristoylation sites.

amino acids 9-14, 15-20, 19-24, 33-38, 34-39, 39-44, 43-48, 61-66, 70-75, 78-83, 83-88, 87-92, 110-115

238/615

FIGURE 237

CAGGATGCAGGGCCGCGTGGCAGGGAGCTGCGCTCCTCTGGGCCTGCTCCTGGTCTGTCTTCATCTCCCAGGCCT
CTTTGCCCCGAGCATCGGTGTTGTGGAGGAGAAAGTTTCCCAAACCTTCGGGACCAACTTGCCCTCAGCTCGGACA
ACCTTCCTCCACTGGCCCCCTCTAACTCTGAACATCCGCAGCCCGCTCTGGACCTTAGGTCTAATGACTTGGCAAG
GGTTCCTCTGAAGCTCAGCGTGCCTCCATCAGATGGCTTCCCACCTGCAGGAGGTTCTGCAGTGCAGAGGTGGCC
TCCATCGTGGGGGCTGCCTGCCATGGATTCTTGGCCCCCTGAGGATCCTTGGCAGATGATGGCTGCTGCGGCTGA
GGACCGCCTGGGGGAAGCGCTGCCTGAAGAACTCTCTTACCTCTCCAGTGTGCGGCCCTCGCTCCGGGCAGTGG
CCCTTTGCCTGGGGAGTCTTCTCCCGATGCCACAGGCCTCTCACCTGAGGCTTCACTCCTCCACCAGGACTCGGA
GTCCAGACGACTGCCCCGTCTAATTCACTGGGAGCCGGGGGAAAAATCCTTTCCCAACGCCCTCCCTGGTCTCT
CATCCACAGGGTTCTGCCTGATCACCCTGGGGTACCCTGAATCCCAGTGTGTCTTGGGGAGGTGGAGGCCCTGG
GACTGGTTGGGGAACGAGGCCCATGCCACACCCTGAGGGAATCTGGGGTATCAATAATCAACCCCAGGTACCAG
CTGGGGAAATATTAATCGGTATCCAGGAGGCAGCTGGGGAAATATTAATCGGTATCCAGGAGGCAGCTGGGGGAA
TATTAATCGGTATCCAGGAGGCAGCTGGGGGAATATTCATCTATACCCAGGTATCAATAACCCATTTCTCCTGG
AGTTCTCCGCCCTCCTGGCTCTTCTTGGAACATCCCAGCTGGCTTCCCTAATCCTCCAAGCCCTAGGTTGCAGTG
GGGCTAGAGCACGATAGAGGGAAACCAACATTGGGAGTTAGAGTCCTGCTCCCGCCCCTTGCTGTGTGGGCTCA
ATCCAGGCCCTGTTAACATGTTTCCAGCACTATCCCCACTTTTCAGTGCCTCCCCTGCTCATCTCCAATAAAATA
AAAGCACTTATGAAA
AAA

239/615

FIGURE 238

MQGRVAGSCAPLGLLLVLHLPGLFARSIGVVEEKVSNFGTNLPQLGQPSSTGPSNSEHPQPALDPRSNDLARV
PLKLSVPPSDGFPFAGGSAVQRWPPSWGLPAMDSWPPEDPWQMMAAAAEEDRLGEALPEELSYLSSAAALAPGSGP
LPGESSPDATGLSPEASLLHQDSESRRRLPRSNSLGAGGKILSQRPWSLIHRVLPDHPWGTLPNPSVSWGGGGPGT
GWGTRMPHPEGIWGINNQPPGTSWGNINRYPGGSWGNINRYPGGSWGNINRYPGGSWGNIHLYPGINNPFPFPGV
LRPPGSSWNIPAGFPNPPSPRLQWG

Important features of the protein:

Signal peptide:

amino acids 1-26

Casein kinase II phosphorylation sites.

amino acids 56-59, 155-158

N-myristoylation sites.

amino acids 48-53, 220-225, 221-226, 224-229, 247-252, 258-263, 259-264, 269-274, 270-275, 280-285, 281-286, 305-310

240/615

FIGURE 239

GGGCGTCTCCGGCTGCTCCTATTGAGCTGTCTGCTCGCTGTGCCCGCTGTGCCTGCTGTGCCCGCGCTGTGCGCCG
CTGCTACCGCGTCTGCTGGACGCGGGAGACGCCAGCGAGCTGGTGATTGGAGCCCTGCGGAGAGCTCAAGCGCCC
AGCTCTGCCCCAGGAGCCAGGCTGCCCCGTGAGTCCCATAGTTGCTGCAGGAGTGGAGCCATGAGCTGCGTCCT
GGGTGGTGTATCCCCTTGGGGCTGCTGTTCTGGTCTGCGGATCCCAAGGCTACCTCCTGCCCAACGTCACTCT
CTTAGAGGAGCTGCTCAGCAAATACCAGCACAAAGCTCTCACTCCCGGGTCCGCAGAGCCATCCCCAGGGAGGA
CAAGGAGGAGATCCTCATGCTGCACAACAAGCTTCGGGGCCAGGTGCAGCCTCAGGCCTCCAACATGGAGTACAT
GGTGAGCGCCGGCTCCGGCCGAGAGGCTGGCACCAGGGGTGGGGCCTGGGCCACCAGCCTGCTCTGTTCCCCAG
CCAGCTCTGTTCCCCAGCCAGTGCGTGTGATGGCTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCCGGCTCTG
TTCTGTTTTGTTTGTGTTTGTGTTTGTGAGACAGGGTCTCACTCTGCCACTGACGCTGGAGTGCAATGGCACAATCGTCA
TGCCCTGAAACCTTAGACTCCCGGGGTAAAGCGATCCTGCTTCAGCCTCCCAAGTAGCTGGAACTACAGGCATGC
ACCATGGTGCCAGCTAGATTTTAAATATTTTGTGGAGATGGGGGTCTTGCTACGTTGCCAGGCTGGTCTTGAA
CTCCTAGGCTCAAGCAATCCTCCTGCCTCAGCCTCTCAAAGTGCTAGGATTATAGGCATGAGTCACCCTGTCTGG
CTCTGGCTCTGTTCTTAACATTCTGCCAAAACAACACACGTGGGTTCCTGTGCAGAGCCTGCCTCGTTGCCTTC
ATGTCACTCTGGTAGCTCCACTGGGAACACAGCTCTCAGCCTTTCCACCTGGAGGCAGAGTGGGGAGGGGGCCC
AGGGCTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCACCCTGACTTCTCCTTAGCCCG
TGTGAGCCTCACTTTCCACTTGGAGAGTCTTCTCGCGTGGTTGCCATGACTGTGAGATAAGTCGAGGCTGTGA
AGGGCCCGGCACAGACTGACCTGCCTCCCCAACCCCTAGGCTTTGCTAACCGGGAAGGAGCTAACGGTGACAGA
AGACAGCCAAGGTCAACCCTCCCGGGTGATGTGATGGGTGTCCAGGTGTGGTTGGGCGATGCTGCTACTTGAC
CCCAAGCTCCAGTGTGGAACTTCCTTCTGGCTGGTTTTCCAGAACTACAGAGGAATGGACCACAGTCTTCCAG
GGTCCCTCCTCGTCCACCAACCGGGAGCCTCCACCTTGGCCATCCGTCAGCTATGAATGGCTTTTTAAACAAACC
CACGTCCCAGCCTGGGTAAACATGGTAAAGCCCCGTCTCTACAAAAAATCCAAGTTAGCCGGGCATGGTGGTGCG
CACCTGTAGTCCCAGCTGCAGTGGGACTGAGGTGGAGGTGGAGGTGGGGGTGGGAGCTGAGGAAGGAGGATCGC
TTGAGCCTGGGAAGTCGAGGCTGCAGTGAGCTGAGATTGCACCACTGCATCCAGCCTGGGTGACAGAGCAAGAC
CCTGTCTCAAAA

241/615

FIGURE 240

MSCVLGGVIPLGLLFLVCGSQGYLLPNVTLLLEELLSKYQHNEHSRVRRAIPREDKEEILMLHNKLRGQVQPQAS
NMEYMVSAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGLRVSSGRGGSRLCSVLFVCFETGSHSATDAGVQ
WHNRHAIKP

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89

242/615

FIGURE 241

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCC
CTTGTCCTCCTCTTGACCCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAG
GAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCAT
CTCCCTTCAGGGACCAGCGTCACCCCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACATTGACAGCCA
TTGAAGCCTGTGTCTTCTTGGCCCCGGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTTCAG
CAGGCCCCACCTCCTGAGTGGCAATAAATAAAATTCGGTATGCTG

243/615

FIGURE 242

MSGGLPLVLLLTLLGSSHGTGPGMTLQLKLKESFLTNSSESSFLELLEKLCLLLHLPSTSVTLHHARSQHHVCNT

244/615

FIGURE 243

GGCAAGTGGAACCACTGGCTTGGTGGATTTTGCTAGATTTTCTGATTTTAAACTCCTGAAAAATATCCCAGAT
AACTGTCATGAAGCTGGTAACTATCTTCCTGCTGGTGACCATCAGCCTTTGTAGTTACTCTGCTACTGCCTTCCT
CATCAACAAAGTGCCCCCTTCCTGTTGACAAGTTGGCACCTTTACCTCTGGACAACATTCTTCCTTTATGGATCC
ATTAAAGCTTCTTCTGAAAACTCTGGGCATTTCTGTTGAGCACCTTGTGGAGGGGCTAAGGAAGTGTGTAATGA
GCTGGGACCAGAGGCTTCTGAAGCTGTGAAGAACTGCTGGAGGCGCTATCACACTTGGTGTGACATCAAGATAA
AGAGCGGAGGTGGATGGGGATGGAAGATGATGCTCCTATCCTCCCTGCCTGAAACCTGTTCTACCAATTATAGAT
CAAATGCCCTAAAATGTAGTGACCCGTGAAAAGGACAAATAAAGCAATGAATACATTA

245/615

FIGURE 244

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59855
<subunit 1 of 1, 93 aa, 1 stop
<MW: 10161, pI: 7.39, NX(S/T): 0
MKLVTIFLLVTISLCSYSATAFLINKVPLPVDKLAPLPLDNILPFMDPLKLLKTLGISV
EHLVEGLRKCVNELGPEASEAVKKLLEALSHLV

Important features:**Signal peptide:**

Amino acids 1-18

246/615

FIGURE 245

TGCTAGGCTCTGTCCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGATCCCTCTATGACT
GCAATGTGAGGTGTCCGGCTTTGCTGGCCCAAGCCTGATAAGCATGAAGCTCTTATCTTTGGTGGCTGTGGT
CGGGTGTGTTGCTGGTGGCCCCAGCTGAAGCCAACAAGAGTTCTGAAGATATCCGGTGCAAATGCATCTGTCCACC
TTATAGAAACATCAGTGGGCACATTTACAACCAGAATGTATCCAGAAGGACTGCAACTGCCTGCACGTGGTGGG
GCCCATGCCAGTGCCCTGGCCATGACGTGGAGGCCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAGCAC
CACCACCATCAAGGTCATCATTGTCTATCTACCTGTCCGTGGTGGGTGCCCTGTTGCTCTACATGGCCTTCTGTAT
GCTGGTGGACCCTCTGATCCGAAAGCCGGATGCATACACTGAGCAACTGCACAATGAGGAGGAGAATGAGGATGC
TCGCTCTATGGCAGCAGCTGCTGCATCCCTCGGGGGACCCCGAGCAAACACAGTCCTGGAGCGTGTGGAAGGTGC
CCAGCAGCGGTGGAAGCTGCAGGTGCAGGAGCAGCGGAAGACAGTCTTCGATCGGCACAAGATGCTCAGCTAGAT
GGGCTGGTGTGGTTGGGTCAAGGCCCAACACCATGGCTGCCAGCTTCAGGCTGGACAAAGCAGGGGGCTACTT
CTCCCTTCCCTCGGTTCCAGTCTTCCCTTTAAAGCCTGTGGCATTTCCTCCTTCTCCCTAACTTTAGAAATG
TTGTAATTTGGCTATTTTGATTAGGGAAGAGGGATGTGGTCTCTGATCTCTGTGTCTTCTTGGGTCTTGGGGTT
GAAGGGAGGGGGAAGGCAGGCCAGAAGGGAATGGAGACATTCGAGGCGGCCTCAGGAGTGGATGCCATCTGTCTC
TCCTGGCTCCACTCTTGCCGCCTTCCAGCTCTGAGTCTTGGGAATGTTGTTACCCTTGAAGATAAAGCTGGGTC
TTCAGGAACCTCAGTGTCTGGGAGGAAAGCATGGCCAGCATTGAGCATGTGTTCCTTTCTGCAGTGGTCTTATC
ACCACTCCCTCCAGCCCCGGCGCCTCAGCCCCAGCCCCAGCTCCAGCCCTGAGGACAGCTCTGATGGGAGAGC
TGGGCCCCCTGAGCCCACTGGGTCTTCAGGGTGCAGTGGGAAGCTGGTGTTCGCTGTCCCCTGTGCACTTCTCGCA
CTGGGGCATGGAGTGCCCATGCATACTCTGTGCCGGTCCCTCACCTGCAGTGGGGGTCTGGGAGTCCCTC
CTCTCCCCAGTGTCCACAGTCACTGAGCCAGACGGTTCGGTTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGA
ACACCACAGCCCCTGACTTGGGTGCTCTTGTCCCTGAACCTTCGTTGTACCAGTGCATGGAGAGAAAATTTG
TCCTCTTGTCTTAGAGTTGTGTGTAATCAAGGAAGCCATCATTAAATTGTTTTATTTCTCTCA

247/615

FIGURE 246

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278

<subunit 1 of 1, 183 aa, 1 stop

<MW: 20574, pI: 6.60, NX(S/T): 3

MKLLSLVAVVGCLLVPPAEANKSSEDIRCKCICPPYRNISGHIYNQNVSQKDCNCLHVVEPMPVPGHDVEAYCLL
CECRYEERSTTTIKVIVYLSVVGALLLYMAFLMLVDPLIRKPDAYTEQLHNEEENEDARSMAAAAASLGGPRA
NTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS**Important features:****Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 90-112

N-glycosylation sites.

amino acids 21-24, 38-41 and 47-50

248/615

FIGURE 247

AATTGTATCTGTGTAATGTTAAAACAAACGAAATAAAATAGAAGGAAAACTTTCTGAGTTTCAAAAACAACAGA
CTAGTACTCTAAAGAACTCTTTAAAACAATTAAGTGTAGGATTGCAGTTATGATTGGATATTATTTAATTCTGT
TTCTGATGTGGGGTTCCCTCCACTGTGTTCTGTGTGCTATTAATATTTACCATTGCAGAAGCTTCATTCAGTGTG
AAAATGAATGCTTAGTGGATCTGTGCCTCTTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAG
TTCCCTCCCTCCGATTGTTCTAAATTAATTGAAAGATGCTGCTGTGGAAAAAGGCATGTATTTAAATCTGTAT
GATTCTCAACCATCTTAGTTGGGAAAGGTCCTTGAAAGCCAATGGAAATACTTTTTTTTTTTCTTGGCACTAAT
CAAGTGAGTGTTACCTTTTCACTTAGTAGGATGTGTTGTACGCTAGTAAAATAGAAACCTGTGTTATTCTCAG
GTATTTTAGAAACAACAGCCATCATTTTATTTTATGTGTGTGTTCTTGGCTGTATTCATAAATTATATATTTTGG
GCTATCAAATATTACTTCATTCAATATAAATAACAATAGTAGAAGTTGTTTACTTAGATATGCTTTCTAGTTGCA
TTTTCTCAGCCTATGTAAGACTACTTTGTTGTAATAGCCTTTGAAATTTACAGTACTGTCTCTCTACTATCTTCA
GATTACTTGATTCAAATAAACCAATTATGTTTGTAAATTGATATTAATAAAACCAGAATAAAAGTTCATATCTACCC

249/615

FIGURE 248

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVENECLVDLCLLRICYKLSGVPNQCRVFLPSDCSK

Important features:

Signal peptide:

amino acids 1-29

250/615

FIGURE 249

AGCGGGTCTCGCTTGGGTTCCGCTAATTTCTGTCTGAGGCGTGAGACTGAGTTCATAGGGTCTGGGTCCCCGA
ACCAGGAAGGGTTGAGGGAACACAATCTGCAAGCCCCCGCGACCCAAGTGAGGGGCCCCGTGTTGGGGTCTCTCC
TCCCTTTGCATTTCCACCCCTCCGGGCTTTGCGTCTTCTGGGGACCCCTCGCCGGGAGATGGCCGCGTTGATG
CGGAGCAAGGATTCGTCTGCTGCTGCTCTCTACTGGCCGCGGTGCTGATGGTGGAGAGCTCACAGATCGGCAGT
TCGCGGGCCAACTCAACTCCATCAAGTCTCTCTGGGCGGGGAGACGCCCTGGTCAGGCCGCCAATCGATCTGCG
GGCATGTACCAAGGACTGGCATTGCGCGGCAGTAAGAAGGGCAAAACCTGGGGCAGGCCTACCCCTGTAGCAGT
GATAAGGAGTGTGAAGTTGGGAGGTATTGCCACAGTCCCCACCAAGGATCATCGGCCTGCATGGTGTGTCGGAGA
AAAAAGAAGCGCTGCCACCGAGATGGCATGTGCTGCCCCAGTACCCGCTGCAATAATGGCATCTGTATCCAGTT
ACTGAAAGCATCTTAACCCCTCACATCCCGGCTCTGGATGGTACTCGGCACAGAGATCGAAACCACGGTCATTAC
TCAAACCATGACTTGGGATGGCAGAATCTAGGAAGACCACACACTAAGATGTCACATATAAAAGGGCATGAAGGA
GACCCCTGCCTACGATCATCAGACTGCATTGAAGGGTTTGTCTGTGCTCGTCATTTCTGGACCAAAATCTGCAAA
CCAGTGTCTCCATCAGGGGGAAGTCTGTACCAAAACAACGCAAGAAGGGTTCTCATGGGCTGGAAATTTTCCAGCGT
TGGCACTGTGCGAAGGGCCTGTCTTGCAAAGTATGGAAAGATGCCACCTACTCCTCAAAGCCAGACTCCATGTG
TGTCAGAAAATTTGATCACCATTGAGGAACATCATCAATTGCAGACTGTGAAGTTGTGTATTTAATGCATTATAG
CATGGTGGAAAATAAGGTTTCAGATGCAGAAGAATGGCTAAAATAAGAAACGTGATAAGAATATAGATGATCACA
AAAGGGAGAAAGAAAACATGAACCTGAATAGATTAGAATGGGTGACAAATGCAGTGCAGCCAGTGTTCATTATG
CAACTTGTCTATGTAATAATGTACACATTTGTGGAAAATGCTATTATTAAGAGAACAAGCACACAGTGGAAATT
ACTGATGAGTAGCATGTGACTTTCCAAGAGTTAGGTTGTGCTGGAGGAGAGGTTTCCTTCAGATTGCTGATTGC
TTATACAAATAACCTACATGCCAGATTTCTATTCAACGTTAGAGTTTAACAAAATACTCCTAGAATAACTTGTTA
TACAATAGGTTCTAAAATAAAATTTGCTAAACAAGAAATGAAAACATGGAGCATTTGTTAATTTACAACAGAAAAT
TACCTTTTGTATTGTAACTACTTCTGCTGTTCAATCAAGAGTCTTGGTAGATAAGAAAAAAATCAGTCAATAT
TTCAAATAATTTGCAAAATAATGGCCAGTTGTTTAGGAAGGCCTTTAGGAAGACAAATAAATAACAAACAAACAG
CCACAAATACTTTTTTTTCAAATTTTAGTTTACCTGTAATTAATAAGAACTGATACAAGACAAAAACAGTTCC
TTCAGATTCTACGGAATGACAGTATATCTCTCTTTATCCTATGTGATTCTGCTCTGAATGCATTATATTTTCCA
AACTATACCCATAAATTTGTGACTAGTAAATACTTACACAGAGCAGAATTTTACAGATGGCAAAAAATTTAAA
GATGTCCAATATATGTGGGAAAAGAGCTAACAGAGAGATCATTATTTCTTAAAGATTGGCCATAACCTATATTTT
GATAGAATTAGATTGGTAAATACATGTATTACATACACTCTGTGGTAATAGAGACTTAAGCTGGATCTGTACTG
CACTGGAGTAAGCAAGAAAATTTGGGAAAACTTTTCTGTTTGTTCAGGTTTTGGCAACACATAGATCATATGTCTG
AGGCACAAGTTGGCTGTTTCATCTTTGAAACCAGGGGATGCACAGTCTAAATGAATATCTGCATGGGATTTGCTAT
CATAATATTTACTATGCAGATGAATTCAGTGTGAGGTCCTGTGTCCGTACTATCCTCAAATTATTTATTTTATAG
TGCTGAGATCCTCAAATAATCTCAATTTTCAGGAGGTTTCAAAAATGTACTCCTGAAGTAGACAGAGTAGTGAGG
TTTCATTGCCCTCTATAAGCTTCTGACTAGCCAATGGCATCATCCAATTTTCTTCCCAAACCTCTGCAGCATCTG
CTTTATTGCCAAAGGGCTAGTTTTCGGTTTTCTGCAGCCATTGCGGTTAAAAATATAAGTAGGATAACTTGTA
ACCTGCATATTGCTAATCTATAGACACCACAGTTTCTAAATCTTTGAAACCCTTTACTACTTTTTTTAACTT
AACTCAGTTCTAAATACTTTGTCTGGAGCACAAAACAATAAAAGGTTATCTTATAGTCGTGACTTTAACTTTT
TAGACCACAATTCACTTTTTAGTTTTCTTTTACTTAAATCCCATCTGCAGTCTCAAATTTAAGTTCTCCAGTAG
AGATTGAGTTTGAGCCTGTATATCTATTAAAAATTTCAACTTCCACATATATTTACTAAGATGATTAAGACTTA
CATTTTCTGCACAGGCTGCAAAAACAAAAATTATAAAGTCCATCCAAGAACCAGTTTGTATAAACAGGT
TGCTATAAGCTTGTGAATGAAAATGGAACATTTCAATCAAACATTTCTATATAACAATTATTATTTACAAT
TTGGTTTCTGCAATATTTTCTTATGTCCACCCTTTTAAAAATTATTATTTGAAGTAATTTATTACAGGAAATG
TTAATGAGATGATTTTCTTATAGAGATATTTCTTACAGAAAGCTTTGTAGCAGAAATATATTTGCAGCTATTGAC
TTTGTAAATTTAGGAAAAATGTATAATAAGATAAAATCTATTAAATTTTCTCCTCTAAAAACTGAAAAAAA
AAAAAAAAAAAAAAAAAAAA

251/615

FIGURE 250

MAALMRSKDSSCCLLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLAFGGSKKGKNLGQA
YPCSSDKECEVGRYCHSPHQSSACMVCRRKKKRCHRDGMCCPSTRCNNGICIPVTESILTPHIPALDGTRHRDR
NHGHYSNHDLGWQNLGRPHTKMSHIKGHEGDPCLRSSDCIEGFCCARHFWTKICKPVLHQGEVCTKQRKKGSHGL
EIFQRCDCAKGLSCKVWKDATYSSKARLHVCQKI

Signal peptide:
amino acids 1-25

252/615

FIGURE 251

TCTCAATCTGCTGACCTCGTGATCCGCCTGACCTTGTAATCCACCTACCTTGGCCTCCCAAAGTGTTGGGATTAC
AGGCGTGAGCCACCGCGCCCGGCCAACATCACGTTTTTAAAAATTGATTTCTTCAAATTCATGGCAAATATTTCC
CTTCCCTTTAACTTCTTATGTGAGAATGAGGAAGGATAGCTGCATTTATTTAGTCAGTTTTTCATTGCATAGTAAT
ATTTTCATGTAGTATTTTCTAAGTTATATTTTAGTAATTCATATGTTTTAGATTATAGGTTTTAACATACTTGTG
AAAATACTTGATGTGTTTTAAAGCCTTGGGCAGAAATCTGTATTGTTGAGGATTGTTCTTTTATCCCCCTTTT
AAAGTCATCCGTCCTTGGCTCAGGATTTGGAGAGCTTGACCACCAAAAATGGCAAACATCACCAGCTCCCAGAT
TTTGGACCAGTTGAAAGCTCCGAGTTTGGGCCAGTTTACCACCACCCCAAGTACACAGCAGAATAGTACAAGTCA
CCCTACAATACTACTTCTTGGGACCTCAAGCCCCAACATCCCAGTCCCTCAGTCCCTCAGTCATCTTGACTTCAA
ATCTCAACCTGAGCCATCCCCAGTTCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCACTGT
TCCTCCTCCTGGTTTGGAGTCCTTTCCTTCCCAGGCAAACTTCGAGAATCAACACCTGGAGACAGTCCCTCCAC
TGTGAACAAGCTTTTGCAGCTTCCCAGCAGCACCATTGAAAATATCTCTGTGTCTGTCCACCAGCCACAGCCCAA
ACACATCAAACCTTGCTAAGCGGCGGATACCCCGAGCTTCTAAGATCCCAGCTTCTGCAGTGGAAATGCCTGGTTC
AGCAGATGTCACAGGATTAAATGTGCAGTTTGGGGCTCTGGAATTTGGGTGAGAACCTTCTCTCTCTGAATTTGG
ATCAGCTCCAAGCAGTGAAAATAGTAATCAGATTTCCCATCAGCTTGTATTGGAAGTCTTAAAGTGAGCCTTTGAA
TACATCTTTTATCAATGACCAGTGCAGTACAGAACTCCACATATACAACCTCCGTCATTACCTCCTGCAGTCTGAC
AAGCTCATCACTGAATTCTGCTAGTCCAGTAGCAATGTCTTCTTATGACCAGAGTTCTGTGCATAACAGGAT
CCCATACCAAAGCCCTGTGAGTTCATCAGAGTCAGCTCCAGGAACCATCATGAATGGACATGGTGGTGGTCTGAAG
TCAGCAGACACTAGACAGTAAGTATAGCAGCAAGCTACTCTTGTGATGGCTGGTGCCAACCAACAGAGGAAAGAG
GATAGCTCACGTGATGTGGAAAACACCAGTTGGTCAATGGCTCATTTCGTTAAAAAGCAGCCCTTTTGCTTTTTTG
TTTTTGGACCAGGTGTTGGCTGTGGTGTATTAGAAATGTCTTAACCACAGCAAGAAGGAGGTGGTGGTCTCATA
TTCTTCTGCCCTAATCAGACTGCACCACAAGTGCAGCATACAGTATGCATTTTAAAGATGCTTGGGCCAGGCGGG
GTGGCTGATGCCATAATCCCAGTGCTTGGGGGGCCAAGGCAGGCAGATTGCCCAAGCTCAGGAGTTTGAGACC
ACCCTGGGCAACATGGTGAAACTCTGTCTCTACTAAAATACGAAAAACTAGCCGGGTGTGGTGGCGCGCGTGCC
TGTAATCCCAGCTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGGCTACAAAGTGAGACTCCGT
CTGAAAAGA

253/615

FIGURE 252

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTTPSTQONSTSHPTT
TTSWDLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAQVTVPPPGLESFSPSQAKLRESTPGDSPSTVNK
LLQLPSTTIENISVSVHQPPKHIKLAKRRIPPASKIPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAP
SSENSNQIPISLYSKSLSEPLNTSLSM TSAVQNSTYTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIYQ
SPVSSSESAPGTIMNGHGGGRSQQTLD SKYSSKLLLSWLVP TKQRKRIAHVMWKTPVGQWLIR

Signal peptide:
amino acids 1-24

FIGURE 253

[illegible]

255/615

FIGURE 254

MELSQMSELMGLSVLLGLLALMATAAVARGWLRAGEERSGRPACQKANGFPDPKSSGSKKQKQYQIRIRKEKPQQH
NFTHRLAAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQREHRSMRANVELDHATLVRFSPPDCRA
FIVWLANGDTLRVFKMTKREDGGYTFTATPEDFPKKHKAPVIDIGIANTGKFIMTASSDTTVLIWSLKGQVLSTI
NTNQMNNTHAHAVSPCGRFVASCFTPDVKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKD
GTWKLWDTDVEYKKKQDPYLLKTGRFEEAAGAAPCRLALSPNAQVLALASGSSIHLYNTRRGEKEECFERVHGEC
IANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGHLKRASNESTRQLQQQLTQAQETLKS LGALKK

Important features:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

256/615

FIGURE 255

ACGGACCGAGGGTTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCCGGGCCAGGTGCCCC
GTCGCAGGTGCCCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGAAGCCCCCTTCCTCGGCGCTGCCAACCC
GCCACCCAGCCCATGGCGAACCCCGGGCTGGGGCTGCTTCTGGCGCTGGGCCTGCCGTTCCCTGCTGGCCCGCTGG
GGCCGAGCCTGGGGGCAAATACAGACCACTTCTGCAAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCC
AGCTCCGATGGCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTGCTC
CTGGCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGGCACCTACCGGCCAGT
AGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGGACTCCAAGGAGACGGTGCAGGGCTGCCTG
CCCATCTAGGTCCCCCTCTCCTGCATCTGTCTCCCTTCATTGCTGTGTGACCTTGGGGAAGGCAGTGCCCTCTCT
GGGCAGTCAGATCCACCCAGTGCTTAATAGCAGGGAAGAAGTACTTCAAAGACTCTGCCCTGAGGTCAAGAGA
GGATGGGGCTATTCACTTTTATATATTTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAAAAA

257/615

FIGURE 256

MANPGLGLLLALGLPFLARWGRAWGQIQTTSANENSTVLPSTSSSSDGNLRPEAITAIIVVFSLLAALLLAVG
LALLVRKLREKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

258/615

FIGURE 257

GCCAGGAATAACTAGAGAGGAACAATGGGGTTATTAGAGGTTTTGTTTTCTCTTAGTTCTGTGCCTGCTGCAC
CAGTCAAATACTTCCTTCATTAAGCTGAATAATAATGGCTTTGAAGATATTGTCTATTGTTATAGATCCTAGTGTG
CCAGAAGATGAAAAAATAATTGAACAAATAGAGGATATGGTGACTACAGCTTCTACGTACCTGTTTGAAGCCACA
GAAAAAGATTTTTTTTTCAAAAATGTATCTATATTAATTCCTGAGAATTGGAAGGAAAAATCCTCAGTACAAAAGG
CCAAAACATGAAAACCATAAACATGCTGATGTTATAGTTGCACCACTACACTCCCAGGTAGAGATGAACCATAC
ACCAAGCAGTTTACAGAAATGTGGAGAGAAAGGCGAATACATTCACCTTCACCCCTGACCTTCTACTTGGAAAAAAA
CAAAATGAATATGGACCACCAGGCAAACTGTTTGTCCATGAGTGGGCTCACCTCCGGTGGGGAGTGTGATGAG
TACAATGAAGATCAGCCTTTCTACCGTGCTAAGTCAAAAAAATCGAAGCAACAAGGTGTTCCGCAGGTATCTCT
GGTAGAAATAGAGTTTATAAGTGTCAAGGAGGCGAGCTGTCTTAGTAGAGCATGCAGAATTGATTCTACAAACAAA
CTGTATGGAAAAGATTGTCAATTCCTTCCTGATAAAGTACAAACAGAAAAAGCATCCATATGTTTATGCAAAAGT
ATTGATTCTGTTTGTGAAATTTTGTAAACGAAAAAACCCATAATCAAGAAGCTCCAAGCCTACAAAACATAAAGTGC
AATTTTGAAGTACATGGGAGGTGATTAGCAATTCAGAGATTTTAAAAACACCATACCCATGGTGACACCACCT
CCTCCACCTGTCTTCTCATTGCTGAAGATCAGTCAAAGAATTGTGTGCTTAGTTCTTGATAAGTCTGGAGCATG
GGGGTAAGGACCGCCTAAATCGAATGAATCAGCAGCAAAACATTTCTGCTGCAGACTGTTGAAAAATGGATCC
TGGGTGGGGATGGTTTCACTTTGATAGTACTGCCACTATTGTAAATAAGCTAATCCAAATAAAAAGCAGTGATGAA
AGAAACACACTCATGGCAGGATTACCTACATATCCTCTGGGAGGAACCTCCATCTGCTCTGGAATTAATATGCA
TTTCAGGTGATTGGAGAGCTACATTCCTCAACTCGATGGATCCGAAGTACTGCTGCTGACTGATGGGGAGGATAAC
ACTGCAAGTTCTTGTATTGATGAAGTGAACAAAGTGGGGCCATTGTTTCAATTTATGCTTTGGGAAGAGCTGCT
GATGAAGCAGTAATAGAGATGAGCAAGATAACAGGAGGAAGTCATTTTTATGTTTCAGATGAAGCTCAGAACAAT
GGCCTCATTGATGCTTTTGGGGCTCTTACATCAGGAAATCTGATCTCTCCAGAACTCCCTTCAGCTCGAAAGT
AAGGGATTAACACTGAATAGTAATGCCTGGATGAACGACACTGTCTAATGATAGTACAGTGGGAAAGGACACG
TTCTTTCTCATCACATGGAACAGTCTGCCTCCAGTATTTCTCTCTGGGATCCAGTGAACAATAATGGAATAAT
TTCAGAGTGGATGCAACTTCCAAATGGCCTATCTCAGTATTCAGGAAGTGCAGAAAGGTGGGCACTTGGGCATAC
AATCTTCAAGCCAAAGCGAACCAGAAACATTAATCTTACAGTAACCTTCTCGAGCAGCAAAATCTTCTGTGCT
CCAATCACAGTGAATGCTAAATGAATAAGGACGTAAACAGTTTCCCAAGCCCAATGATTGTTTACGCAGAAAT
CTACAAGGATATGTACCTGTTCTTGGAGCCAAATGTGACTGCTTTCATTGAATCACAGAATGGACATACAGAAGTT
TTGGAACTTTTGGATAATGGTGCAGGCGCTGATTCTTTCAAGAATGATGGAGTCTACTCCAGGTATTTTACAGCA
TATACAGAAAAATGGCAGATATAGCTTAAAGTTCGGGCTCATGGAGGAGCAAAACACTGCCAGGCTAAAATTACGG
CCTCCACTGAATAGAGCCGCTACATACCAGGCTGGGTAGTGAACGGGGAAATGAAGCAAAACCCGCCAAGACCT
GAAATTGATGAGGATACCTCAGACCACCTTGGAGGATTTAGCCGAACAGCATCCGGAGGTGCATTTGTGGTATCA
CAAGTCCCAAGCCTTCCCTTGCTGACCAATACCCACCAAGTCAAATCACAGACCTTGATGCCACAGTTTATGAG
GATAAGATTATTTTACATGGACAGCACCAGGAGATAATTTTGTGTTGGAAAAGTTCAACGTTATATCATAAGA
ATAAGTGCAAGTATTTCTGATCTAAGAGACAGTTTGTGATGATGCTCTTCAAGTAAATACTACTGATCTGTACCA
AAGGAGGCCAACTCCAAGGAAAGCTTTGCATTTAAACCAGAAAAATATCTCAGAAAGAAAAATGCAACCCACATATT
ATTGCCATTAAAAGTATAGATAAAAGCAATTTGACATCAAAAGTATCCAACATTTGCACAAGTAACCTTGTATTATC
CCTCAAGCAAAATCCTGATGACATTGATCCTACACCTACTCCTACTCCTACTCCTACTCCTGATAAAAGTCATAAT
TCTGGAGTTAATATTTCTACGCTGGTATTGCTGTGATTGGGTCTGTTGTAATTGTTAACTTTATTTTAAAGTACC
ACCATTTGAACCTTAACGAAGAAAAAATCTTCAAGTAGACCTAGAAGAGAGTTTAAAAAACAAACAAATGTAA
GTAAAGGATATTTCTGAATCTTAAATTCATCCCATGTGTGATCATAAACTCATAAAAAATAATTTAAGATGTGCG
GAAAAGGATACCTTGATTAAATAAAACACTCATGGATATGTAACAACTGTCAAGATTAAATTTAATAGTTTCA
TTTATTTGTTATTTATTTGTAAGAAATAGTGTGAACAAAGATCCTTTTTCTACTGATACCTGGTGTATATT
ATTTGATGCAACAGTTTCTGAAATGATTTTCAAAATGCATCAAGAAATTAATATCATCTATCTGAGTAGTCAA
AATACAAGTAAAGGAGAGCAAAATAAACACATTTGGAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA
AAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA

259/615

FIGURE 258

MGLFRGEFVFLVLCLLHQSNSTFIKLNNNGFEDIVIVIDPSVPEDEKIIIEQIEDMVTASTYLFEATEKRFFFKN
VSILIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTECGEKGEYIHFTPDLLLGGKKQNEYGPPG
KLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATRCISAGISGRNRVYKCQGGSCLSRACRIDSTTKLYGKDCQF
FPDKVQTEKASIMFMQSIDSVVEFCNEKTHNQEAPSLQNIKCNRSTWEVISNSEDFKNTIPMVTPPPPPVFSL
KISQRIVCLVLDKSGSMGGKDRLNRMNQAAKHFLQTVENGSWVGMVHFDSTATIVNKLIQIKSSDERNTLMAGL
PTYPLGGTSICSGIKYAFQVIGELHSQLDGSEVLLLLTDGEDNTASSCIDEVKQSGAIVHFIALGRAADEAVIEMS
KITGGSHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLTLNSNAWMNDTVIIDSTVGKDTFFLITWNS
LPSPISLWDPSGTIMENFTVDATSKMAYLSIPGTAKVGTWAYNLQAKANPETLTITVTSRAANSSVPEITVNAKM
NKDVNSFPSPMIVYAEILQGYVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNDBGVYSRYFTAYTENGRYS
LKVRAHGGANTARLKLRLPPLNRAAYIPGWVVNGEIEANPPRPEIDEDTQTTLDEFSRTASGGAFVVSQVPSLPLP
DQYPPSQITDLDATVHEDKIILTWTAPGDNFDVGKVQRYIIRISASILDRLDSFDDALQVNTTDLSPKEANSKES
FAFKPENISEENATHIFIAIKSIDKSNLTSKVSNIQVTLFIPQANPDDIDPTPTPTPTPTPDKSHNSGVNISTL
VLSVIGSVVIVNFILSTTI

Signal peptide:

amino acids 1-21

Putative transmembrane domains:

amino acids 284-300, 617-633

Leucine zipper pattern.

amino acids 469-491, 476-498

N-glycosylation site.amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592, 628-632,
811-815, 832-836, 837-841, 852-856, 896-900

260/615

FIGURE 259

CGCCGGAGGCAGCGGGCGGTGGCGCAGCGGGCAGATGGGCGTTGTCTCAGAGGACGACTTTTCAGCACAGTTCAA
ACTCCACCTACGGAACCACAAGCAGCAGTCTCCGAGCTGACCAGGAGGCAGTCTTGAGAAGCTGCTGGACCGCC
CGCCCCCTGGCCTGCAGAGGCCCCGAGGACCGCTTCTGTGGCACATACATCATCTTCTTCAGCCTGGGCATTGGCA
GTCTACTGCCATGGAACCTCTTTATCACTGCCAAGGAGTACTGGATGTTCAAACCTCCGCAACTCCTCCAGCCCAG
CCACCGGGGAGGACCCTGAGGGCTCAGACATCCTGAACCTACTTTGAGAGCTACCTTGCCGTTGCCTCCACCGTGC
CCTCCATGCTGTGCCTGGTGGCCAACTTCTGCTTGTCAACAGGGTTGCAGTCCACATCCGTGTCTGGCCTCAC
TGACGGTCATCCTGGCCATCTTCATGGTGATAACTGCACTGGTGAAGGTGGACACTTCTCCTGGACCCGTTGGTT
TTTTTGCGGTCAACATTGTCTGCATGGTGATCCTCAGCGGTGCCCTCCACTGTCTTCAGCAGCAGCATCTACGGCA
TGACCGGCTCCTTTCTATGAGGAACCTCCAAGCACTGATATCAGGAGGAGCCATGGGCGGGACGGTCAGCGCCG
TGGCCTCATTGGTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTTCTGACGGCCACCA
TCTTCTCGTGCTCTGCATGGGACTTACCTGCTGCTGTCCAGGCTGGAGTATGCCAGGTACTACATGAGGCCTG
TTCTTGCGGCCCATGTGTTTTCTGGTGAAGAGGAGCTTCCCCAGGACTCCCTCAGTGCCCTTCGGTGGCCTCCA
GATTCATTGATTCACACACACCCCTCTCCGCCCCATCCTGAAGAAGACGGCCAGCCTGGGCTTCTGTGTCACT
ACGCTCTTCTTCATCACCAGCCTCATCTACCCCGCGTCTGCACCAACATCGAGTCCCTCAACAAGGGCTCGGGCT
CACTGTGGACCACCAAGTTTTTTCATCCCCCTCACTACCTTCTCCTGTACAACCTTGTGACCTATGTGGCCGGC
AGCTCACCGCCTGGATCCAGGTGCCAGGGCCCAACAGCAAGGCGCTCCCAGGGTTCTGTGCTCCTCCGGACCTGCC
TCATCCCCCTCTTCTGTGCTCTGTAACCTACCAGCCCCGCTCCACCTGAAGACTGTGGTCTTCCAGTCCGATGTGT
ACCCCGCACTCCTCAGCTCCTGCTGGGGCTCAGCAACGGCTACCTCAGCACCTTGGCCCTCCTTACGGGCCTA
AGATTGTGCCCAGGGAGCTGGCTGAGGCCACGGGAGTGGTGATGTCCTTTTATGTGTGCTTGGGCTTAACACTGG
GCTCAGCCTGCTCTACCCTCCTGGTGCACCTCATCTAGAAGGGAGGACACAAGGACATTGGTGTTCAGAGCCTT
TGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGGCCATGGAGGAAAGGCCATAAGTTTTCACTTGGGGACAGAGAG
CAGAGCACACTCGGGCCTCATCCCTCCCAAGATGCCAGTGAGCCACGTCCATGCCCATTCCGTGCAAGGCAGATA
TTCCAGTCATATTAACAGAACTCCTGAGACAGTTGAAGAAGAAATAGCACAAATCAGGGGTACTCCCTTCACA
GCTGATGGTTAACAATCCACCTTCTTTCTAGCCCTTCAAAGATGCTGCCAGTGTTCGCCCTAGAGTTATTACAAA
GCCAGTGCCAAAACCCAGCCATGGGCTCTTGCAACCTCCAGCTGCGCTCATTCCAGCTGACAGCGAGATGCAA
GCAAATGCTCAGCTCTCCTTACCCTGAAGGGGTCTCCCTGGAATGGAAGTCCCCTGGCATGGTCAGTCTCAGGC
CCAAGACTCAAGTGTGCACAGACCCCTGTGTTCTGCGGGTGAACAACCTGCCCACTAACCAGACTGGAAAACCCAG
AAAGATGGGCCTTCCATGAATGCTTCATTCCAGAGGGACCAGAGGGCCTCCCTGTGCAAGGGATCAAGCATGTCT
GGCCTGGGTTTTCAAAAAAGAGGGATCCTCATGACCTGGTGGTCTATGGCCTGGGTCAAGATGAGGGTCTTTCA
GTGTTCTGTTTACAACATGTCAAAGCCATTGGTTCAAGGGCGTAATAAATACTTGCGTATTCAAAAA

261/615

FIGURE 260

MAVSEDDFQHSSNSTYGTSSSLRADQEALLEKLLDRPPPGLQRPEDRFCGTYYIFFSLGIGSLLPWNEFITAK
EYWMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPSMLCLVANFLLVNRVAVHIRVLASLTVILAI FMVIT
ALVKVDTSSWTRGFFAVTIVCMVILSGASTVFSSSIYGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSD
VRNSALAFFLTATIFLVLCMGLYLLLSRLEYARYYMRPVLAHVFSGEEELPQDSL SAPSVASRFIDSHTPPLRP
ILKKTASLGFCVTYVFFITS LIYPAVCTNIESLNKGSGSLWTTKFFIPLTTFLLYNFADLCGRQLTAWIQVPGPN
SKALPGFVLLRTCLIPLFVLCNYQPRVHLKTVVFQSDVYPALLSSLLGLSNGYLSTLALLYGPKIVPRELAEATG
VMSFYVCLGLTLGSACSTLLVHLI

Transmembrane domain:

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252, 305-330,
448-472

262/615

FIGURE 261

CGGACGCGTGGGCTGCTGGTGGGAAGGCCTAAAGAAGCTGGAAAGCCACTCTCTTGAACACCACACCTGTTTA
AAGAACCTAAGCACCATTAAAGCCACTGGAAATTTGTGTCTAGTGGTTGTGGGTGAATAAAGGAGGGCAGAAAT
GGATGATTTTCTCTCCATTAGCCTGCTGTCTCTGGCTATGTTGGTGGGATGTTACGTGGCCGGAATCATTCCCTT
GGCTGTTAATTTCTCAGAGGAACGACTGAAGCTGGTGACTGTTTTGGGTGCTGGCCTTCTCTGTGGAAGTGTCT
GGCAGTCATCGTGCCTGAAGGAGTACATGCCCTTTATGAAGATATTCTTGAGGGAAAACACCACCAAGCAAGTGA
AACACATAATGTGATTGCATCAGACAAAGCAGCAGAAAAATCAGTTGTCCATGAACATGAGCAGCCACGACCA
CACACAGCTGCATGCCTATATTGGTGTTCCTCGTTCTGGGCTTCGTTTTCATGTTGCTGGTGGACCAGATTGG
TAACTCCCATGTGCATTCTACTGACGATCCAGAAGCAGCAAGGTCTAGCAATTCCAAAATCACCACCACGCTGGG
TCTGGTTGTCCATGCTGCAGCTGATGGTGTTCGTTTGGGAGCAGCAGCATCTACTTCACAGACCAGTGTCCAGTT
AATTGTGTTTGTGGCAATCATGCTACATAAGGCACCAGCTGCTTTTGGACTGGTTTCTTCTTGATGCATGCTGG
CTTAGAGCGGAATCGAATCAGAAAGCACTTGCTGGTCTTTGCATTGGCAGCACCAGTTATGTCCATGGTGACATA
CTTAGGACTGAGTAAGAGCAGTAAAGAAGCCCTTTAGAGGTGAACGCCACGGGAGTGGCCATGCTTTTCTCTGC
CGGGACATTTCTTTATGTTGCCACAGTACATGTCTCCCTGAGGTGGGCGGAATAGGGCAGCCACAAGCCCCGA
TGCCACGGGAGGGAGAGGCCCTCAGCCGCCTGGAAGTGGCAGCCCTGGTTCTGGGTGCTCATCCCTCTCATCCT
GTCAGTAGGACACCAGCATTAATGTTCAAGGTCCAGCCTTGGTCCAGGGCCGTTTGCCATCCAGTGAGAACAGC
CGGCAGGTGACAGCTACTCACTTCCTCAGTCTCTTGTCTCACCTTGCGCATCTCTACATGTATTCCTAGAGTCCA
GAGGGGAGGTGAGGTTAAACCTGAGTAATGGAAAAGCTTTTAGAGTAGAAAACACATTTACGTGTCAGTTAGCTA
TAGACATCCCATTGTGTTATCTTTTAAAGGCCCTTGACATTTTGCCTTTTAAATATTTCTCTTAACCTATTCTC
AGGGAAGATGGAATTTAGTTTTAAGGAAAAGAGGAGAAGCTTCATACTCACAATGAAATAGTGATTATGAAAATAC
AGTGTCTGTAAATTAAGCTATGTCTCTTCTTCTTAGTTTAGAGGCTCTGCTACTTTATCCATTGATTTTTAACA
TGGTTCCACCAGTGAAGACTGGTGCTTTAGCATCTATGCCACATGCGTTGATGGAAGGTGATAGCACCCTCA
CTTAGATGCTAAAGGTGATTCTAGTTAATCTGGGATTAGGGTCAGGAAAATGATAGCAAGACACATTGAAAGCTC
TCTTTTACTCAAAAGAGATATCCATTGAAAAGGGATGTCTAGAGGGATTTAAACAGCTCCTTTGGCACGTGCCT
CTCTGAATCCAGCCTGCCATTCCATCAAATGGAGCAGGAGAGGTGGGAGGAGCTTCTAAAGAGGTGACTGGTATT
TTGTAGCATTCCCTTGTCAGTTCTCCTTTGCAGAAATACCTGTCTCCACATTCCCTAGAGAGGAGCCAAGTTCTAGT
AGTTTCAGTTCTAGGCTTTCCCTCAAGAACAGTCAGATCACAAAGTGTCTTTGGAATTAAGGGATATTAATTT
TAAGTGATTTTGGATGGTTATTGATATCTTTGTAGTAGCTTTTTTTTAAAGACTACCAAAATGTATGGTTGTCC
TTTTTTTTTGTTTTTTTTTTTTTTTAATTATTTCTCTTAGCAGATCAGCAATCCCTCTAGGGACCTAAATACTAGG
TCAGCTTTGGCGACACTGTGTCTCTCACATAACCACCTGTAGCAAGATGGATCATAAATGAGAAGTGTTCCT
ATTGATTTAAAGCTTATTGGAATCATGTCTCTTGTCTCTTCGTCTTTCTTTGCTTTTCTTCTAATCTTTCCCTC
TAGCCTCTCCTCGCCACAATTTGCTGCTTACTGCTGGTGTAAATATTTGTGTGGGATGAATCTTATCAGGACAA
CCACTTCTCGAACTGTAATAATGAAGATAATAATATCTTTATTCTTTATCCCCCTTCAAAGAAATACCTTTGTG
TCAAATGCCGCTTTGTTGAGCCCTTAAATACCACCTCTCATGTGTAAATTGACACAATCACTAATCTGGTAAT
TTAAACAATTGAGATAGCAAAAGTGTTTAACAGACTAGGATAATTTTTTTTTCATATTGCCAAAATTTTTGTAA
ACCCTGTCTTGTCAAATAAGTGATAATATTGTATTATTAATTTATTTTACTTTCTATACCATTTCAAACACA
TTACACTAAGGGGGAACCAAGACTAGTTTCTTCAGGCGAGTGGACGTAGTAGTTGTAAAAACGTTTCTATGAC
GCATAAGCTAGCATGCCTATGATTTATTTCTTCATGAATTTGTCACTGGATCAGCAGCTGTGGAAATAAAGCTT
GTGAGCCCTCTGCTGGCCACAGTGAGGAAAGTAGCACAAATAGGATACAGTTGTATGTAGTCATTGGCAACAATT
GCATACAATTTTACTACCAAGAGAAGGTATAGTATGGAAAGTCCAAATGACTTCCTTGATTGGATGTTAACAGCT
GACTGGTGTGAGACTTGAGTTTCATCTAGTCCTTCAAACATATATGGTTGCCTAGATTCTCTCTGGAAGTGC
TTTGTCAAATAAATAGCAGATTGTAGTGTCAAAAAA

263/615

FIGURE 262

MDDFISISLLSLAMLVGCYVAGIIPLAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHALYEDILEGKHHQAS
ETHNVIASDKAAEKSVVHEHEHSDHTQLHAYIGVSLVLGFVFMLLVDQIGNSHVHSTDDPEAARSSNSKITTTL
GLVVHAAADGVALGAAASTSQTSVQLIVFVAIMLHKAPAAFGLVSFLMHAGLERNRIRKHLVLFALAAPVMSMT
YLGLSKSSKEALSEVNATGVAMLFSAFTFLYVATVHVLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPLI
LSVGHQH

Signal peptide:
amino acids 1-18

Transmembrane domain:
amino acids 37-56, 106-122, 211-230, 240-260, 288-304

264/615

FIGURE 263

CTCCTTAGGTGGAAACCCTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAAGACCATACGTCCCCGG
GCAGGGGTGACAACAGGTGTCATCTTTTGTATCTCGTGTGTGGCTGCCTTCCCTATTTCAAGGAAAGAC
GCCAAGGTAATTTTGAACCCAGAGGAGCAATGATGTAGCCACCTCCTAACCTTCCCTTCTTGAACCCCC
AGTTATGCCAGGATTTACTAGAGAGTGTCAACTCAACCAGCAAGCGGCTCCTTCGGCTTAACCTTGTTGG
TTGGAGGAGAGAACCTTTGTGGGGCTGCGTTCTCTTAGCAGTGCTCAGAAGTGACTTGCCTGAGGGTG
GACCAGAAGAAAGGAAGGTCCCCTCTTGTCTGTGGCTGCACATCAGGAAGGCTGTGATGGGAATGAA
GGTGAACAACTTGGAGATTTCACTTCAGTCATTGCTTCTGCTGCAAGATCATCCTTTAAAAGTAGAGA
AGCTGCTCTGTGTGGTGGTTAACTCCAAGAGGCAGAACTCGTTCTAGAAGGAAATGGATGCAAGCAGC
TCCGGGGGCCCCAAACGCATGCTTCTGTGGTCTAGCCCCAGGGAAGCCCTTCCGTGGGGGGCCCCGGCT
TTGAGGGATGCCACCGGTTCTGGACGCATGGCTGATTTCTGAATGATGATGGTTCGCCGGGGGCTGCT
TGGCTGGATTTCCCGGGTGGTGGTTTTGCTGGTGTCTCTGCTGTGCTATCTCTGTCTGTACATGT
TGGCCTGCACCCCAAAAGGTGACGAGGAGCAGCTGGCACTGCCAGGGCCAACAGCCCCACGGGGAAG
GAGGGGTACAGGCCGTCCTTCAGGAGTGGGAGGAGCAGCACCGCCAATACGTGAGCAGCCTGAAGCG
GCAGATCGCACAGCTCAAGGAGGAGCTGCAGGAGAGGAGTGAGCAGCTCAGGAATGGGCAGTACCAAG
CCAGCGATGCTGCTGGCCTGGGTCTGGACAGGAGCCCCCAGAGAAAACCCAGGCCGACCTCCTGGCC
TTCCTGCACTCGCAGGTGGACAAGGCAGAGGTGAATGCTGGCGTCAAGCTGGCCACAGAGTATGCAGC
AGTGCCTTTCGATAGCTTTACTCTACAGAAGGTGTACCACTGGAGACTGGCCTTACC CGCCGACCTTACC
AGGAGAAGCCTGTGAGGAAGGACAAGCGGGATGAGTTGGTGGAAAGCCATTGAATCAGCCTTGGAGACC
CTGAACAATCCTGCAGAGAACAGCCCCAATCACCGTCTTACACGGCCTCTGATTTTCATAGAAGGGAT
CTACCGAACAGAAAGGGACAAAGGGACATTGTATGAGCTCACCTTCAAAGGGGACCACAAACACGAAT
TCAAACGGGCTCATCTTATTTTCGACCATTCAGCCCCATCATGAAAGTGAAAAATGAAAAGCTCAACATG
GCCAACACGCTTATCAATGTTATCGTGCTCTAGCAAAAAGGGTGGACAAGTCCGGCAGTTCATGCA
GAATTTTCAGGGAGATGTGCATTGAGCAGGATGGGAGAGTCCATCTCACTGTTGTTTACTTTGGGAAAG
AAGAAATAAATGAAGTCAAAGGAATACTTGAAAACCTTCCAAAGCTGCCAACTTCAGGAACCTTACC
TTCATCCAGCTGAATGGAGAATTTTCTCGGGGAAAGGGACTTGATGTTGGAGCCCCGCTTGGGAAAGG
AAGCAACGTCCTTCTCTTTTTCTGTGATGTGGACATCTACTTCACATCTGAATTCCTCAATACGTGTA
GGCTGAATACACAGCCAGGGAAGAAGGTATTTTATCCAGTTCCTTTTTCAGTCAGTACAATCCTGGCATA
ATATACGGCCACCATGATGTCAGTCCCTCCCTTGGAACAGCAGCTGGTCATAAAGAAGGAACTGGATT
TTGGAGAGACTTTGGATTTGGGATGACGTGTGAGTATCGGTGAGCTTCATCAATATAGGTGGGTTTG
ATCTGGACATCAAAGGCTGGGGCGGAGAGGATGTGCACCTTTATCGCAAGTATCTCCACAGCAACCTC
ATAGTGGTACGGACGCCCTGTGCGAGGACTCTTCCACCTTGGCATGAGAAGCGCTGATGGACGAGCT
GACCCCCGAGCAGTACAAGATGTGCATGCAGTCCAAGGCCATGAACGAGGCATCCACGGCCAGCTGG
GCATGCTGGTGTTCAGGCACGAGATAGAGGCTCACCTTCGCAAAACAGAAACAGAAAGACAAAGTAGCAAA
AAAACATGAACCTCCAGAGAAGGATTGTGGGAGACACTTTTCTTTCTTTTGAATTTACTGAAAGTG
GCTGCAACAGAGAAAAGACTTCCATAAAGGACGACAAAAGAATTGGACTGATGGGTGAGAGATGAGAA
AGCCTCCGATTTCTCTCTGTTGGGCTTTTTACAACAGAAATCAAAATCTCCGCTTTGCCTGCAAAAGT
AACCAGTTGCACCCTGTGAAGTGTCTGACAAAGGCAGAATGCTTGTGAGATTATAAGCCTAATGGTG
TGGAGGTTTTGATGGTGTTTACAATACTGAGACCTGTTGTTTTGTGTGCTCATTGAAATATTCATG
ATTTAAGAGCAGTTTTGTAAAAAATTCATTAGCATGAAAGGCAAGCATATTTCTCCTCATATGAATGA
GCCTATCAGCAGGGCTCTAGTTTCTAGGAATGCTAAAATATCAGAAGGCAGGAGAGGAGATAGGCTTA
TTATGATACTAGTGAGTACATTAAGTAAAAATAAATGGACCAGAAAAGAAAAGAAACCATAAATATCG
TGTCATATTTTCCCCAAGATTAACCAAAAATAATCTGCTTATCTTTTGGTGTCTTTTAACTGTCT
CCGTTTTTTTTCTTTTATTTAAAAATGCACTTTTTTTCCCTTGTGAGTTATAGTCTGCTTATTTAATTA
CCACTTTGCAAGCCTTACAAGAGAGCACAAGTTGGCCTACATTTTTATATTTTTTAAGAAGATACCTT
GAGATGCATTATGAGAACTTTCAGTTCAAAGCATCAAATTGATGCCATATCCAAGGACATGCCAAATG
CTGATTCTGTCAGGCACTGAATGTGAGGCATTGAGACATAGGGAAGGAATGGTTTGTACTAATACAGA
CGTACAGATACTTTCTCTGAAGAGTATTTTCGAAGAGGAGCAACTGAACACTGGAGGAAAAGAAAATG
ACACTTTCTGCTTTACAGAAAAGGAACTCATTGAGCTGGTGATATCGTGATGTACCTAAAAGTCAG
AAACCACATTTTCTCCTCAGAAGTAGGGACCGCTTTCTTACCTGTTTAAATAAACCAGTATACCGT
GTGAACCAACAATCTCTTTTCAAACAGGGTGCTCCTCCTGGCTTCTGGCTTCCATAAGAAGAAATG
GAGAAAAATATATATATATATATATATATTTGTGAAAGATCAATCCATCTGCCAGAATCTAGTGGGATG
GAAGTTTTTGTACATGTTATCCACCCAGGCCAGGTGGAAGTAACTGAATTATTTTTTAATTAAGC
AGTTCTACTCAATCACCAGATGCTTCTGAAAATTGCATTTTATTACCATTTCAAACATTTTTTAA
AATAAATACAGTTAACATAGAGTGGTTTTCTTCATTCATGTGAAAATTATTAGCCAGCACCAGATGCAT
GAGCTAATTATCTCTTTGAGTCCTTGCTTCTGTTTGTCTCACAGTAAACTCATTTGTTTAAAGCTTCAA
GAACATTCAAGCTGTTGGTGTGTTAAAAATGCATTTGATTGATTTGTACTGGTATTGATGAAATTT
AATTAAAAACACAGGCCATGAATGGAAGGTGGTATTGCACAGCTAATAAAATATGATTTGTGGATATGAA

265/615

FIGURE 264

MMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQEWEEQHRNYVSSL
KRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFLHSQVDKAEVNAGVKLATEYAAVPFDS
FTLQKVYQLETGLTRHPEEKPVKDKRDELVEAIESALETLNNPAENSPNHRPYTASDFIEGIYRTERDKGTYE
LTFKGDHKHEFKRLILFRPFSPIMKVKNELNMANTLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVY
FGKEEINEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNLCRLNT
QPGKKVFYPVLF SQYNPGI IYGHDAVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDDLKGGWGED
VHLYRKYLHSNLIVVRTPVRLFHLWHEKRCMDLTPQYKCMQSKAMNEASHGQLGMLVFRHEIEAHLRKQKQ
KTSSKKT

266/615

FIGURE 265

GGATGCGAGAAAGCCTCAGTGTGCTCTTCTGGCCTGGGTCTGCTTCTCTTCTACGCTGGCATTGCCCTCTTCA
CCAGTGGCTTCTGCTCACCCGTTTGGAGCTACCAACCATAGCAGCTGCCAAGAGCCCCAGGCCCTGGGTCCC
TGCCATGGGGGAGCCAAGGAAACCTGGGGCCTGCTGGATGGCTTCCCGATTTTCGCGGGTGTGTGGTGCTGA
TAGATGCTCTGCGATTTGACTTCGCCCAGCCCCAGCATTACACGTGCCTAGAGAGCCTCCTGTCTCCCTACCCT
TCCTGGGCAAACCTAAGCTCCTTGCGAGGATCCTGGAGATTTCAGCCCCACCATGCCCGGCTCTACCGATCTCAGG
TTGACCCTCCTACCACCACCATGCAGCGCCTCAAGGCCCTCACCCTGGCTCACTGCCTACCTTTATTGATGCTG
GTAGTAACCTTCGCCAGCCAGCCATAGTGAAGACAATCTCATTAAGCAGCTCACCAGTGCAGGAAGGCGTGTAG
TCTTCATGGGAGATGATACCTGGAAAGACCTTTTCCCTGGTGCTTCTCCAAAGCTTCTTCTTCCCATCCTTCA
ATGTCAGAGACCTAGACACAGTGGACAATGGCATCCTGGAACACCTCTACCCACCATGGACAGTGGTGAATGGG
ACGTGCTGATTGCTCACTTCTGGGTGTGGACCACTGTGGCCACAAGCATGGCCCTACCACCCTGAAATGGCCA
AGAACTTAGCCAGATGGACCAGGTGATCCAGGGACTTGTGGAGCGTCTGGAGAATGACACACTGCTGGTAGTGG
CTGGGGACCATGGGATGACCACAAATGGAGACCATGGAGGGGACAGTGAAGTGGAGGTCTCAGCTGCTCTCTTTC
TGTATAGCCCCACAGCAGTCTTCCCCAGCACCCACAGAGGAGCCAGAGGTGATTCTCAAGTTAGCCTTGTGC
CCACGCTGGCCCTGCTGCTGGGCCTGCCATCCCATTGGGAATATCGGGGAAGTGATGGCTGAGCTATTCTCAG
GGGTGAGGACTCCAGCCCCACTCCTCTGCTTTAGCCCCAGCCTCAGCTCTCCATCTCAATGCTCAGCAGGTGT
CCCCATTTCTTACCTACTCAGCTGCTACTCAGGACCTTCAAGCTAAGGAGCTTCATCAGCTGCAGAACCTCT
TCTCCAAGGCCTCTGCTGACTACCACTGGCTTCTCCAGAGCCCCAAGGGGGCTGAGGCGACACTGCCGACTGTGA
TTGCTGAGCTGCAGCAGTCTGCGGGGAGCTCGGGCCATGTGCATCGAGTCTTGGGCTCGTTTCTCTCTGGTCC
GCATGGCGGGGGTACTGCTCTTGGCTGCTTCTGCTTTATCTGCCTGCTGGCATCTCAGTGGGCAATATCCC
CAGGCTTTCCATTCTGCCCTCTACTCCTGACACCTGTGGCCTGGGGCCTGGTTGGGGCCATAGCGTATGCTGGAC
TCCTGGGAACCTATTGAGCTGAAGCTAGATCTAGTGCTTCTAGGGGCTGTGGCTGCAGTGAGCTCATTCCTCCCTT
TTCTGTGGAAGCCTGGGCTGGCTGGGGGTCCAAGAGGCCCTGGCAACCCTGTTTCCCATCCCTGGGCCCCGTCC
TGTACTCCTGCTGTTTTGCTTGGCTGTGTTCTTCTCTGATAGTTTTGTTGTAGCTGAGGCCAGGGCCACCCCT
TCCTTTTGGGCTCATTCATCCTGCTCCTGGTTGTCCAGCTTCACTGGGAGGGCCAGCTGCTTCCACCTAAGCTAC
TCACAATGCCCCGCTTGGCACTTCAGCCACAACAAACCCCCACGGCACAATGGTGCATATGCCCTGAGGCTTG
GAATTGGGTTGCTTTTATGTACAAGGCTAGCTGGGCTTTTTCATCGTTGCCCTGAAGAGACACCTGTTTGCCACT
CCTCTCCCTGGCTGAGTCTCTGGCATCCATGGTGGGTGGTGCAGCCAAGAATTTATGGTATGGAGCTTGTGTGG
CGGCGCTGGTGGCCCTGTTAGCTGCCGTGCGCTTGTGGCTTCGCGCTATGTTAATCTCAAGAGCCCCGAGCCAC
CCATGCTCTTTGTGCGCTGGGACTGCCCCCTAATGGCATTTGGTACTGCTGCCTACTGGGCATTGGCCTCGGGGG
CAGATGAGGCTCCCCCGTCTCCGGGTCTGGTCTCTGGGGCATCCATGGTGTGCTCGGCTGGGCTGTAGCAGGGC
TGGCTGCTTCAGGGCTCGCGCTGCTGCTCTGGAAGCCTGTGACAGTGTGGTGAAGGCTGGGGCAGGCGCTCCAA
GGACCAGGACTGTCTCACTCCCTTCTCAGGCCCCCCCCACTTCTCAAGCTGACTTGGATTATGTGGTCCCTCAA
TCTACCGACACATGCAGGAGGAGTTCGGGGCCGCTTAGAGAGGACCAATCTCAGGGTCCCCTGACTGTGGCTG
CTTATCAGTTGGGGAGTGTCTACTCAGCTGCTATGGTCACAGCCCTCACCCTGTTGGCCTTCCACTTCTGCTGT
TGCATGCGGAGCGCATCAGCCTTGTGTTCTGCTTCTGTTTCTGCAGAGCTTCTTCTCCTACATCTGCTTGTG
CTGGGATACCCGTCACCACCCCTGGTCTTTTACTGTGCCATGGCAGGCAGTCTCGGCTTGGGCCCTCATGGCCA
CACAGACCTTCTACTCCACAGGCCACCAGCCTGTCTTTCAGCCATCCATTGGCATGCAGCCTTCGTGGGATTCC
CAGAGGGTCATGGCTCCTGTACTTGGCTGCCTGCTTTGCTAGTGGGAGCCAAACACCTTTGCCCTCCCACCTCCTCT
TTGCAGTAGGTTGCCCACTGCTCCTGCTCTGGCCTTTTCTGTGTGAGAGTCAAGGGCTGCGGAAGAGACAGCAGC
CCCCAGGGAATGAAGCTGATGCCAGAGTCAGACCCGAGGAGGAAGAGGAGCCACTGATGGAGATGCGGCTCCGGG
ATGCGCCTCAGCACTTCTATGCAGCACTGCTGCAGCTGGGCTCAAGTACCTCTTTATCCTTGGTATTTCAGATT
TGGCCTGTGCCTTGGCAGCCTCCATCCTTCGAGGCATCTCATGGTCTGGAAAGTGTGTTGCCCTAAGTTCATAT
TTGAGGCTGTGGGCTTCAATTGTGAGCAGCGTGGGACTTCTCCTGGGCATAGCTTTGGTGATGAGAGTGGATGGT
CTGTGAGCTCCTGGTTCAGGCAGCTATTTCTGGCCAGCAGAGGTAGCCTAGTCTGTGATTACTGGCACTTGGCT
ACAGAGAGTGTGGAGAACAGTGTAGCCTGGCCTGTACAGGTACTGGATGATCTGCAAGACAGGCTCAGCCATAC
TCTTACTATCATGCAGCCAGGGGCCGCTGACATCTAGGACTTCATTATTCTATAATTTCAGGACCACAGTGGAGTA
TGATCCCTAATCCTGATTGGATGCATCTGAGGGACAAGGGGGCGGTCTCCGAAGTGAATAAAATAGGCCGG
GCGTGGTGACTTGCACCTATAATCCCAGCACTTTGGGAGGCAGAGGTGGGAGGATTGCTTGGTCCCAGGAGTTCA
AGACCAGCCTGTGGAACATAACAAGACCCCGTCTCTACTATTTAAAAAAGTGAATAAAATGATAATAT

267/615

FIGURE 266

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809
<subunit 1 of 1, 1089 aa, 1 stop
<MW: 118699, pI: 8.49, NX(S/T): 2
MQKASVLLFLAWVCFIFYAGIALETSGFLLTRLELTNHSSCQEPGPGSLPWGSQKPGACWMASRFSRVVLVI
DALRFDFAPQHQSHVPREPPVSLPFLGKLSSLRILEIQPHHARLYRSQVDPPTTMMQRLKALTGSLPTFIDAG
SNFASHAIVEDNLIKQLTSAGRRVFMGDDTWKDLFPAGFSKAFPPSFNVRLDTVDNGILEHLYPTMDSGEWD
VLIAHFLGVDHCGHKHGHPEMAKKLSQMDQVIQGLVERLENDTLLVVAGDHGTTNGDHGGDSELEVSAALFL
YSPTAVFPSTPPEEPEVIPQVSLVPTLALLLGLPIIPFGNIGEVMAELFSGGEDSQPHSSALAQASALHLNAQQVS
RFLHTYSAATQDLQAKELHQLQNLFSKASADYQWLLQSPKGAETLPTVIAELQQFLRGARAMCIESWARFSLVR
MAGGTALLAASCFCICLLASQWAI SPGFPPCPLLLTPVAWGLVGAIAYAGLLGTIELKLDLVLLGAVAAVSSFLPF
LWKAWAGWGSKRPLATLFPPIPGPVLLLLLFR LAVFFSDFS FVVAEARATPFLLG SFILLLVQLHWEGQLLPKLL
TMPRLGTSATTNPPRHNGAYALRLGIGLLLCTRLAGLFHRCPEETPVCHSSPWLSPPLASMVGGRAKNLWYGACVA
ALVALLAAVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPPRLRVLVSGASMLPRAVAGL
AASGLALLLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHMQEEFRGRLETKSQGPLTVAA
YQLGSVYSAAMVTALTLLAFPLLLLHAERISLVFLLLFLQS FLLLHLLAAGIPVTTPGPFTVPWQAVSAWALMAT
QTFYSTGHQPVPFPAIHWHA AFVGFPEGHGSCTWLPALLVGANTFASHLLFAVGCPLLLLLWPFLLCESQGLRKRQQP
PGNEADARVRPEEEEEPLMEMRLRDAPQH FYAALLQLGLKYLFI LGIQILACALAASILRRHLMVWKVFAPKFIF
EAVGFIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domains:amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850, 1016-1034,
1052-1070**Leucine zipper pattern.**

amino acids 843-864

N-glycosylation sites.

amino acids 37-40, 268-271

FIGURE 267

FIGURE 267

[illegible]

269/615

FIGURE 268

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812
><subunit 1 of 1, 337 aa, 1 stop
><MW: 37668, pI: 6.27, NX(S/T): 1
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWBPASYPECGNNAQSPIDIQTDSVTFDPLPALQPHGYDQPGTE
PLDLHNNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPGSEHQINSEATFAELHIVHYDSDSYDSLSEA
AERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSV
LWTVFYRRSQISMEQLEKLGTLFSTEEPSKLLVQNYRALQPLNORMVFASFQAGSSYTTGEMLSLGVGILVG
CLCLLLAVYFIARKIRKKRLENRKSVVFTSAQATTEA
```

Important features of the protein:**Signal peptide:**

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

270/615

FIGURE 269

GTGGCGCTGGCGGTTGCTGTCAGCTGATTCCCGGGGTTGGTGGCAGCGGCGGTAGCAGCAATGACTTTCTCCTG
GGGAACCCGTTTCAGTCTCCAGTGGGACAGCGCATCGAGAAAGCCACAGATGGCTCCCTGCAGAGCGAGGACTGG
GCCCTCAACATGGAGATCTGCGACATCATCAACGAGACGGAGGAAGGTCCCAAAGATGCCCTCCGAGCAGTAAAG
AAGAGAATCGTGGGGAATAAGAACTTCCACGAGGTGATGCTGGCTCTCACAGTCTTAGAAACCTGTGTCAAGAAC
TGCGGGCACCCTTCCACGTGCTGGTGGCCAGCCAGGACTTCGTGGAGAGTGTGCTGGTGAGGACCATCCTGCCC
AAGAACAACCCACCCACCATCGTGCATGACAAAGTGCTCAACCTCATCCAGTCCTGGGCTGACGCGTTCCGCAGC
TCGCCCCGATCTGACAGGTGTGGTCACCATCTATGAGGACCTGCGGAGGAAAGGCCTGGAGTTCCCCATGACTGAC
CTGGACATGCTGTCACCCATCCACACACCCAGAGGACCGTGTTCAACTCAGAGACACAATCAGGACAGGATTCTG
TGGGCACTGACTCCAGCCAGCAAGAGGACTCTGGCCAGCATGCTGCCCCCTCTGCCCCCCCCGCCCCATACTCTCCG
GTGACACGCCCCATAGCACCAACCCCGGAACAGATTGGGAAGCTGCGCAGTGAGCTGGAGATGGTGAAGTGGGAACG
TGAGGGTGATGTCGGAGATGCTGACGGAGCTGGTGCCACCCAGGCCGAGCCCGCAGACCTGGAGCTGCTGCAGG
AGCTCAACCGCACGTGCCGAGCCATGCAGCAGCGGGTCTGAGTGATACCCTGCTCCGGGCCCCATGCCCAAGGA
GCCCTTCAGAGCCCACACTGCCAGTCGAGGCCTGGCTGGAGGCTGGCCACAGTGGAAATTCTGCCGAGCCTATTG
TCCCTACCTGCTCTGCTGCATGGGGCCCCATGGCTTTGGCTGGCCACTGAGGGTAGGGTGTGGAGGTGTGGAGG
CCCCCTGAGGAGCTGCGGCGGCCCCAGGTACGAAGCTGCAACTCTGCGCGCAGTGGGCGAGATCTCATCAGCCCCA
GGCTGCAGGTGAGGCTTCAGGGGATGCTGGGGCCCCACTGCCCTCCGCTGCCTTGCCCTCCATCCTTCTCTGT
TCCTTCTGGCCGGGCACACAGCACTGGGGCTCACCTCTTGGTTGATCCTCTTGTAAGTGGGAGAGGTGCCTTTTG
TATCCCCAATTAAAGGTAGAAAACC

271/615

FIGURE 270

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62813
><subunit 1 of 1, 209 aa, 1 stop
><MW: 23465, pI: 7.57, NX(S/T): 1
MDFLLGNPFSSPVGQRIEKATDGSLSQSEDWALNMEICDIINETEEGPKDALRAVKKRIVGNKNFHEVMLALTVLE
TCVKNCGRHFHVLVASQDFVESVLVRTILPKNNPPTIVHDKVLNLIQSWADAFRSSPDLTGVVITYEDLRRKGLE
FPMTDLDMLSPIHTPRGPCSTQRHNQDRILWALTPASKRTLASMLPLCPPRPYSPVTRP
```

Important features of the protein:**Signal peptide:**

Amino acids 1-15

N-glycosylation site:

Amino acids 41-45

N-myristoylation sites:

Amino acids 6-12;23-29

272/615

FIGURE 271

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTCTCTGCGGGGAGACGCCAGCCTGCGTCTGCCATGGGGC
TCGGGTTGAGGGGCTGGGGACGTCTCTGCTGACTGTGGCCACCGCCCTGATGCTGCCCCTGAAGCCCCCGCAG
GCTCCTGGGGGGCCAGATCATCGGGGGCCACGAGGTGACCCCCACTCCAGGCCCTAATGGCATCCGTGCGCT
TCGGGGGCAACATCACTGCGGAGGCTTCCTGCTGCGAGCCCGCTGGGTGGTCTCGGCCGCCCACTGCTTCAGCC
ACAGAGACCTCCGCACTGGCCTGGTGGTGTGGGCGCCACGTCTGAGTACTGCGGAGCCCACCCAGCAGGTGT
TTGGCATCGATGCTCTCACCACGCACCCCGACTACCACCCCATGACCCACGCCAACGACATCTGCCTGCTGCGGC
TGAACGGCTCTGCTGTCTGGGCCCTGCAGTGGGGCTGCTGAGGCTGCCAGGAGAAAGGGCCAGCCCCCACAG
CGGGGACACGGTGCCGGGTGGCTGGCTGGGGCTTCGTGTCTGACTTTGAGGAGCTGCCGCCTGGACTGATGGAGG
CCAAGGTCCGAGTGCTGGACCCGGACGTCTGCAACAGCTCCTGGAAGGGCCACCTGACACTTACCATGCTCTGCA
CCCGCAGTGGGGACAGCCACAGACGGGGCTTCTGCTCGGCCGACTCCGGAGGGCCCTGGTGTGCAGGAACCGGG
CTCACGGCCTCGTTTCCTTCTCGGGCCTCTGGTGGGCGACCCCAAGACCCCGACGTGTACACGCAGGTGTCCG
CCTTTGTGGCCTGGATCTGGGACGTGGTTCGGCGGAGCAGTCCCCAGCCGGCCCCCTGCCTGGGACCACCAGGC
CCCCAGGAGAAGCCGCCTGAGCCACAACCTTGCGGCATGCAAAATGAGATGGCCGCTCCAGGCCTGGAATGTTCCG
TGGCTGGGCCCCACGGGAAGCCTGATGTTCAAGGTTGGGGTGGGACGGGCAGCGGTGGGGCACACCCATTCCACA
TGCAAAGGGCAGAAGCAAACCCAGTAAATGTTAACTGACAAAAAAAAAAAAAAAAAAGAAA

273/615

FIGURE 272

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845
><subunit 1 of 1, 283 aa, 1 stop
><MW: 30350, pI: 9.66, NX(S/T): 2
MGLGLRGWGRPLLTVATALMLPVKPPAGSWGAIIGGHEVTPHSRPFYMASVRFGGQHHCGGFLLRARWVVSAAHC
FSHRDLRTGLVVLGAHVLSTAEPTQQVFGIDALTTHPDYHPMTHANDICLLRLNGSAVLGPAVGLLRPLPGRRARF
PTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPDVCNSSWKGHLLTLMCTRSKDSHRRGFCSADSGGFLVCR
NRAHGLVSFSGLWCGDPKTPDVYTQVSAFVAWIWDVVRSSPQPGPLPGTTRPPGEAA
```

Signal peptide:
amino acids 1-30

274/615

FIGURE 273

GAAGTTCGCGAGCGCTGGCTATGGGTCTGGGGCGCGGGCTGGCGGGCGCTGCTGGCGGTGCTGGCGCTCGGGACAG
GAGACCCAGAAAGGGCTGCGGCTCGGGGCGACACGTTCTCGGCGCTGACCAGCGTGGCGCGCGCCCTGGCGCCCCG
AGCGCCGGCTGCTGGGGCTGCTGAGGCGGTACCTGCGCGGGGAGGAGGCGCGGCTGCGGGACCTGACTAGATTCT
ACGACAAGGTACTTTCTTTGTCATGAGGATTCAACAACCCCTGTGGCTAACCCCTGCTTGCAATTTACTCTCATCA
AACGCCCTGCAGTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGGATG
GCTATGAGAAGGTGGAGCAAGACCTTCAGCCCTTTGAGGACCTTGAGGGAGCAGCAAGGGCCCTGATGCGGCTGC
AGGACGTGTACATGCTCAATGTGAAAGGCCTGGCCCCGAGGTGTCTTTCAGAGAGTCACTGGCTCTGCCATCACTG
ACCTGTACAGCCCCAAACGGCTCTTTCTCTCACAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCCTATGACA
TGGGGGATTATTACCATGCCATTCCATGGCTGGAGGAGGCTGTCACTCTCTTCCGAGGATCTTACGGAGAGTGGA
AGACAGAGGATGAGGCAAGTCTAGAAGATGCCCTTGGATCACTTGGCCTTTGCTTATTTCCGGGCGAGGAAATGTTT
CGTGTGCCCTCAGCCTCTCTCGGGAGTTCTTCTCTACAGCCAGATAATAAGAGGATGGCCAGGAATGTCTTGA
AATATGAAAGGCTCTTGCGCAGAGAGCCCCAACACGCTGGTAGCTGAGGCTGTATCCAGAGGCCCAATATACCCC
ACCTGCAGACCAGAGACACCTACGAGGGGCTATGTACAGCCCTGGGTTCCCAGCCCACTCTCTACCAGATCCCTA
GCCTCTACTGTTCCCTATGAGACCAATTCCAACGCTACCTGCTGCTCCAGCCCATCCGGAAGGAGGTCATCCACC
TGGAGCCCTACATTGCTCTTACCATGACTTCGTCACTGACTCAGAGGCTCAGAAAATTAGAGAACTTGCAGAAC
CATGGCTACAGAGGTCAGTGGTGGCATCAGGGGAGAAGCAGTTACAAGTGGAGTACCGCATCAGCAAAAGTGCCT
GGCTGAAGGACACTGTTGACCCAAAACCTGGTGACCCTCAACCACCGCATTGCTGCCCTCACAGGCCTTGATGTCC
GGCCTCCCTATGCAGAGTATCTGCAGGTGGTGAAGTATGGCATCGGAGGACACTATGAGCCTCACTTTGACCATG
CTACGTACCAAGCAGCCCCCTCTACAGAAATGAAGTCAGGAAACCGAGTTGCAACATTTATGATCTATCTGAGCT
CGGTGGAAGCTGGAGGAGCCACAGCCTTCATCTATGCCAACCTCAGCGTGCCTGTGGTTAGGAATGCAGCACTGT
TTTGGTGAACCTGCACAGGAGTGGTGAAGGGGACAGTGACACACTTCATGCTGGCTGTCTGTCTGCTGGTGGGAG
ATAAGTGGGTGGCCAAAGTGGATACATGAGTATGGACAGGAATTCCGCAGACCCTGCAGCTCCAGCCCTGAAG
ACTGAAGTGTGGCAGAGAGAAGCTGGTGGAGTCTGTGGCTTTCCAGAGAAGCCAGGAGCCAAAAGCTGGGGTA
GGAGAGGAGAAAGCAGAGCAGCCTCCTGGAAGAAGGCCTTGTCACTTTGTCTGTGCCTCGCAATCAGAGGCAA
GGGAGAGGTTGTTACCAGGGGACACTGAGAATGTACATTTGATCTGCCCCAGCCACGGAAGTCAGAGTAGGATGC
ACAGTACAAAGGAGGGGGGAGTGGAGGCCTGAGAGGGAAGTTTCTGGAGTTCAGATACTCTCTGTTGGGAACAGG
ACATCTCAACAGTCTCAGGTTGATCAGTGGGTCTTTTGGCACTTTGAACCTTGACCACAGGGACCAAGAAGTGG
CAATGAGGACACCTGCAGGAGGGGCTAGCCTGACTCCAGAACTTTAAGACTTTCTCCCCACTGCCTTCTGCTGC
AGCCCAAGCAGGGAGTGTCCCCCTCCCAGAAGCATATCCCAGATGAGTGGTACATTATATAAGGATTTTTTTTAA
GTTGAAAACAACCTTTCTTTTCTTTTGTATGATGGTTTTTTAACACAGTCATTAAAAATGTTTATAAATCAAAA

275/615

FIGURE 274

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64849
><subunit 1 of 1, 544 aa, 1 stop
><MW: 61126, pI: 6.40, NX(S/T): 2
MGPGARLAALLAVLALGTGDPERAAARGDTFSALTSVARALAPERRLGLLRRYLRGEEA
RLRDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHSLEASENIRALKDGY
EKVEQDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRTGSAITDLYSPKRLFSLT
GDDCFQVGKVAIDMGDYYHAIPWLEEAVSLFRGSYGEWKTEDEASLEDALDHLAFAYFRA
GNVSCALSLSREFLLYSPDNKRMARNVLKYERLLAESPNHVVAEAVIQRPNI PHLQTRDT
YEGLCQTLGSOPTLYQIPSLYCSYETNSNAYLLLQPIRKEVIHLEPYIALYHDFVSDSEA
QKIRELAEPWLQRSVVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNHRIAALTGLDVRP
PYAEYLQVVNYGIGGHHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLSSEAGGATAFIY
ANLSVPVVRNAALFWWNLHRSGEGSDTLHAGCPVLVGDKWVANKWIEHYGQEFRRPCSS
SPED
```

Important features of the protein:**Signal peptide:**

Amino acids 1-19

Leucine zipper pattern:

Amino acids 34-56;41-63

Ribonucleotide reductase small subunit signature:

Amino acids 340-356

N-glycosylation sites:

Amino acids 242-246;482-486

Cell attachment sequence:

Amino acids 27-30

Tyrosine kinase phosphorylation site:

Amino acids 189-198

N-myristoylation sites:Amino acids 4-10;135-141;153-159;164-170;241-247;303-309;309-315;
457-463;473-479

276/615

FIGURE 275

GGCAACATGGCTCAGCAGGCTTGCCCCAGAGCCATGGCAAAGAATGGACTTGTAATTTGCATCCTGGTGATCACC
TTACTCCTGGACCAGACCACCAGCCACACATCCAGATTAAGCCAGGAAGCACAGCAAACGTCGAGTGAGAGAC
AAGGATGGAGATCTGAAGACTCAAATTGAAAAGCTCTGGACAGAAGTCAATGCCTTGAAGGAAATTCAGCCCTG
CAGACAGTCTGTCTCCGAGGCCTAAAGTTCAAGAAGATGCTACCTTGCTTCAGAAGGTTTGAAGCATTTCAT
GAGGCCAATGAAGACTGCATTTCCAAAGGAGGAATCCTGGTTATCCCCAGGAACCTCCGACGAAATCAACGCCCTC
CAAGACTATGGTAAAAGAGCCTGCCAGGTGTCAATGACTTTTGGCTGGGCATCAATGACATGGTCACGGAAGGC
AAGTTTGTGACGTCAACGGAATCGCTATCTCCTTCAACTGGGACCGTGCACAGCCTAACGGTGGCAAGCGA
GAAAACGTGTCTCTTCTCCCAATCAGCTCAGGGCAAGTGGAGTGATGAGGCCTGTGCGAGCAGCAAGAGATAC
ATATGCGAGTTCACCATCCCTAAATAGGTCTTTCTCCAATGTGTCTCCAAGCAAGATTCATCATAACTTATAGG
TTCATGATCTCTAAGATCAAGTAAAAATCATAATTTTTACTTTATTAATAAATTGCAACACAAGATCAATGTCCAT
AGCAATATGATAGCATCAGCCAATTTTGCTAACACATTTCTTTGGGATTTTGCCCTTCTCTGGGGTATAGGGGATC
AGAAATATGATCCATGTGCACGCAGATAAAATGGCTTCTGTAAACAGACTAAAACTTTCTCTCTAGTCTTTC
TCACTTGTAACAAACCCAGTTTGTFTTCAAAAAATCAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTT
AGGCTACCTGAAAGATTTTCCCTTGAAGTTTAGCGTATGTTTACTAACAAAAATTCCTACATCAGAGACTCT
AGGTGCTATATAATCCAAAACTTTTCAGCCTGTGTCTCATTCTGTCCCATGCTGGCAATAACCTTGTGAGCC
CATTACCCTTATTTTGAATTGCTCCATCTCCTGGTGGGACTTGATCTTGTCTGCCATATCAGAACACAAACCCC
TGAAGAGGTTCTGATTTGATTTTTTTTTTTTCTTCATGCCTACCCCTTTTTTTTGGAAAGTTTCCAGCCGCAATTTGA
AATGAAATGACAAGGTGTATATTTGATCAATTTTCATTCCACCATTCGATTACAACTCTAACTTAAATGGGTA
ACCCTAAGGCATATCAAAGAAGCAGATTGCATGATAACGGAAATAGAAAAAAGAACCTACATTTATTTTGCTT
TAGCATCCTTACTCTCACCTTTTATGAGATTGAGAGTGGACTTACATTTCTTTTTTACATTTTCGTATATTTAT
TTTTTTTAGCCATCATTATATGTTTAAGTCTATTATGGGCAACCAATCTTTGGAAGCTGAAAAGTGAATTTAAAG
AATGCTATCTTGGAAAATTGCATACGTCTGTGCAATTTTTTATTCTGCCTAGTGCTATTCTGCTTGTTTAACTAG
ATTGTACAAAATAAATTTCATTGCTTAATATCAAATTACAAAGTTTAGACTTGGAGGGAAATGGGCTTTTGAAG
CAAACAATTTTAAATATATTTGTTCTTCAAATAAATAGTGTTTAAACATTGAATGTGTTTTGTGAACAATATCC
CACTTTGCAAACTTTTAACTACACATGCTTGAATTAAGTTTTAGCTGTTTTTCATTGCTCAATAATAAAGCCTGAA
TTCTGATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

277/615

FIGURE 276

MAQQACPRAMAKNGLVICILVITLLLDQTTSHTSRLKARKH\$KRRVRDKDGD\$DLKTQIEKLWTEVNALKEIQALQT
VCLRGTKVHKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQDYGKRSLPGVND\$FWLGINDMVTEGKF
VDVNGIAISFLNWDRAQPN\$GGKRENCVLF\$QSAQGKWSDEACR\$SKRYICEFTIPK

278/615

FIGURE 277

GAGATAGGGAGTCTGGGTTTAAGTTCCCTGCTCCATCTCAGGAGCCCCCTGCTCCCACCCCTAGGAAGCCACCAGAC
TCCACGGTGTGGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCCACGAGCGCTGGCTGAGGGACCGAGCC
GGAGAGCCCCGGAGCCCCCGTAACCCGCGCGGGGAGCGCCAGGATGCGCGCGGGGACTCGGAGCAGGTGCGCT
ACTGCGCGCGCTTCTCCTACCTCTGGCTCAAGTTTTCACTTATCATCTATTCCACCGTGTCTGGCTGATTGGGG
CCCTGGTCTGTCTGTGGGCATCTATGCAGAGGTTGAGCGGCAGAAATATAAAACCCTTGAAAGTGCCTTCCTGG
CTCCAGCCATCATCCTCATCCTCCTGGGCGTCGTATGTTTATGGTCTCCTTCATTGGTGTGCTGGCGTCCCTCC
GTGACAACCTGTACCTTCTCCAAGCATTTCATGTACATCCTTGGGATCTGCCTCATCATGGAGCTCATTTGGTGGCG
TGGTGGCCTTGACCTTCCGGAACCAGACCATTGACTTCCCTGAACGACAACATTCGAAGAGGAATTGAGAACTACT
ATGATGATCTGGACTTCAAAAACATCATGGACTTTGTTTCAGAAAAAGTTCAAGTGTGTGGCGGGGAGGACTACC
GAGATTGGAGCAAGAATCAGTACCACGACTGCAGTGCCCTGGACCCCTGGCCTGTGGGGTGCCCTACACCTGCT
GCATCAGGAACACGACAGAAGTTGTCAACACCATGTGTGGCTACAAAACATTCGACAAGGAGCGTTTCAGTGTGC
AGGATGTCATCTACGTGCGGGGCTGCACCAACGCCGTGATCATCTGGTTCATGGACAACATACACCATCATGGCGT
GCATCCTCCTGGGCATCCTGCTTCCCCAGTTCCCTGGGGGTGCTGCTGACGCTGCTGTACATCACCCGGTGGAGG
ACATCATCATGGAGCACTCTGTCACTGATGGGCTCCTGGGGCCCGTGCCAAGCCAGCGTGGAGGCGGCAGGCA
CGGGATGCTGCTTGTGCTACCCCAATTAGGGGCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTCTGGGATAGC
ACCTCTCAGTCAACATCGTGGGGCTGGACAGGGCTGCGGCCCTCTGCCACACTCAGTACTGACCAAAGCCAGG
GCTGTGTGTGCTGTGTGTAGGTCCCACGGCCTCTGCCTCCCCAGGGAGCAGAGCCTGGGCCTCCCTAAGAGGC
TTTCCCCGAGGCAGCTCTGGAATCTGTGCCACCTGGGGCCTGGGGAACAAGGCCCTCCTTTCTCCAGGCCCTGGG
CTACAGGGGAGGGAGAGCCTGAGGCTCTGCTCAGGGCCATTTCATCTCTGGCAGTGCCTTGGCGGTGGTATTCA
AGGCAGTTTTGTAGCACCTGTAATTGGGGAGAGGGAGTGTGCCCTCGGGGAGGAGGGAAGGGCATCTGGGGAA
GGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCCATGGCCAGGTTGGCCTCTTCTCAGCCTCCAGGTGCCTT
GAGCCCTCTTGCAAGGGCGGCTGCTTCCCTGAGCCTAGTTTTTTTTTACGTGATTTTTGTAACATTCATTTTTTT
GTACAGATAACAGGAGTTTCTGACTAATCAAAGCTGGTATTTCCCCGCATGTCTTATTCTTGCCCTTCCCCAAC
CAGTTTGTTAATCAAACAATAAAACATGTTTTGTTTTGTTTTTAAAAA

279/615

FIGURE 278

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863
><subunit 1 of 1, 294 aa, 1 stop
><MW: 33211, pI: 5.35, NX(S/T): 3
MPRGDSEQVRYCARFSYLWLKFSLLIYSTVFWLIGALVLSVGIYAEVERQKYKTLES AFLAPAILILLGVVMFM
VSFIGVLASLRONLYLLQAFMYILGICLIMELIGGVVALTFRNQTIDFLNDNIRRG IENYYDDLDFKNIMDFVQK
KFKCCGGEDYROWSKNQYHDCSAPGPLACGVPTCCIRNTTEVVNTMCGYKTIDKERFSVQDVIYVRGCTNAVII
WFMDNYTIMACILLGILLPQFLGVLLTLLYITRVEDIIMEHSVTDGLLGPGAKPSVEAAGTGCCLCYPN

Signal peptide:
amino acids 1-44

Transmembrane domains:
amino acids 22-42, 57-85, 93-116, 230-257

280/615

FIGURE 279

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACCTTGCTGCCCTCTGACACCTGGGAAGAT
GGCCGGCCCGTGGACCTTCACCCCTTCTCTGTGGTTTGTGGCAGCCACCTTGATCCAAGCCACCTCAGTCCCAC
TGCAGTTCTCATCCTCGGCCCCAAAAGTCATCAAAGAAAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAG
CATCCTGCAGCAGCTGCCGCTGCTCAGTGCCATGCGGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCT
GGTGAACACCGTCCCTGAAGCACATCATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAAGCC
CTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCAACACGCCCTGGTCAA
GACCATCGTGGAGTTCCACATGACGACTGAGGCCCAAGCCACCATCCGCATGGACACCAGTGAAGTGGCCCCAC
CCGCTGGTCCCTCAGTGACTGTGCCACCAGCCATGGGAGCCTGCGCATCCAAGTGTGTATAAGCTCTCCTTCCT
GGTGAACGCCTTAGCTAAGCAGGTATGAACCTCCTAGTGCCATCCCTGCCAATCTAGTGAAAAACCAGCTGTG
TCCCGTGATCGAGGCTTCCTTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCCATTTCCCTCAG
CATTGACCGTCTGGAGTTTGACCTTCTGTATCCTGCCATCAAGGGTGACACCATTCAGCTCTACCTGGGGGCCAA
GTTGTTGGACTCACAGGGAAAGGTGACCAAGTGGTTCAATAACTCTGCAGCTTCCCTGACAATGCCACCCCTGGA
CAACATCCCGTTTCAGCCTCATCGTGAGTCAGGACGTGGTGAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGA
ATTCATGGTCTGTGGACTCTGTGCTTCCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGCTGATCAATGA
AAAGGCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCCGAGTTTTTTATAGA
CCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGCTGGAAAGTGTTCCTCCAGTGAAGCCCTCCGCCCTTTGTT
CACCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTACACCAAAGGTGACCAACTTATACTCAACTGAATAA
CATCAGCTCTGATCGGATCCAGCTGATGAACCTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCAT
CACTGAGATCATCCACTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTGATTGGT
GAAGGCCTTGGGATTCGAGGCAGCTGAGTCCTCACTGACCAAGGATGCCCTTGTGCTTACTCCAGCCTCCTTGTG
GAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAGGGAAGGCTGGGTCCCAGCTGGGAGT
ATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAATCAATAAACACTTGCCCTGTGAAAAA

281/615

FIGURE 280

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881
><subunit 1 of 1, 484 aa, 1 stop
><MW: 52468, pI: 7.14, NX(S/T): 3
MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDNATSILQQLPLLSAMREKPAGGIPVLGS
LVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPLVKTIIVEFHMTTEAQATIRMDTSASGP
TRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMNLLVPSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISL
SIDRLEFDLLYPAIKGDTIQLYLGAKLLDSQGKVTKWFNNSAASLTMPITLDNIPFSLIVSQDVVKAAVAVALSPE
EFMVLLDSVLPESAHLKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEALRPL
FTLGIEASSEAQFYTKGQQLILNLNNISSDRIQLMNSGIGWFPDVLKNIITEIHSILLPNQNGKLRSGVPVSL
VKALGFEEAESSLTkdALVLTpASLWKpSPVSQ

Important features of the protein:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

282/615

FIGURE 281

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCTTTCCCCGCGTTCT
CTTTCCACCTTTCTCTTCTTCCACCTTAGACCTCCCTTCTGCCCCTCCTTTCTGCCCACCGCTGCTTCTGGC
CCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGGGGTCTGTGGGTTGATCTGTGGCCCCTGTGCCCTCCGTGTC
CTTTTCGTCTCCCTTCTTCCCGACTCCGCTCCCGGACCAGCGGCTGACCCTGGGGAAAGGATGGTTCCCGAGGT
GAGGGTCTCTCCTCCTTGTGGGACTCGCGCTGCTCTGGTTCCCCCTGGACTCCCACGCTCGAGCCCGCCAGA
CATGTTCTGCCTTTTCCATGGGAAGAGATACTCCCCCGGCGAGAGCTGGCACCCCTACTTGGAGCCACAAGGCCT
GATGTACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGTTACCGCCTCCACTGTCCGCTGTCCA
CTGCCCCCAGCCTGTGACGGAGCCACAGCAATGCTGTCCCAAGTGTGTGGAACCTCACACTCCCTCTGGACTCCG
GGCCCCACCAAAGTCCTGCCAGCACAACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTT
CCCCTCCCGCCTGCCCAACCAGTGTGTCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCCTCACAACTG
CCCCGAACCAGGCTGCCAGCACCCCTCCCACTGCCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGTGA
GCAATCGGATGAAGAGGACAGTGTGCAGTGCCTCCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGATGC
TGGGAGAAAGAGAGGCCCGGGCACCCAGCCCCCACTGGCCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTT
CAGACCCAAGGGAGCAGGCAGCACAACCTGTCAAGATCGTCCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGG
CGGGAAGACGTACTCCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGCCCCCTTGCCTGCATCCTATG
CACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGTACCCCTGCCGTACCCCGAGAA
AGTGGCTGGGAAGTGCTGCAAGATTGCCCAGAGGACAAAGCAGACCCCTGGCCACAGTGAGATCAGTTCTACCAG
GTGTCCCAAGGCACCGGGCCGGGTCTCGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTTGC
CCTGGAACACGAGGCCCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAACTGAGGCTCA
GAGAGGTGAAGTACCTGGCCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGAAAGTCAGGAAGC
AAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCACGAAGGTCACTGGAACGTCCTCCTAG
CCCAGACCTGGAGCTGAAGGTCACGGCCAGTCCAGACAAAGTGACCAAGACATAACAAAGACCTAACAGTTGCA
GATATGAGCTGTATAATTGTTGTTATTATATATTAATAAATAAGAAGTGCATTACCCTCAAAAAAAAAAAAAA
AAAAAA

283/615

FIGURE 282

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902
><subunit 1 of 1, 451 aa, 1 stop
><MW: 49675, pI: 7.15, NX(S/T): 1
MVPEVRVLSSLLGLALLWFPLDSHARARPD MFCLFHGKRYSPGESWHPYLEPQGLMYCLRCTCSEGAHVSCYRLH
CPPVHCPQPVTEPQQCCPKC VEPHTPSGLRAPPKSCQHNGTMYQHGEIFSAHELFPSRLPNQCVLCSCTEGQIYC
GLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEEDSVQSLHGVRHPQDPCSSDAGRKRGPPTAPTGLSAPLSF
IPRHFPRPKGAGSTTVKIVLKEKHKKACVHGGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPTTEYPC
RHPEKVAGKCKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKLVKDE
ETEAQRGEVPGPRPHSQNLPLDSQESQEARLPERGTALPTARWPPRRSLERLPSDPGAEGHGQSRQSDQDITKT
```

Signal peptide:
amino acids 1-25

284/615

FIGURE 283

GCGATGGTGCGCCCGGTGGCGGTGGCGGCGGCGGTTGCGGAGGCTTCCTTGGTTCGGATTGCAACGAGGAGAAGAT
GACTGACCAACCGACTGGCTGAATGAATGAATGGCGGAGCCGAGCGCGCCATGAGGAGCCTGCCGAGCCTGGGCG
GCCTGCGCCTGTGTGTCTGCGCCGCCGCCGCCGCCGCTCGCCTCAGCCGCCCTCGGCGGGGAATGTCACCGGTG
GCGCGGGGGCGCGGGGACAGTGAGCGCGTCGCCGGGCCCGGTTGCGGGGCGAGCCAGCCACCCCTTCCTTA
GGGCGACGGCTCCCACGGCCAGGCCCGAGGACCGGGCCCCCGCGCGCCACCGTCCACCGACCCCTGGCTGCGA
CTTCTCCAGCCAGTCCCGGAGACCACCCCTCTTGGGCGACTGCTGGACCCTCTTCCACCACCTTTAGGGCGC
CGCTCGGCCCTCGCCGACCACCCCTCCGGCGGCGGAACGCACTTCGACCACCTCTCAGGCGCCGACCAGACCCG
CGCCGACCACCCCTTCGACGACCACTGGCCCGGCGCCGACCACCCCTGTAGCGACCACCGTACCGGCGCCACGA
CTCCCCGAGCCCGACCCCGATCTCCCCAGCAGCAGCAACAGCAGCGTCCTCCCCACCCACCTGCCACCGAGG
CCCCCTCTTCGCCTCCTCCAGAGTATGTATGTAAGTCTGTGGTTGGAAGCCTGAATGTGAATCGCTGCAACC
AGACCACAGGGCAGTGTGAGTGTGCGCCAGGTTATCAGGGGCTTCACTGTGAAACCTGCAAGAGGGCTTTTACC
TAAATTACACTTCTGGGCTCTGTGAGCCATGTGACTGTAGTCCACATGGAGCTCTCAGCATACCGTGCAACAGGT
AAGCAACAGAGGGTGGAAGTGAAGTTTATTTTATTTTAGCAAGGGAAAAAAAAGGCTGCTACTCTCAAGGACCA
TACTGGTTTAAACAAAGGAGGATGAGGGTCATAGATTTACAAAATATTTTATATACTTTTATTCTTACTTTAT
ATGTTATATTTAATGTCAGGATTTAAAAACATCTAATTTACTGATTTAGTTCTTCAAAGCACTAGAGTCGCCAA
TTTTTCTCTGGGATAATTTCTGTAAATTTTCATGGGAAAAAATTATTGAAGAATAAATCTGCTTTCTGGAAGGGCT
TTCAGGCATGAAACCTGCTAGGAGGTTTAGAAATGTTCTTATGTTTATTAATATAACATTGGAGTTTGAGGAAAT
TTGTTGTTTGGTTTATTTTTCTCTCTAATCAAAATTCTACATTTGTTTCTTTGGACATCTAAAGCTTAACCTGGG
GGTACCCTAATTTATTTAACTAGTGGTAAGTAGACTGGTTTACTCTATTTACCAGTACATTTTTGAGACCAAAA
GTAGATTAAGCAGGAATTATCTTTAACTATTATGTTATTTGGAGGTAATTTAATCTAGTGGAATAATGTACTGT
TATCTAAGCATTTGCCTTGTAAGTGAAGTAATATTCTTTGACCTTATGTGAGGCACTTGGCTTTTTGTG
GACCCCAAGTCAAAAACTGAAGAGACAGTATTAATAATGAAAAAATAATGACAGGTTATACTCAGTGTAACC
TGGGTATAACCCAGATCTGCTGCCACTTACGAGCTGTGTTCTTGGGCAAGTAATTTCTTTCACTGAGCTTGT
TTCTTCTCAAGGTTGTTGTGAAGATTAATGAGTTGATATATATAAAATGCCTAGCACATGTCACTCAATAAATT
CTGTTTGTGTTTAAATTTCAAAGGAATATTATGGACTGAAATGAGAGAACATGTTTTAAGAACTTTTAGCTCCTTG
ACAAAGAAGTGCTTTTATACTTTAGCACTAAATATTTTAAATGCTTTATAAATGATATTATACTGTTATGGAATAT
TGTATCATATTGTAGTTTATTAATAATGTAGAAGAGGCTGGGCGCGGTGGCTCACGCCCTGTAATCCTAGCACTTT
GGGAGGCCAAGGCGGTGGATCACTTGAGGCCAGGAGTTCTAGATGAGCCTGGCCAGCACAGTGAAACCCCGTCT
CTACTAAAAATACAAACAAATTAGCTGGGCGTGGTGGCACACACCTGTAGTCCCAGCTACTCGGGAGGCTGAGGC
AGGAGAATCGGTTGAACCCGGGAGGTGGAGTTGCAGTGAGCTGAGATCGCGCCACTGCACTCCAGCCTGGTGAG
AGAGGGAGACTCTGTCTTAAAAAAA

285/615

FIGURE 284

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRSLSLGGGLALLCCAAAAA AVASAASAGNVTGGGGAAGQVDASPGPGLRGEP SHFFPRATAPTAQAPRTGPPRA
TVHRELAATSPAQSPETTP LWATAGPSSTTFQAPLGPSPTTPPAERTSTTSQAPTRPAPTTLSTTTGPAPTPV
ATTVPAPTTTPRTTPDLPSSSNSSVLPTPPATEAPSSPPPEYVCNC SVVGS LNVNRCNQTTGQCECRPGYQGLHC
ETCKEGFYLNYSGLCQPCDCSPHGALSIPCNR

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

EGF-like domain cysteine pattern signature.

amino acids 214-226.

FIGURE 285

FIGURE 285

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCAGACATGCTGCTGCTGCTGCTGCCCTGCTCTGGGG
AGGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTTCGGTGACGGTGCAGGAAGGCCTGTGT
GTCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCATGGCTGGATTTACCCCTGGCCCAGTAGTTCATGGCTACTGG
TTCGGGAAGGGGCAATACAGACCCAGGATGCTTCAGTGGCCACAACCAACCCAGCTCGGGCAGTGTGGGAGG
ACTCGGGACCGATTCCACCTCCTTTGGGGACCACATACCAAGAAATGCACCTGAGCATCAGAGATGCCAGAAGA
AGTGATGCGGGGAGATACTTCTTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAAACATCACCGGCTCTCT
GTGAATGTGACAGCTGTGACCCACAGGCCAACATCCTCATCCAGGCACCCCTGGAGTCCGGCTGCCCCAGAAT
CTGACCTGCTCTGTGCCCTGGGCCTGTGACAGGGGACACCCCTTATGATCTCCTGGATAGGGACCTCCGTGTCC
CCCTGGACCCCTCCACCACCCGCTCCTCGGTGCTCACCTCATCCACAGCCCCAGGACCATGGCACCGCTC
ACCTGTGAGGTGACCTTCCCTGGGGCCAGCGTGACCACGAAACAGACCGTCCATCTCAACGTGTCTTACC CGCCT
CAGAACTTGACCATGACTGTCTTCCAAGGAGACGGCACAGTATCCACAGTCTTGGGAAATGGCTCATCTCTGTCA
CTCCAGAGGGCCAGTCTCTCGCCTGGTCTGTGCAATTGATGCAAGTTGACAGCAATCCCCCTGCCAGGCTGAGC
CTGAGCTGGAGAGGCTGACCTCTGCGCCCTCACAGCCCTCAAACCGGGGGTGCTGGAGCTGCCCTGGGTGCAC
CTGAGGAGTGCACTGAATTACCTCACAGAGCTCAGAACCCCTCTCGGTCTCAGCAGGTCTACTGTAACGTCTCC
CTGCAGAGCAAAGCCACATCAGGAGTGACTCAGGGGGTGGTTCGGGGGAGCTGGAGCCACAGCCCTGGTCTTCCGT
TCTTCTGCGTTCATCTTCTGTTGTAGTGAGGTCTGACAGGAAGAAATCGGCAAGGCCAGCAGCGGGCGTGGGAGAT
ACGGGCATAGAGGATGCAAACGCTGTACGGGGTTCAGCCCTCTCAGGGGGCCCTGACTGAACCTTGGGCAGAAGAC
AGTCCCCAGACAGCCCTCCCCAGCTTCTGCCCCGCTCCTAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTC
AGCTTCCAGATGGTGAAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGAGATCAAGATC
CACAGATTGAGAAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCCCTCAGGCAAGGGAGAAGTCAGAGGC
TGATTCTTGATAGAAATTAACAGCCCTCAACGTGATGAGCTATGATAACACTATGAATTATGTGCAGAGTGAAGAGC
ACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAATCCACACTGTGCCCTCCCTTTTATTTTTTAACTAAAG
ACAGACAAATTCTTA

287/615

FIGURE 286

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVOEGLCVHVPCSFYPSHGWIYPGPVVHGYWFREGANTDQDAPVA
TNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKGSIKWNYKHHRLSVNVTALTHRPNILI
PGTLESGCPQNLTCVWPWACEQGTTPMISWIGTSVSPDPSTTRSSVLTLPQPDHGTSLTCQVTFPGASVTN
KTVHLNVSYPQNLMTVFQGDGTVSTVLGNGSSLSLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPS
NPGVLELPWWHLRDAAEFTCRAQNPLGSQQVYLNVSLSQKATSGVTQGVVGGAGATALVFLSFCVIFVVVRSCRK
KSARPAAGVGDTGIEDANAVRGSAQGPLTEPWAEDSPPDQPPASARSSVGEGLQYASLSFQMKPWDSRGQE
ATDTEYSEIKIHR

Signal peptide:
amino acids 1-15

Transmembrane domain:
amino acids 351-370

288/615

FIGURE 287

CGCGAGCTGAGAGGAGCAGGTAGAGGGGCAGAGGCGGGACTGTCTGTTGGGGAGCCGCCAGGAGGCTCCTCAG
GCCGACCCAGACCCCTGGCTGGCCAGGATGAAGTATCTCCGGCACCGGCGGCCCAATGCCACCCTCATTCTGGCC
ATCGGCGCTTTCACCCTCCTCCTCTTCAGTCTGTAGTGTACACCCACCTGCAAGGTCCAGGAGCAGCCACCG
GCGATCCCCGAGGCCCTGGCCTGGCCCACTCCACCCACCCGCCAGCCCCGGCCCCGTGCCATGCCAACACCTCT
ATGGTCACCCACCCGGACTTCGCCACGCAGCCGCAGCACGTTTCAAGAACTTCCTCCTGTACAGACACTGCCGCCAC
TTTCCCCTGCTGCAGGACGTGCCCCCTCTAAGTGCGCGCAGCCGGTCTTCCTGCTGCTGGTGATCAAGTCTCTC
CCTAGCAACTATGTGCGCCGCGAGCTGCTGCGGCGCACGTGGGGCCGCGAGCGCAAGGTACGGGGTTTGCAGCTG
CGCTCCTCTTCCTGGTGGGCACAGCCTCCAACCCGCACGAGGCCCGCAAGGTCAACCGGCTGCTGGAGCTGGAG
GCACAGACTCACGGAGACATCCTGCAGTGGGACTTCCACGACTCCTTCTTCAACCTCACGCTCAAGCAGGTCTTG
TTCTTACAGTGGCAGGAGACAAGGTGCGCCAACGCCAGCTTCGTGCTCAACGGGGATGATGACGTCTTTGCACAC
ACAGACAACATGGTCTTCTACCTGCAGGACCATGACCCTGGCCGCCACCTCTTCGTGGGGCAACTGATCCAAAAC
GTGGGCCCCATCCGGGCTTTTGGAGCAAGTACTATGTGCCAGAGGTGGTGACTCAGAATGAGCGGTACCCACCC
TATTGTGGGGGTGGTGGCTTCTTGCTGTCCCGCTTACGCGCGCTGCCCTGCGCCGTGCTGCCCATGTCTTGGAC
ATCTTCCCCATTGATGATGTCTTCTGGGTATGTGTCTGGAGCTTGAGGGACTGAAGCCTGCCTCCACAGCGGC
ATCCGCACGTCTGGCGTGCGGGCTCCATCGCAACACCTGTCTCCTTTGACCCCTGCTTCTACCGAGACCTGCTG
CTGGTGACCCGCTTCTTACCTTATGAGATGCTGCTCATGTGGGATGCGCTGAACCAGCCCAACCTCACCTGCGGC
AATCAGACACAGATCTACTGAGTCAGCATCAGGGTCCCCAGCCTCTGGGCTCCTGTTTCCATAGGAAGGGGCGAC
ACCTTCCTCCAGGAAGCTGAGACCTTTGTGGTCTGAGCATAAGGGAGTGCCAGGGAAGGTTTGAGGTTTGATGA
GTGAATATTCTGGCTGGCGAACTCCTACACATCCTTCAAAACCCACCTGGTACTGTTCCAGCATCTTCCCTGGAT
GGCTGGAGGAACCTCAGAAAAATATCCATCTTCTTTTGTGGCTGCTAATGGCAGAAGTGCCTGTGCTAGAGTTCC
AACTGTGGATGCATCCGTCCCGTTTGGTCAAAGTCTTACTTCCCTGCTCTCACCTACTCACAGACGGGATGCTA
AGCAGTGCACCTGCAGTGGTTTAATGGCAGATAAGCTCCGTCTGCAGTTCAGGCCAGCCAGAACTCCTGTGTC
CACATAGAGCTGACGTGAGAAATATCTTTCAGCCCAGGAGAGGGGTCCTGATCTTAACCCCTTCTGGGTCTC
AGACAACTCAGAAGGTTGGGGGGATACCAGAGAGGTGGTGAATAGGACCGCCCCCTCCTTACTTGTGGGATCAA
ATGCTGTAATGGTGGAGGTGTGGGCAGAGGAGGGAGGCAAGTGTCTTTGAAAGTTGTGAGAGCTCAGAGTTTCTG
GGTCCCTCATTAGGAGCCCCCATCCCTGTGTTCCTCAAGAATTTCAGAGAACAGCACTGGGGCTGGAATGATCTTT
AATGGGCCCCAAGGCCAACAGGCATATGCCTCACTACTGCCTGGAGAAGGGAGAGATTTCAGGTCTCCAGCAGCCT
CCCTCACCCAGTATGTTTTACAGATTACGGGGGGACCGGTGAGCCAGTGACCCCTGCAGCCCCCAGCTTCAGG
CCTCAGTGTCTGCCAGTCAAGCTTCACAGGCATTGTGATGGGGCAGCCTTGGGGAATATAAAATTTTGTGAAGAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

289/615

FIGURE 288

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65413

<subunit 1 of 1, 372 aa, 1 stop

<MW: 42515, pI: 8.92, NX(S/T): 6

MKYLRRHRPNATLILAIGAFTLLLFSLVSPPTCKVQEOPPAIPEALAWPTPPTRPAPAPCHANTSMVTHPDFAT
QPQHVQNFLLYRHCRHFPLLQDVPPSKCAQPVFLLLVIKSSPSNYVRRELLRRTWGRERKVRGLQLRLLFLVGTA
SNPHEARKVNRLLLELEAQTHGDILQWDFHDSFFNLTLKQVLFQWQETRCANASFVLNGDDVFAHTDNMVFYLO
DHDPGRHLFVQGQLIQNVGPIRAFWSKYVPEVVTQNERYPYCGGGGFLLSRFTAAALRRAAHVLDIFPIDDVFL
GMCLELEGLKPASHSGIRTSGVRAPSQHLSSFDPFCFYRDLLLVHREFLPYEMLLMWDALNQPNLTCGNQTQIY

Important features:**Type II transmembrane domain:**

Amino acids 15-34

N-glycosylation sites:

Amino acids 10-14;64-68;184-188;202-206;362-366;367-371

TonB-dependent receptor proteins signature 1:

Amino acids 1-32

N-myristoylation sites:

Amino acids 308-314;316-322

290/615

FIGURE 289A

CGCGCTCCCCGCGCGCCTCCTCGGGCTCCACGCGTCTTGCCCCGAGAGGCAGCCTCCTCCAGGAGCGGGGCCCT
GCACACCAATGGCCCCCGGGTGGGCAGGGGTGCGCGCCGCCGTGCGCGCCCCGCCTGGCGCTGGCCTTGCGCGTGGC
GAGCGTCTGAGTGGGCTCCAGCCGTGCGCTGCCCCACCAAGTGACCTGCTCCGCTGCCAGCGTGGACTGCCA
CGGGCTGGGCTCCGCGCGGTTCCTCGGGGCATCCCCGCAACGCTGAGCGCCTTGACCTGGACAGAAATAATAT
CACCAGGATCACCAAGATGGACTTCGCTGGGCTCAAGAACCTCCGAGTCTTGATCTGGAAGACAACCAGGTCAG
CGTCATCGAGAGAGGCGCCTTCCAGGACCTGAAGCAGCTAGAGCGACTGCGCCTGAACAAGAATAAGCTGCAAGT
CCTTCCAGAATTGCTTTTCCAGAGCAGCCGAAGCTCACCAGACTAGATTTGAGTGAAAACCAGATCCAGGGGAT
CCCAGGAAGGCGTTCCGCGGCATCACCAGTGTGAAGAACCTGCAACTGGACAACAACCACATCAGCTGCATTGA
AGATGGAGCCTTCCGAGCGCTGCGCGATTTGGAGATCCTTACCTTCAACAACAACAACATCAGTCGCATCCTGGT
CACCAGCTTCAACCACATGCCGAAGATCCGAACCTGCGCCTCCACTCCAACCACCTTACTGCGACTGCCACCT
GGCTGGCTCTCGGATTGGCTGCGACAGCGACGACAGTTGGCCAGTTCACACTCTGCATGGCTCCTGTGCATTT
GAGGGGCTTCAACGTGGCGGATGTGCAAGAAGGAGTACGTGTGCCCAGCCCCCACTCGGAGCCCCATCCTG
CAATGCCAACTCCATCTCCTGCCCTTCCGCTGACGTCGAGCAATAACATCCTGGACTGTGAGGAAAGGCTT
GATGGAGATTCTGCCAACTTGCCGGAGGGCATCGTCGAATACGCTAGAACGAAGTCCATCAAAGCCATCCC
TGCAGGAGCCTTCAACAGTACAAGAACTGAAGCAATAGACATCAGCAAGAATCAGATATCGGATATTGCTCC
AGATGCCTTCCAGGGCTGAAATCACTCACATCGCTGGTCTCTGTATGGGAACAAGATCACCAGATTGCCAAGGG
ACTGTTTGATGGGCTGGTGTCCCTACAGCTGCTCCTCCTCAATGCCAACAAGATCAACTGCCTGCGGGTGAACAC
GTTTCAGGACCTGCAGAACCTCAACTTGCTCTCCCTGTATGACAACAAGCTGCAGACCATCAGCAAGGGGCTCTT
CGCCCCCTGTCAGTCCATCCAGACACTCCACTTAGCCCCAAAACCCATTTGTGTGCGACTGCCACTTGAAGTGGCT
GGCGACTACCTCCAGGACAACCCCATCGAGACAAGCGGGGCCGCTGCAGCAGCCGCGCGGACTCGCCAACAA
GCGCATCAGCCAGATCAAGAGCAAGAAGTTCGCTGCTCAGGCTCCGAGGATTACCGCAGCAGGTTTCAGCAGCGA
GTGCTTCATGGACCTCGTGTGCCCCGAGAAGTGTGCTGTGAGGGCAGGATTGTGGACTGCTCCAACCAGAAGCT
GGTCCGCATCCCAAGCCACCTCCCTGAATATGTACCGACCTGCGACTGAATGACAATGAGGTATCTGTTCTGGA
GGCCACTGGCATCTTCAAGAAGTTGCCAACCTGCGGAAATAAATCTGAGTAACAATAAGATCAAGGAGGTGCG
AGAGGGAGCTTTCGATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAGGGAACCAGCTGGAGACCGTGCACGG
GCGCTGTTCCGTGGCCTCAGTGGCCTCAAAACCTTGATGCTGAGGAGTAACTTGATCAGCTGTGTGAGTAATGA
CACCTTTGCCGGCCTGAGTTCCGTGAGACTGCTGTCCCTCTATGACAATCGGATCACCACCATCACCCCTGGGGC
CTTACCACGCTTGTCTCCCTGTCCACCATAAACCTCCTGTCCAACCCCTTCAACTGCAACTGCCACCTGGCCTG
GCTCGGCAAGTGGTTGAGGAAGAGGCGGATCGTCAGTGGGAACCCTAGGTGCCAGAAGCCATTTTCTCTCAAGGA
GATTCCTCATCCAGGATGTGGCCATCCAGGACTTACCTGTGATGGCAACGAGGAGAGTAGCTGCCAGCTGAGCCC
GCGCTGCCCGGAGCAGTGACCTGTATGGAGACAGTGGTGCGATGCAGCAACAAGGGGCTCCGCGCCCTCCCCAG
AGGCATGCCCAAGGATGTGACCGAGCTGTACCTGGAAGGAAACCACCTAACAGCCGTGCCAGAGAGCTGTCCGC
CCTCCGACACCTGACGCTTATTGACCTGAGCAACAACAGCATCAGCATGCTGACCAATTACACCTTCAGTAACAT
GTCTACCTCTCCACTCTGATCCTGAGCTACAACCGGCTGAGGTGCATCCCCGTCCACGCCTTCAACGGGCTGCG
GTCCCTGCGAGTGCTAACCTCCATGGCAATGACATTTCCAGCGTTCTTGAAGGCTCCTTCAACGACCTCACATC
TCTTTCCCATCTGGCGCTGGGAACCAACCCACTCCACTGTGACTGCAGTCTTCGTTGGCTGTGCGAGTGGGTGAA
GGCGGGGTACAAGGAGCCTGGCATCGCCCGCTGCAGTAGCCCTGAGCCCATGGCTGACAGGCTCCTGCTCACCAC
CCCAACCCACCGCTTCCAGTGCAAGGGCCAGTGGACATCAACATTGTGGCCAATGCAATGCCTGCCTCTCCAG
CCCGTCAAGAATAACGGGACATGACCCAGGACCTGTGGAGCTGTACCGCTGTGCCTGCCCC

291/615

FIGURE 289B

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCAACACCTGCATCCAGAACCCCTGTCAGCATGGAGGCACC
TGCCACCTGAGTGACAGCCACAAGGATGGGTTTCAGCTGCTCCTGCCCTCTGGGCTTTGAGGGGCAGCGGTGTGAG
ATCAACCCAGATGACTGTGAGGACAACGACTGCGAAAACAATGCCACCTGCGTGGACGGGATCAACAACCTACGTG
TGTATCTGTCCGCTAACTACACAGGTGAGCTATGCGACGAGGTGATTGACCACTGTGTGCCTGAGCTGAACCTC
TGTCAGCATGAGGCCAAGTGCATCCCCCTGGACAAAGGATTTCAGCTGCGAGTGTGTCCCTGGCTACAGCGGGAAG
CTCTGTGAGACAGACAATGATGACTGTGTGGCCCAAGTGCCGCCACGGGGCCCACTGCGTGGACACAATCAAT
GGCTACACATGCACCTGCCCCCAGGGCTTCAGTGGACCTTCTGTGAACACCCCCACCCATGGTCTTACTGCAG
ACCAGCCCATGCGACCACTACGAGTGCCAGAACGGGGCCCACTGCATCGTGGTGCAGCAGGAGGCCACCTGCCGC
TGCCCAACAGGCTTCGCGGCCCCAGATGCGAGAAGCTCATCACTGTCAACTTCGTGGGCAAAGACTCCTACGTG
GAACTGGCCTCCGCCAAGGTCCGACCCAGGCCAACATCTCCCTGCAGGTGGCCACTGACAAGGACAACGGCATC
CTTCTCTACAAAGGAGACAATGACCCCTGGCACTGGAGCTGTACCAGGGCCACGTGCGGCTGGTCTATGACAGC
CTGAGTTCCCCTCCAACCACAGTGTACAGTGTGGAGACAGTGAATGATGGGCAGTTTCACAGTGTGGAGCTGGTG
ACGCTAAACAGACCCCTGAACCTAGTAGTGAGCAAAAGGAATCCAAAGAGCCTGGGGAAGCTCCAGAAGCAGCCA
GCAGTGGGCATCAACAGCCCCCTCTACCTTGAGGGCATCCCCACCTCCACCGGCCTCTCCGCCTTGCGCCAGGGC
ACGGACCGGCCTCTAGGCGGCTTCCACGGATGCATCCATGAGGTGCGCATCAACAACGAGCTGCAGGACTTCAAG
GCCCTCCCACCACAGTCCCTGGGGGTGTCAACAGGCTGCAAGTCTGCACCGTGTGCAAGCACGGCCTGTGCCGC
TCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGCCGCCAGGCTGGACCGGCCCACTCTGCGACCAGGAGGCCCGG
GACCCCTGCCTCGGCCACAGATGCCACCATGGAAAATGTGTGGCAACTGGGACCTCATACATGTGCAAGTGTGCC
GAGGGCTATGGAGGGGACTTGTGTGACAACAAGAATGACTCTGCCAATGCCTGCTCAGCCTTCAAGTGTCAACAT
GGGCAGTGCCACATCTCAGACCAAGGGGAGCCCTACTGCCTGTGCCAGCCCGGCTTTAGCGGCGAGCACTGCCAA
CAAGAGAATCCGTGCCTGGGACAAGTAGTCCGAGAGGTGATCCGCCGCCAGAAAGGTTATGCATCATGTGCCACA
GCCTCCAAGGTGCCCATCATGGAATGTCGTGGGGGCTGTGGGCCCCAGTGCTGCCAGCCCACCCGCAGCAAGCGG
CGGAAATACGTCTTCCAGTGCACGGACGGCTCCTCGTTTGTAGAAGAGGTGGAGAGACACTTAGAGTGCAGCTGC
CTCGCGTGTTCCTAAGCCCCCTGCCCGCCTGCCTGCCACCTCTCGGACTCCAGCTTGATGGAGTTGGGACAGCCAT
GTGGGACCCCTGGTGATTTCAGCATGAAGGAAATGAAGCTGGAGAGGAAGGTAAAGAAGAAGAGAATATTAAGTA
TATTGTAAATAAACAAAAAATAGAACTTAAAAAAAAAAAAAAAAAAAAA

292/615

FIGURE 290

MAPGWAGVGA AVRARLALALASVLSGPPAVACPTKCTCSAASVDC HGLGLRAVPRGIPRNAERLDLDRNNITR
ITKMDFAGLKNLRVLHLEDNQVSVIERGAFQDLKQLERLRNLNKNLQVLPELLFQSTPKLTRLDLSENQIQGIPR
KAFRGITDVKNLQLDNNHISCIEDGAFRALRDL EILTLNNNNISRI LVT SFNHMPKIRTLRLHSNHLYCDCHLAW
LSDWLRQRRTVGQFTLCMAPVHLRGFNVADVQKKEYVCPAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLME
IPANLPEGIVEIRLEQNSIKAIPAGAFQYKKLKRIDISKNQISDIAPDAFQGLKSLTSLVLYGNKITEIAKGLF
DGLVSLQLLLLNANKINCLRVNTFQDLQNLNLLSLYDNKLQ TISKGLFAPLQSIQTLHLAQNPFCVDCHLKWLAD
YLQDNPIETSGARCSSPRRLANKRISQIKSKKFRCSGSEDYRSRFSSECFMDLVCPEKCRCEGTIVDCSNQKLV R
IPSHLPEYVTDLRLNDNEVSVLEATGIFKKLPNLRKINLSNNKIKEVREGAFDGAASVQELMLTGNQLETVHGRV
FRGLSGLKTLMLRSNLISCVSNDTFAGLSSVRLLSLYDNRI TITPGAFTTLVSLSTINLLSNPFNCNCHLAWLG
KWLRRRIVSGNPRCQKPFFLKEIPIQDVAIQDFTCDGNEESSCQLSPRCPEQCTCMETTVVRC SNKGLRALPRGM
PKDVTLEYLEGNHILTAVPRELSALRHITLIDLSNNSISMLTNYTFSNMSHLSTLILSYNRLRCIPVHAFNGLRSL
RVLT LHGNDISSVPEGSFNDLTSLSHLALGTNPLHCD CSLRWLSEWVKAGYKEPGIARCSSPEPMADRLLLTPT
HRFQCKGPVDINIVAKCNACLSSPCKNNGTCTQDPVELYRCACPYSYKGDCTVPINTC IONPCQHGGTCHLSDS
HKDGFSCSCPLGFEGQRC EINPDDCEDNDCENNATCVDGINNYVCICPPNYTGELCDEVIDHCVPELNLCQHEAK
CIPLDKGFSCCECVPGYSGKLCETDNDDCVAHKCRHGAQCVD TINGYTCTCPQGFSGPFCEHPPPMVLLQTSPCDQ
YECQNGAQCI VVQQEPTCRCP PGFAGPRCEKLITVNFVGKDSYVELASAKVRPQANISLQVATDKDNGILLYKGD
NDPLALELYQGHVRLVYDSLSSPPTTVYSVETVNDGQFHSVELVTLNQT LNLVVDKGT PKSLGKLQKQPAVGINS
PLYLGGIPTSTGLSALRQGTDRPLGGFHGCIHEVRINNELQDFKALPPQSLGVSPGCKSCTVCKHGLCRSVEKDS
VVCECRPGWTGPLCDQEARDPCLGHRCHHGKCVATGT SYMCKCAEGYGGDLCDNKNSANACSAFKCHHGQCHIS
DQGEPYCLCQPGFSGEHCQQENPCLGQVVREVIRROKGYASCATASKVPIMECRGGCGPQCCQPTRSKRRKYVFQ
CTDGS SFVEEVERHLECGCLACS

Signal peptide:
amino acids 1-27

293/615

FIGURE 291

GGATGCAGGACGCTCCCCTGAGCTGCCTGTCACCGACTAGGTGGAGCAGTGTTCCTCCGCAGACTCAACTGAGA
AGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTTCAGTTCTGTCTCCGGCAGGCTTTGAGGATGAAGGCTG
CGGGCATTCTGACCCTCATTGGCTGCCTGGTCACAGGCGCCGAGTCCAAAATCTACACTCGTTGCAAACTGGCAA
AAATATTCTCGAGGGCTGGCCTGGACAATTACTGGGGCTTCAGCCTTGGAAGCTGGATCTGCATGGCATATTATG
AGAGCGGCTACAACACCACAGCCCCGACGGTCCTGGATGACGGCAGCATCGACTATGGCATCTTCCAGATCAACA
GCTTCGCGTGGTGCAGACGCGGAAAGCTGAAGGAGAACAACCACTGCCATGTCGCCTGCTCAGCCTTGATCACTG
ATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGAGACACAAGGAATGAACTATTGGCAAGGCT
GGAAGAAACATTGTGAGGGCAGAGACCTGTCCGAGTGGAAAAAGGCTGTGAGGTTTCCTTAAACTGGAAGCTGGAC
CCAGGATGCTTTGCAGCAACGCCCTAGGATTTGCAGTGAATGTCCAAATGCCTGTGTCATCTTGTCCCGTTTCCT
CCAATATTCCTTCTCAAACTTGAGAGGGAAAATTAAGCTATACTTTAAGAAAATAAATATTTCCATTTAAATGTC

294/615

FIGURE 292

MKAAGILTLIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAPTVLDDGSIDYGIF
QINSFAWCRRGKLENNHCHVACSALITDDLTDALICARKIVKETQGMNYWQGWKKHCEGRDLSEWKKGCEVS

Signal peptide:
amino acids 1-19

295/615

FIGURE 293

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTGTACCCAAGGAAAG
TGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGCTGTTTCTCATAGCGACCACCAGAGGA
TGGAGTACAGATGAGGCTAATACTTACTTCAAGGAATGGACCTGTTCTTCGTCTCCATCTCTGCCCAGAAGCTGC
AAGGAAATCAAAGACGAATGTCCTAGTGCATTTGATGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATCTAC
CAGACCTTCTGTGACATGACCTCTGGGGGTGGCGGCTGGACCCTGGTGGCCAGCGTGCATGAGAATGACATGCGT
GGGAAGTGCACGCTGGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCCAGAGGGGGACGGCAAC
TGGGCCAACTACACACCTTTGGATCTGCAGAGGGCGCCACGAGCGATGACTACAAGAACCCTGGCTACTACGAC
ATCCAGGCCAAGGACCTGGGCATCTGGCACGTGCCCAATAAGTCCCCATGCAGCACTGGAGAAACAGCTCCCTG
CTGAGGTACCGCACGGACACTGGCTTCCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCA
GTGAAATATGGAGAAGGAAAGTGTGGACTGACAACGGCCCCGTGATCCCTGTGGTCTATGATTTTGGCGACGCC
CAGAAAACAGCATCTTATTACTCACCCCTATGGCCAGCGGGAATTCAGTGCGGGATTTGTTTCAGTTTCAGGGTATTT
AATAACGAGAGAGCAGCCAACGCCTTGTGTGCTGGAATGAGGGTCACCGGATGTAACACTGAGCATCACTGCATT
GGTGGAGGAGGATACTTTCCAGAGGCCAGTCCCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATAT
GGAATCATGTTGGTTACAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGTTGAGAGTTT
TGTGGGAGGGAACCCAGACCTCTCCTCCCAACCATGAGATCCCAAGGATGGAGAACAACCTTACCCAGTAGCTAGA
ATGTTAATGGCAGAAGAGAAAACAATAAATCATATTGACTCAAGAAAAAAA

296/615

FIGURE 294

MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTENGVIYQTFCDMTSG
GGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFGSAEAATSDDYKNPGYYDIQAKDLGIW
HVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGIYQKYPVKYGEKGCWTDNGPVIPVVYDFGDAQKTASYSP
YGQREFTAGFVQFRVFNNERAANALCAGMRVTGCNTEHHCIGGGGYFPEASPQCGDFSGFDWSGYGTHVGYSSS
REITEAAVLLFYR

297/615

FIGURE 295

CAGGCCATTTGCATCCCACTGTCCCTGTGTTCTGGAGCCAGGCCACACCGTCCTCAGCAGTGTCTGTGTTAAAAA
CGCCAAGCTGAATATATCATGCCCCCTATTAAAACTTGTACATGGCTCCCCATTGGTTTTTGGAGAAAAGTTCAAG
CTTTTACCTTGGTGTCTGCCCTGTATCCCAGTGTTCAGGCTGGCTAGACGGCGGAAGAAGATCCTATTTTACTGT
CACTTCCCAGATCTGCTTCTCACCAGAGAGATTCTTTTCTTAAACGACTATACAGGGCCCCAATTGACTGGATA
GAGGAATACACCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTCACAGCTGCTGTTTTTAAGGAAACA
TTCAAGTCCCTGTCTCACATAGACCCTGATGTCCTCTATCCATCTCTAAATGTCACCAGCTTTGACTCAGTTGTT
CCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCTGCTGCTCTCCATCAACAGATACGAAAGGAAG
AAAAATCTGACTTTGGCACTGGAAGCCCTAGTACAGCTGCGTGGAAGATTGACATCCCAAGATTGGGAGAGGGTT
CATCTGATCGTGGCAGGTGGTTATGACGAGAGAGTCTGGAGAATGTGGAACATTATCAGGAATTGAAGAAAATG
GTCCAACAGTCCGACCTTGGCCAGTATGTGACCTTCTTGAGGTCTTTCTCAGACAAAACAGAAAATCTCCCTCCTC
CACAGCTGCACGTGTGTGCTTTACACACCAAGCAATGAGCACTTTGGCATTGTCCCTCTGGAAGCCATGTACATG
CAGTGGCCAGTCATTGCTGTTAATTCGGGTGGACCTTGGAGTCCATTGACCACAGTGTACAGGGTTTCTGTGT
GAGCCTGACCCGGTGCCTTCTCAGAAGCAATAGAAAAGTTTCATCCGTGAACCTTCCTTAAAAGCCACCATGGGC
CTGGCTGGAAGAGCCAGAGTGAAGGAAAAAATTTCCCTGAAGCATTACAGAACAGCTCTACCGATATGTTACC
AACTGCTGGTATTAATCAGATTGTTTTTAAGATCTCCATTAATGTCATTTTTATGGATTGTAGACCCAGTTTGA
AACCAAAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTTAAAAAATAAACTTGAGTCTTGAATGTGAGCCA
CTTTCCTATATACCACACCTCCCTGTCCACTTTTCAGAAAAACCATGTCTTTTATGCTATAATCATTCCAAATTT
TGCCAGTGTTAAGTTACAAATCTGGTGTCAATCCATGTTTCAGCAGAGTATTTTAATTATATTTTCTCGGGATTAT
TGCTCTTCTGTCTATAAATTTTGAATGATACTGTGCCTTAATTGGTTTTTCATAGTTTAAAGTGTGTATCATTATCA
AAGTTGATTAATTTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTTCCAGATTCAATCCACCGAAGTGT
TCACTGTCTCTGTTAGGGAATTTTGTGTTGCTGCTTTGCCTGGATCCATAGCGAGAGTGTCTGTATTTTT
TTTAAGATAATTTGTATTTTTGCACACTGAGATATAATAAAAGGTGTTTATCATAAAAAAAAAAAAAAAAAA

298/615

FIGURE 296

MPLLKLVHGSPLVFGEKFKLFTLVSACIPVFRLLARRRKKILFYCHFDPDLLTKRDSFLKRLYRAPIDWIEEYTTG
MADCILVNSQFTAAVFKETFKSLSHIDPDVLYPSLNVTSFDSVVPKLDLVPKGKKFLLLSINRYERKKNLTLA
LEALVQLRGRLTSQDWERVHLIVAGGYDERVLENVEHYQELKKMVQQSDLGQYVTFLRSFSDKQKISLLHSCTCV
LYTPSNEHFGIVPLEAMYMOCPIAVNSGGPLESIDHSVTGFLCEPDVHFSEAEKFIREFSLKATMGLAGRAR
VKEKFSPEAFTEQLYRYVTKLLV

Signal peptide:

amino acids 1-15

299/615

FIGURE 297

GACTACGCCGATCCGAGACGTGGCTCCCTGGGCGGCAGAACCAATGTTGGACTTCGCGATCTTCGCCGTTACCTTC
TTGCTGGCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCAGACAAGCTGCAGGAATTCAGGGATTACT
CCAACTGAAGAAAAAGATGGTAATCTTCAGATATTGTGAATAGTGGAGTTTGCATGAGTTCCTGGTTAATTTG
CATGAGAGATATGGGCCTGTGGTCTCCTTCTGGTTTGGCAGGCGCCTCGTGGTTAGTTTGGGCACTGTTGATGTA
CTGAAGCAGCATATCAATCCCAATAAGACATCGGACCCTTTGAAACCATGCTGAAGTCATTATTAAGGTATCAA
TCTGGTGGTGGCAGTGTGAGTGAAAACCATGAGGAAAAAATTGTATGAAAATGGTGTGACTGATTCTCTGAAG
AGTAACTTTGCCCTCCTCTAAAGCTTTCAGAAGAATTATTAGATAAATGGCTCTCCTACCCAGAGACCCAGCAC
GTGCCCCCTCAGCCAGCATATGCTTGGTTTTGCTATGAAGTCTGTTACACAGATGGTAATGGGTAGTACATTTGAA
GATGATCAGGAAGTCATTCGCTTCCAGAAGAATCATGGCACAGTTTGGTCTGAGATTGGAAAAGGCTTTCTAGAT
GGGTCACCTTGATAAAAAACATGACTCGGAAAAAACAATATGAAGATGCCCTCATGCAACTGGAGTCTGTTTTAAGG
AACATCATAAAAGAACGAAAAGGAAGGAACCTTCAGTCAACATATTTTCATTGACTCCTTAGTACAAGGGAACCTT
AATGACCAACAGATCCTAGAAGACAGTATGATATTTCTCTGGCCAGTTGCATAATAACTGCAAAATTGTGTACC
TGGGCAATCTGTTTTTTAACCACCTCTGAAGAAGTTCAAAAAAAATTATATGAAGAGATAAACCAAGTTTTTGA
AATGGTCCTGTACTCCAGAGAAAATTGAGCAGCTCAGATATTGTCAGCATGTGCTTTGTGAACTGTTCTGA
GCCAACTGACTCCAGTTTCTGCCCAGCTTCAAGATATTGAAGGAAAAATTGACCGATTTATTATTCCTAGAGAG
ACCTCGTCCTTTATGCCCTTGGTGTGGTACTTCAGGATCCTAATACTTGGCCATCTCCACACAAGTTTGATCCA
GATCGGTTTGATGATGAATTAGTAATGAAACTTTTTCTCACTTGGATTCTCAGGCACACAGGAGTGTCCAGAG
TTGAGGTTTGATATATGGTGACCACAGTACTTCTAGTGTATTGGTGAAGAGACTGCACCTACTTTCTGTGGAG
GGACAGGTTATTGAAACAAAGTATGAACTGGTAACATCATCAAGGGAAGAAGCTTGGATCACTGTCTCAAAGAGA
TATTAAATTTTTATACATTTAAATCATTGTAAATTGATTGAGGAAAAACAACCATTTAAAAAAAATCTATGTTG
AATCCTTTTATAAACAGTATCACTTTGTAATATAAACACCTATTTGTACTTAA

300/615

FIGURE 298

MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLHERYGPVVSFWFGR
RLVVSLGTVDLVKQHINPNKTSDFETMLKSLRLRYQSGGGSVSENHMRKKLYENGVTDSLKSNFALLKLSEELL
DKWLSYPETQHVPLSQHMLGFAMKSVTQMVMGSTFEDDQEVIRFQKNHGTWVSEIGKGFLDGS�DKNMTRKKQYE
DALMQLESVLRNIIKERKGRNFSQHIFIDSLVQGNLNDQQILEDSMIFSLASCIITAKLCTWAICFLTTSSEVQK
KLYEEINQVFGNGPVTPEKIEQLRYCQHVLCEVVRTAKLTPVSAQLQDIEGKIDRFIIPRETLVLYALGVVLQDP
NTWPSPHKFDPPDRFDDELVMKTFSSLGFSGTQECPELRFAYMVTTVLLSVLVKRLHLLSVEGQVIETKYELVTSS
REEAWITVSKRY

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 271-290

301/615

FIGURE 299

CTAGATTTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACTTCCAGCCTCAGAGACCGCCGCCCTT
GTCCCCGAGGGCCATGGGCCGGGTCTCAGGGCTTGTCCTCTCGCTTCTGACGCTCCTGGCGCATCTGGTGGT
CGTCATCACCTTATTCTGGTCCCGGGACAGCAACATACAGGCCTGCCTGCCTCTCACGTTACCCCCGAGGAGTA
TGACAAGCAGGACATTCAGCTGGTGGCCGCGCTCTCTGTACCCCTGGGCCTCTTTGCAGTGGAGCTGGCCGTTT
CCTCTCAGGAGTCTCCATGTTCAACAGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGTGGC
CCTGTCCTTCTTCATATTCGAGCGTTGGGAGTGCCTACGTATTGGTACATTTTTGTCTTCTGCAGTGCCCTTCC
AGCTGTCACTGAAATGGCTTTATTTCGTCACCGTCTTTGGGCTGAAAAAGAAACCCTTCTCATACCTTCATGACG
GGAACCTAAGGACGAAGCCTACAGGGGCAAGGCGCGCTTCGTATTCTTGGAAGAAGGAAGGCATAGGCTTCGGTT
TTCCCCTCGGAACTGCTTCTGCTGGAGGATATGTGTTGGAATAATTACGTCTTGAGTCTGGGATTATCCGCATT
GTATTTAGTGCTTTGTAATAAAATATGTTTTGTAGTAACATTAAGACTTATATACAGTTTTAGGGGACAATTAAA
AAAAAAAAA

302/615

FIGURE 300

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLGLFAVELAGFLSGV
SMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCSALPAVTEMALFVTVEGLKKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

303/615

FIGURE 301

CTGGGACCCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAGATGCAACTGACTCGCTGCTGC
TTCGTGTTCCCTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGGATGATGGTCCTCCCGGCTCAGAGGAC
CCTGAGCGTGATGACCACGAGGGCCAGCCCCGCCCCGGGTGCCTCGGAAGCGGGGCCACATCTCACCTAAGTCC
CGCCCCATGGCCAATTCCACTCTCTAGGGGTGCTGGCCCCGCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCC
CCCAACCGCCCGAACCACAGCCCCCACCCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTACTCC
AACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGGAAGATTGTGGACCATGGCAATGGGACCTTCAGCGTC
CACTTCCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCCTCGTGCCCCCAGTAAAGCTGTAGAGTTC
CACCAGGAACAGCAGATCTTCATCGAAGCCAAGGCCTCCAAAATCTTCAACTGCCGGATGGAGTGGGAGAAGGTA
GAACGGGGCCGCCGGACCTCGCTTTGCACCCACGACCCAGCCAAGATCTGCTCCCGAGACCACGCTCAGAGCTCA
GCCACCTGGAGCTGCTCCAGCCCTTCAAAGTCGTCTGTGTCTACATCGCCTTCTACAGCACGGACTATCGGCTG
GTCCAGAAGGTGTGCCAGATTACAACCTACCATAGTGATACCCCTACTACCCATCTGGGTGACCCGGGGCAGGC
CACAGAGGCCAGGCCAGGGCTGGAAGGACAGGCCTGCCATGCAGGAGACCATCTGGACACCGGGCAGGGAAGGG
GTTGGGCCTCAGGCAGGGAGGGGGGTGGAGACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAG
AGAAAGGGTCCCAAGTGCTGGTCCCAACCTGAAGCTGTGGAGTGAAGTAGATCACAGGAGCACTGGAGGAGGAGTG
GGCTCTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCCGAGGCCTGTGGGCAG
GCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGCCCTTGGTTCTTGCCATCCTGAGGAAAGATA
GCAACAGGGAGGGGGAGATTTTCATCAGTGTGGACAGCCTGTCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAG
GAGCCAGTCAGCAGGGTGGGGTGGGGCCAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCCCTGTC
GTGTGCTGAGCATGGCATGAGGCTGAAGTGGCAACCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCT
CCAGCCAGGCCACCCCTTTCCAAAATCCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATTGCTGATGGCACA
CCCATCCTTAAGCTAAGACAGGACGATTGTGGTCCTCCACACTAAGGCCACAGCCATCCGCGTGCTGTGTGTC
CCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAGCATCCATGTCCCGGAGAGGGGTCCCTCAACAGTCAGCC
TCACCTGTGACAGCGGGGTCTCCCGGATCTGGATGGCGCCGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGGC
CGGGCCGACAGCATGTGCTGGATCTGTCTGTGTGTCTGTCTGTGGGTGGGGGAGGGGAGGGAAGTCTTGTGA
AACCCTGATTGCTGACTTTTGTGTGAAGAATCGTGTCTTGGAGCAGGAAATAAAGCTTGCCCCGGGGCA

304/615

FIGURE 302

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521

><subunit 1 of 1, 252 aa, 1 stop

><MW: 28127, pI: 8.91, NX(S/T): 5

QLTRCCFVFLVQGSLLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMANSTLLGLLAPPGEA
WGILQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNISISLVP
PSKAVEFHQEQQIFIEAKASKIFNCRMWEKVERGRRTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVVCVYIAF
YSTDYRLVQKPCPDYNYHSDTPYYPSG

Important features of the protein:**Signal peptide:**

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

305/615

FIGURE 303

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCCTGCGCTCGCCCTTTATGTCT
TCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGAGCTTTCTTCTGGTTGGTGTCTCTACTGA
TTTCGTCCCTTGTTTGGTTCATGGCAAGAGTCATTATTGACAACAAAGATGGACCAACACAGAAATATCTGCTGA
TCTTTGGAGCGTTTGTCTCTGTCTATATCCAAGAAATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCA
GTGAAGGTTTGAAGAGTATAAACCAGGTGAGACAGCACCTCTATGCGACTGCTGGCCTATGTTTCTGGCTTGG
GCTTTGGAATCATGAGTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGGCCAGGCACAGTGGGCA
TTCATGGAGATTCTCCTCAATTCTTCCTTTATTTCAGCTTTTCATGACGCTGGTCATTATCTTGCTGCATGTATTCT
GGGGCATTGTATTTTTTGTGAGCTGTGAGAAGAAAAAGTGGGGCATCCTCCTTATCGTTCTCCTGACCCACCTGC
TGGTGTGAGCCAGACCTTCATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTATATAATCCTGGTGCTCA
TGGGCACCTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTCTGCCAAGACAAGA
ACTTTCTTCTTTACAACCAGCGCTCCAGATAAACCCTCAGGGAACCAGCACTTCCCAAACCGCAGACTACATCTTTA
GAGGAAGCACAACTGTGCCTTTTCTGAAAATCCCTTTTCTGGTGGAATTGAGAAAGAAATAAACTATGCAGATA

306/615

FIGURE 304

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658
><subunit 1 of 1, 257 aa, 1 stop
><MW: 28472, pI: 9.33, NX(S/T): 0
MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDNKGPTQKYLLIFG
AFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGFGIMSGVFSFVNTLSDSLGP GTVGIHG
DSPQFFLYSAFMTLVIIILLHVFWGIVFFDGCEKKKWGILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGT
WAFLAAGGSCRSLKLCCLLCQDKNFLLYNQSR

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

FIGURE 305

[illegible]

308/615

FIGURE 306

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQSNQVFPSLSLIPLTQM
LTLGPDHLHLNPAAGMTFGTQTHPLTLGGGLNVQQQLHPHVLPIFVTQLGAQGTLISSEE
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGS LPAGGAGVNPATQGTPAGRLPTPSG
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

Signal peptide:

amino acids 1-16

FIGURE 307

FIGURE 307

AAAAAAAAAAAA

310/615

FIGURE 308

MRWILFIGALIGSSICGQEKFFGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFNRPVDVLVPSVSLQA
FKSFLRSQGLEAYVTIEDLQALLDNEDDEMQRHNEGQERSNNFNFGAYHSLEAIYHEMDNIAADFPDLARRVKIG
HSFENRPMYVLKFSTGKGVRPAPVWLNAGIHSREWISQATAIWTARKIVSDYQRDPATISILEKMDIFLLPVANP
DGYVYTQTQNRLWRKTRSRNPGSSCIGADPNRNWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVDIFIQKHGN
FKGFIDLHSYSQLLMYPYGYSVKKAPDAEELDKVARLAALASVSGTEYQVGPTCTTVYPASGSSIDWAYDNGI
KFAFTFELRDTGTGFLLPANQIIPTAEETWLGLKTIMEHVRDNL

Signal peptide:
amino acids 1-16

311/615

FIGURE 309

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCCAGCCTGAGTCCAAGAT
TCTTCCCAGGAACACAAACGTAGGAGACCCACGCTCCTGGAAGCACCAGCCTTTATCTTTCACCTTCAAGTCCC
CTTTCTCAAGAATCCTCTGTTCTTTGCCCTCTAAAGTCTTGGTACATCTAGGACCCAGGCATCTTGCTTTCCAGC
CACAAAGAGACAGATGAAGATGCAGAAAGGAAATGTTCTCCTTATGTTTGGTCTACTATTGCATTTAGAAGCTGC
AACAAATTCCAATGAGACTAGCACCTCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGCCAC
CAACTCTGGGTCCAGTGTGACCTCCAGTGGGGTCAGCACAGCCACCATCTCAGGGTCCAGCGTGACCTCCAATGG
GGTCAGCATAGTCCACCAACTCTGAGTTCATACAACTCCAGTGGGATCAGCACAGCCACCAACTCTGAGTTCAG
CACAGCGTCCAGTGGGATCAGCATAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCAC
CAACTCTGAGTCCAGCACACCCTCCAGTGGGGCCAGCACAGTCCACCAACTCTGGGTCCAGTGTGACCTCCAGTGG
AGCCAGCACTGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGAGTCTAG
CACACTCTCCAGTGGGGCCAGCACAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCTAGCACAGCCAC
CAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAG
GGCCAGCACTGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAG
AACGACCTCCAATGGGGCTGGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGGCCAGCACAGCCAC
CAACTCTGACTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGG
GGCCAGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGGCTAGCACAGCCACCAACTCTGACTCCAG
CACAACTCCAGTGGGGCCGGCACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTGGGATCAGCACAGTCCAC
CAATTCGAGTCCAGCACACCCTCCAGTGGGGCCAACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGG
GGCCAACACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAG
CACAACTCCAGTGGGGTCAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCTAGCACAGCCAC
CAACTCTGACTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCTAGCACAGTGTCCAGTGG
GATCAGCACAGTCCCAATTCGAGTCCAGCACAACTCCAGTGGGGCCAACACAGCCACCAACTCTGGGTCCAG
TGTGACCTCTGCAGGCTCTGGAACAGCAGCTCTGACTGGAATGCACACAACTTCCCATAGTGCATCTACTGCAGT
GAGTGAGGCAAAGCCTGGTGGGTCCCTGGTGCCGTGGGAAATCTTCCTCATCACCTGGTCTCGGTTGTGGCGGC
CGTGGGGCTCTTTGCTGGGCTCTTCTTCTGTGTGAGAAACAGCCTGTCCCTGAGAAACACCTTTAACACAGCTGT
CTACCACCCTCATGGCCTCAACCATGGCCTTGGTCCAGGCCCTGGAGGGAATCATGGAGCCCCCACAGGCCAG
GTGGAGTCTTAATGGTTCTGGAGGAGACCAGTATCATCGATAGCCATGGAGATGAGCGGGAGGAACAGCGGGCC
CTGAGCAGCCCCGGAAGCAAGTGCCGCTTCTCAGGAAGGAAGAGACCTGGGCACCCAAGACCTGGTTTCCTTT
CATTCATCCCAGGAGACCCCTCCCAGCTTTGTTGAGATCCTGAAAATCTTGAAGAAGGTATTCCTCACCTTTCT
TGCTTTTACCAGACACTGGAAAGAGAATACTATATTGCTCATTAGCTAAGAAATAAATACATCTCATCTAACAC
ACACGACAAAGAGAAGCTGTGCTTGCCCCGGGGTGGGTATCTAGCTCTGAGATGAACTCAGTTATAGGAGAAAAC
CTCCATGCTGGACTCCATCTGGCATTCAAATCTCCACAGTAAAATCCAAGACCTCAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

312/615

FIGURE 310

MKMQKGNVLLMFGLLLHLEAATNSNETST SANTGSSVISSGASTATNSGSSVTSSGVSTATIS
GSSVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSESS
TPSSGASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSSTTS
SGASTATNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTTSNGA
GTATNSESSTTSSGASTATNSDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSSGASTA
TNSDSSTTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGANTATNS
ESSTVSSGASTATNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSTTSSEASTATNSESS
TVSSGISTVTNSESSTTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAVSEAKPGGS
LVPWEIFLITLVSVVAAVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGPGPGGNHGAP
HRPRWSPNWFWRPVS SIAMEMSGRNSGP

Signal peptide:
amino acids 1-20

Transmembrane domain:
amino acids 510-532

313/615

FIGURE 311A

CTAAGCCGGAGGATGTGCAGCTGCGGGCGGGCGCGGGCTACGAAGAGGACGGGGACAGGCGCGCTGCGAACCGA
GCCAGCCAGCCGGAGGACGCGGGCAGGGCGGGACGGGAGCCCGGACTCGTCTGCCGCCGCCGCTCGTCGCCGCTCG
TGCCGGCCCCGCGTCCCGCGCGCGAGCGGGAGGAGCCCGCCACCTCGCGCCGAGCCGCCGCTAGCGCGCGC
CGGGCATGGTCCCCTCTTAAAGGCGCAGGCCGCGGGCGGGGGCGGGTGTGCGGAACAAAGCGCCGGCGCGGG
CCTGCGGGCGGCTCGGGGGCCGCGATGGGCGCGGGCGGGCCCGCGCGCGGGCGGGCGCTGCCCGGGCGGGCCTCG
CGGCGCTAGGGCGGGCTGGCCTCCGTGGGCGGGGGCAGCGGGCTGAGGGCGCGCGGAGCCTGCGGCGGGCGGGC
GGCGGGCGGGCGGGCCCGGGCGGGCGGAGCGGGCGGGGCTGCGGGCGGGCGGGCGGGCTGGCTCAGCGTGC
TGCTCGGGCTCGTCTGGGCTTCGTGCTGGCCTCGCGGCTCGTCTGCCCGGGGCTTCCGAGCTGAAGCGAGCGG
GCCCACGGCGCGCGCCAGCCCCGAGGGTGCCTGCGGGCAGGCGGGCGGGCTTCCAGGCGGGCGGGCGGGC
CGATGGCGCGGGGGCGAGCTCTGGCCGCCCGGCTCGGACCCAGATGGCGGGCCCGCGCGAGCAACTTCTCT
TCGTGGGAGTCATGACCGCCAGAAATACCTGCAGACTCGGGCCGTGGCCGCTTACAGAACATGGTCCAAGACAA
TTCTGGGAAAGTTCAGTTCCTTCAAGTGAGGGTTCGACACATCTGTACCAATTCCAGTAGTCCACTACGGG
GTGTGGACGACTCTACCGCCCCAGAGAAGTCTTCATGATGCTCAAGTACATGCACGACCACTACTTGGACA
AGTATGAATGGTTTATGAGAGCAGATGATGACGTGTACATCAAAGGAGACCGTCTGGAGAACTTCTGAGGAGTT
TGAACAGCAGCGAGCCCTCTTCTTGGGCAGACAGGCTGGGCACCACGGAAGAAATGGGAAACTGGCCCTGG
AGCCTGGTGAGAACTTCTGATGGGGGGGCTGGCGTGATCATGAGCCGGGAGGTGCTTCGGAGAATGGTGCCGC
ACATTGGCAAGTGTCTCGGGAGATGTACACCACCCATGAGGACGTGGAGGTGGGAAGGTGTGTCCGGAGGTTT
CAGGGGTGAGTGTGTCTGGTCTTATGAGATGCGGCAGCTTTTTTATGAGAATTACGAGCAGAACAAAAGGGGT
ACATTAGAGATCTCCATAACAGTAAATTCACCAAGCTATCACATTACACCCCAACAAAACCCACCTACCAGT
ACAGGCTCCACAGCTACATGCTGAGCCGCAAGATATCCGAGCTCCGCCATCGCACAAATACAGCTGCACCGCGAAA
TTGTCTGATGAGCAATACAGCAACACAGAAATTCATAAAGAGGACCTCCAGCTGGGAATCCCTCCCTCTTCA
TGAGGTTTCAGCCCCGCCAGCGAGAGGAGATTCTGGAATGGGAGTTTCTGACTGGAAAATACTTGTATTTCGGCAG
TTGACGGCCAGCCCCCTCGAAGAGGAATGGACTCCGCCAGAGGGAAGCCTTGGACGACATTGTATGCAGGTCA
TGGAGATGATCAATGCCAACGCCAAGACCAGAGGGCGCATCATTGACTTCAAAGAGATCCAGTACGGCTACCGCC
GGGTGAACCCCATGTATGGGGCTGAGTACATCTGGACCTGCTGCTTCTGTACAAAAGCACAAAGGGAAGAAAA
TGACGGTCCCTGTGAGGAGGCACGCGTATTTACAGCAGACTTTCAGCAAAATCCAGTTTGTGGAGCATGAGGAGC
TGGATGCACAAGAGTTGGCCAAGAGAATCAATCAGGAATCTGGATCCTTGTCTTTCTCTCAAACCTCCCTGAAGA
AGCTCGTCCCCTTTCAGCTCCCTGGGTGCAAGAGTGAGCACAAAGAACCCAAAGATAAAAAGATAACATACTGA
TTCTTTGTCTGGGCGTTTCGACATGTTTGTGAGATTATGGGAAACTTTGAGAAGACGTGTCTTATCCCCAATC
AGAAGCTCAAGCTCGTGGTCTGCTTTTCAATTCTGACTCCAACCTGACAAGGCCAAACAAGTTGAAGTATGA
GAGATTACCGCATTAAAGTACCCTAAAGCCGACATGCAGATTTTGCCTGTGTCTGGAGAGTTTTCAAGAGCCCTGG
CCCTGGAAGTAGGATCCTCCCAGTTTAAACAATGAATCTTGTCTTCTTCTGCGACGTGACCTCGTGTCTTACTA
CAGAATTCCTTCAGCGATGTCGAGCAATACAGTTCTGGGCCAACAAATATATTTTCCAATCATCTTCAGCCAGT
ATGACCCAAAGATTGTTATAGTGGGAAAGTTCCAGTGACAACCATTTTGCCTTTACTCAGAAAAGTGGCTTCT
GGAGAACTATGGGTTTGGCATCACGTGTATTTATAAGGAGATCTTGTCCGAGTGGGTGGCTTTGATGTTTCCA
TCCAAGGCTGGGGGCTGGAGGATGTGGACCTTTTCAACAAGTTGTCCAGGCAGGTTTGAAGACGTTTAGGAGCC
AGGAAGTAGGAGTAGTCCACGTCCACCATCCTGTCTTTGTGATCCCAATCTTGACCCCAACAGTACAAAATGT
GCTTGGGGTCCAAAGCATCGACCTATGGGTCCACCCAGCAGCTGGCTGAGATGTGGCTGGAAAAAATGATCCAA
GTTACAGTAAAGCAGCAATAATAATGGCTCAGTGAGGACAGCCTAATGTCCAGCTTTGCTGGAAAAGACGTTTT
TAATTATCTAATTTATTTTCAAAAATTTTGTATGATCAGTTTGAAGTCCGTATACAAGGATATATTTTAC
AAGTGGTTTTCTTACATAGGACTCCTTTAAGATTGAGCTTTCTGAACAAGAAGGTGATCAGTGTTCCTTTTGA
CACATCTTCTGTGAACATTATGTAGCAGACCTGCTTAACCTTGACTTGAAATGTACCTGATGAACAAAATTT
TTTAAAAAATGTTTTCTTTTGAACCTTTGCTCCAGTCCATATGGCAGAAAACGTGAACATTCTGCAAGTAT
TATTGTAACAAAACACTGTAATCTGTTAAATGTTCTGTTGTGATTGTTAACATTCCACAGATTCTACCTTTTGT
GTTTTGTTTTTTTTTTTACAATTGTTTTAAAGCCATTTTCATGTTCCAGTTGTAAGATAAGGAAATGTGATAATA
GCTGTTTCATCATTGTCTTCAGGAGAGCTTTCAGAGTTGATCATTTCCTCTCATGGTACTCTGCTCAGCATGGC
CACGTAGGTTTTTTTTGTTTGTGTTTTGTTTGTGTTTTTGGAGACGGAGTCTCACTCTGTTACCCAGGCTGGAATG
CAGTGGCGCAATCTTGGCTCACTTTAACCTCCACTTCCCTGGTTCAAGCAATCCCTGCCTTTGCCTCCCGAGT
AGCTGGGATTACAGGCACACACCACCGCCAGNTAGTTTTTTTTGTATTTTGTAGTAGAGACGGGTTTACCAT
GCAAGCCAGCTGGCCACGTAGGTTTTAAAGCAAGGGGCGTGAAGAAGGCACAGTGAAGTATGTGGCTGTTCTCG
TGGTAGTTCATTTCGGCTAAATAGACCTGGCATTAAATTTCAAGAAGGATTGGCATTCTCTTCTGACCCCTT
CTCTTAAAGGGTAAATATTAATGTTTGAATGACAAAGATGAATTATTACAATAAATCTGATGTACACAGACT
GAAACATACACATACACCTAATCAAAACGTTGGGGAATAATGATTTGGTTTTGTTCTTTTCATCTGTCTG
TGTTATGTGGGTGGAGATGGTTTTTATTCTTTTATTACTGTTTTGTTTTATCCTTTGTATCTGAAATACCTTTAA

314/615

FIGURE 311B

TTTATTTAATATCTGTTGTTTCAGAGCTCTGCCATTTCTTGAGTACCTGTTAGTTAGTATTATTTATGTGTATCGG
GAGTGTGTTTAGTCTGTTTTATTTGCAGTAAACCGATCTCCAAAGATTTCTTTTGGAAACGCTTTTCCCCCTCC
TTAATTTTTATATTCCTTACTGTTTTACTAAATATTAAGTGTTCCTTGACAATTTGGTGCTCATGTGTTTGGG
GACAAAAGTGAAATGAATCTGTCATTATACCAGAAAGTTAAATTCTCAGATCAAATGTGCCTTAATAAATTTGTT
TTCATTTAGATTTCAAACAGTGATAGACTTGCCATTTTAATACACGTCATTGGAGGGCTGCGTATTTGTAAATAG
CCTGATGCTCATTGGAAAAATAAACAGTGAACAATATTTTCTATTGTACTTTTCGAACCATTTTGTCTCATT
ATTCCTGTTT TAGCTGAAGAATTGTATTACATTTGGAGAGTAAAAACTTAAACACGAAAAA

315/615

FIGURE 312

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836
><subunit 1 of 1, 802 aa, 1 stop
><MW: 91812, pI: 9.52, NX(S/T): 3
MAARGRAWLSVLLGLVLGFVLASRLVLPRASELKRAGPRRRASPEGCRSGQAAASQAGGARG
DARGAQLWPPGSDPDGGPRDRNFLFVGVMATAQKYLQTRAVAAYRTWSKTIPGKVQFFSSEGSD
TSVPIPVVPLRGVDDSYPPQKKSEFMMLKYMHDHYLDKYEFMRADDDVYIKGDRLNFLRSLN
SSEPLFLGQTGLGTTEEMGKLALEPGENFCMGGPGVIMSREVLRRMVPHIGHKCLREMYTTHE
VEVGRCVRRFAGVQCVWSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPNKNPPYQYRL
HSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQLGIPPSFMRFPQPRQEEILEWEL
LTGKYLYSAVDGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQGYRRVNP
MYGAEYILDLLLLYKKHKGKKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKRINQESGSL
SFLSNLKKLVFPQLPGSKSEHKEPKDKKINILIPLSGRFDMFVRFMGNFEKTCLIPNQNVKL
VLLFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQFNESLLFFC
DVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSDNHFAFTQKTGFWRNYGF
GITCIYKGD LVRVGGFDVSIQGWGLEDDVLFNKVVQAGLKTFRSQEVGVVHVHHPVFCDPNLD
PKQYKMCLGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA
```

Signal peptide:

amino acids 1-23

316/615

FIGURE 313

GGCCGGACGCCTCCGCGTTACGGGATGAATTAACGGCGGGTTCCGCACGGAGGTTGTGACCCC
TACGGAGCCCCAGCTTGCCACGCACCCCACTCGGCGTCGCGCGGCGTGCCCTGCTTGTCACA
GGTGGGAGGCTGGAACATCAGGCTGAAAAACAGAGTGGGTACTCTCTTCTGGGAAGCTGGCA
ACAAATGGATGATGTGATATATGCATTCCAGGGGAAGGGAAATTGTGGTGCTTCTGAACCCAT
GGTCAATTAACGAGGCAGTTTCTAGCTACTGCACGTACTTCATAAAGCAGGACTCTAAAAGCT
TTGGAATCATGGTGTGATGGAAAGGGATTTACTTTATACTGACTCTGTTTTGGGGAAGCTTTT
TTGGAAGCATTTCATGCTGAGTCCCTTTTTACCTTTGATGTTTGTAACCCATCTTGGTATC
GCTGGATCAACAACCGCCTTGTGGCAACATGGCTCACCTACCTGTGGCATTATTGGAGACCA
TGTTTGGTGTAAGAGTGATTATAACTGGGGATGCATTTGTTCTGGAGAAAGAAGTGTCATTA
TCATGAACCATCGGACAAGAATGGACTGGATGTTCTGTGGAATTGCCTGATGCGATATAGCT
ACCTCAGATTGGAGAAAAATTTGCCTCAAAGCGAGTCTCAAAGGTGTTCTGGATTGTGGTGGG
CCATGCAGGCTGCTGCCTATATCTTCATTCATAGGAAATGGAAGGATGACAAGAGCCATTTTCG
AAGACATGATTGATTACTTTTGTGATATTCACGAACCACTTCAACTCCTCATATCCCAGAAG
GGACTGATCTCACAGAAAACAGCAAGTCTCGAAGTAATGCATTTGCTGAAAAAATGGACTTC
AGAAATATGAATATGTTTTACATCCAAGAACTACAGGCTTTACTTTTGTGGTAGACCGTCTAA
GAGAAGGTAAGAACCTTGATGCTGTCCATGATATCACTGTGGCGTATCCTCACAACATTCCTC
AATCAGAGAAGCACCTCCTCCAAGGAGACTTTCCAGGGAAATCCACTTTCACGTCCACCGGT
ATCCAATAGACACCCTCCCCACATCCAAGGAGGACCTTCAACTCTGGTGCCACAAACGGTGGG
AAGAGAAAGAAGAGAGGCTGCGTTCCCTTCTATCAAGGGGAGAAGAATTTTTATTTTACCGGAC
AGAGTGTCATTCCACCTTGCAAGTCTGAACTCAGGGTCCTTGTGGTCAAATTGCTCTCTATAC
TGTATTGGACCCTGTTTACGCCCTGCAATGTGCCTACTCATATATTTGTACAGTCTTGTTAAGT
GGTATTTTATAATCACCATTGTAATCTTTGTGCTGCAAGAGAGAATATTTGGTGGACTGGAGA
TCATAGAACTTGATGTTACCGACTTTTACACAAACAGCCACATTTAAATTCAAAGAAAAATG
AGTAAAGATTATAAGGTTTGCCATGTGAAAACCTAGAGCATATTTTGGAAATGTTCTAAACCTT
TCTAAGCTCAGATGCATTTTGTGATGACTATGTGCAATATTTCTTACTGCCATCATTATTTGT
TAAAGATATTTTGCACCTAATTTTGTGGGAAAAATATTGCTACAATTTTTTTTAAATCTCTGAA
TGTAATTTTCGATACTGTGTACATAGCAGGGAGTGATCGGGGTGAAATAACTTGGGCCAGAATA
TTATTAAACAATCATCAGGCTTTTAAA

317/615

FIGURE 314

MHSRGREIVVLLNPWSINEAVSSYCTYFIKQDSKSGIMVSWKGIYFILTLFWGSFFGSI FML
SPFLPLMFVNPSWYRWINNRLVATWLTLPVALLETMFGVKVIITGDAFVPGERSVIIMNHRTR
MDWMFLWNCLMRYSYLRLEKICLKASLKGVPFGFGWAMQAAAYIFIHRKWKDDKSHFEDMIDYF
CDIHEPLQLLIFPEGTDLTENSKSRSNFAEKNGLQKYEYVLHPRTTGFTFVVDRLREGKNLD
AVHDITVAYPHNIPQSEKHLQGDFFPREIHFHVHRYPIDTLPTSKEDLQLWCHKRWEEKEERL
RSFYQGEKNFYFTGQSVIPPCKSELRVLVVKLLSILYWTLFSPAMCLLIYLYSLVKWYFIITI
VIFVLQERIFGGLEIIEIACYRLLHKOPHLNSKKNE

Important features of the protein:

Signal peptide:

amino acids 1-22

Transmembrane domains:

amino acids 44-63, 90-108, 354-377

318/615

FIGURE 315

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTGA
CCTCCAAATCATCCATCCACCCCTGCTGTCTGTTTTCATAGTGTGAGATCAACCCACAGG
AATATCCATGGCTTTTGTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTGAGGACAGTG
GCAAGTCACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCTCCTG
CTCCCTCTTTCCTGAGACCACTGCAGAGGCTATGGAAGTGCAGTTCTTCAGGAATCAGTTCCA
TGCTGTGGTCCACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACAGTATCG
AGGGAGAAGTGAAGTTTGTGAAGGACTCCATTGCAGGGGGGCGTGTCTCTTAAGGCTAAAAA
CATCACTCCCTCGGACATCGGCCTGTATGGGTGCTGGTTTCAGTTCCCAGATTTACGATGAGGA
GGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCCTCTCATTTCCATCGTGGGATA
TGTTGACGGAGGTATCCAGTTACTCTGCCTGTCTCAGGCTGGTTCCCCCAGCCACAGCCAA
GTGGAAAGTCCACAAGGACAGGATTTGTCTTCAGACTCCAGAGCAAATGCAGATGGGTACAG
CCTGTATGATGTGGAGATCTCCATTATAGTCCAGGAAAATGCTGGGAGCATATTGTGTTCCAT
CCACCTTGCTGAGCAGAGTCATGAGGTGGAATCCAAGGTATTGATAGGAGAGACGTTTTTCCA
GCCCTCACCTTGGCGCCTGGCTTCTATTTTACTCGGGTTACTCTGTGGTGGCCTGTGTGGTGT
TGTCATGGGGATGATAATTGTTTTCTTCAAATCCAAAGGGAAAATCCAGGCGGAAGTGGACTG
GAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGGAAACACGCAGTGGAGGTGACTCT
GGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAAGTGAACCCATAGAAA
AGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCTTCTCA
GGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGGACAAAATGTAGGGTGGTATGT
GGGAGTGTGTCGGGATGACGTAGACAGGGGGAAGAACAATGTGACTTTGTCTCCCAACAATGG
GTATTGGGTCTCAGACTGACAACAGAACATTTGTATTTACATTCAATCCCCATTTTATCAG
CCTCCCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTTCCTGGACTATGAGGGTGGGACCAT
CTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACCCTGCTGACATGTCAGTTTGAAGG
CTTGTTGAGACCCTATATCCAGCATGCGATGTATGACGAGGAAAAGGGGACTCCCATATTCAT
ATGTCCAGTGTCTGGGGATGAGACAGAGAAGACCCTGCTTAAAGGGCCCCACACCACAGACC
CAGACACAGCCAAGGGAGAGTGTCTCCCGACAGGTGGCCCCAGCTTCCTCTCCGGAGCCTGCGC
ACAGAGAGTCACGCCCCCCTCTCCTTTAGGGAGCTGAGGTTCTTCTGCCCTGAGCCCTGCA
GCAGCGGCAGTCACAGCTTCCAGATGAGGGGGGATTGGCCTGACCCTGTGGGAGTCAGAAGCC
ATGGCTGCCCTGAAGTGGGGACGGAATAGACTCACATTAGGTTTAGTTTGTGAAAAGTCCATC
CAGCTAAGCGATCTTGAACAAGTCACAACCTCCCAGGCTCCTCATTTGCTAGTCACGGACAGT
GATTCCTGCCTCACAGGTGAAGATTAAAGAGACAACGAATGTGAATCATGCTTGAGGTTTGA
GGGCACAGTGTGCTAATGATGTGTTTTATATTATACATTTTCCCACCATAAACTCTGTTT
GCTTATTCCACATTAATTTACTTTTCTCTATACCAAATCACCCATGGAATAGTTATTGAACAC
CTGCTTTGTGAGGCTCAAAGAATAAAGAGGAGGTAGGATTTTCACTGATTCTATAAGCCCAG
CATTACCTGATACCAAAACCAGGCAAAGAAAACAGAAGAAGAGGAAGGAAAAGTACAGGTCCA
TATCCCTCATTAACACAGACACAAAATTTCTAAATAAAATTTTAAACAAATTAAGTAAACAAT
ATATTTAAAGATGATATATACTACTCAGTGTGGTTTGTCCCACAAATGCAGAGTTGGTTTAA
TATTTAAATATCAACCAGTGTAAATTCAGCACATTAATAAAGTAAAAAAGAAAACCATAAAAA
AAAAA

319/615

FIGURE 316

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866
><subunit 1 of 1, 466 aa, 1 stop
><MW: 52279, pI: 6.16, NX(S/T): 2
MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHAV
VHLYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEEAT
WELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGYSLY
DVEISIIVQENAGSILCSIHAEQSHEVESKVLIGETFFQSPWRLASILLGLLCGALCGVVM
GMIIVFFKSKGKIQAELDWRKKGQAELRDARKHAVEVTLDPEAHKLCVSDLKTVTHRKAP
QEVPHSEKRFTRKSVVASQGFQAGRHYWEVDVGQNVGWYGVCRDDVDRGKNNVTLSPNNGYW
VLRLTTEHLYFTFNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLLTCQFEGLL
RPYIQHAMYDEEKGTPIFICPVSWG

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

320/615

FIGURE 317

GCACCTGCGACCACCGTGAGCAGTCATGGCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTTC
TGGGCTTGTCCTGGCTCTGTCGCTGCTGCTGCCCCAAGGCCTTCCTGTCCCGCGGGAAGCGGCA
GGAGCCGCCGCCGACACCTGAAGGAAAATTGGGCCGATTTCCACCTATGATGCATCATCACCA
GGCACCCCTCAGATGGCCAGACTCCTGGGGCTCGTTTCCAGAGGTCTCACCTTGCCGAGGCATT
TGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGGAAGAGGTCTGATGGG
GCAGATTATTCCAATCTACGGTTTTGGGATTTTTTTATATATACTGTACATTCTATTTAAGGT
AAGTAGAATCATCCTAATCATATTACATCAATTGAAAATCTAATATGGCGATAAAAATCATTGT
CTACATTAAAACTTCTTATAGTTCATAAAATTATTTCAAATCCATCATCTCTTTAAATCCTGC
CTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTTCAAGTTTACATAAGAATGTTTACTCAA
TGTTTAAGTGTTTTGCCCCAAAATTCACAATAACAAGGCAGAACTAGGACTTGAACATGGAT
CTTTTGGTTCTTAATCCAGTGAGTGATACAATTCAATGCACTCCCCTGCCA

321/615

FIGURE 318

MAYSTVQRVALASGLVLALSLLLPAFLSRGKRQEPPTPEGKLGFRPPMMHHHQAPSDGQTP
GARFQRSHLAEAFKAKGSGGGAGGGGSGRGLMGQIIPYGFIFLYILYILFKVSRIILIILHQ

322/615

FIGURE 319

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTAG
GAAAAGAGTTTGTGGGAACCTGGGTTATCGGCCTCGTCATCTTCATATCCCTGATTGTCCT
GGCAGTGTGCATTGGACTCACTGTTTATTATGTGAGATATAATCAAAGAAGACCTACAATTA
CTATAGCACATTGTCATTTACAACCTGACAACTATATGCTGAGTTTGGCAGAGAGGCTTCTAA
CAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGAAAAATGCATTTTATAAATCTCC
ATTAAGGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTCAGTCAACAGAAGCATGGAGTGTT
GGCTCATATGCTGTTGATTTGTAGATTTCACTCTACTGAGGATCCTGAAACTGTAGATAAAAT
TGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTAGATCCTCA
CTCAGTTAAAATTAATAAATCAACAAGACAGAAACAGACAGCTATCTAAACCATTGCTGCGG
AACACGAAGAAGTAAACTCTAGGTGAGAGTCTCAGGATCGTTGGTGGGACAGAAGTAGAAGA
GGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGTGGAGCAACCTT
AATTAATGCCACATGGCTTGTGAGTGCTGCTCACTGTTTTACAACATATAAGAACCCTGCCAG
ATGGACTGCTTCCTTTGGAGTAACAATAAAACCTTCGAAAATGAAACGGGGTCTCCGGAGAAT
AATTGTCCATGAAAAATACAAACACCCATCACATGACTATGATATTTCTCTTGACAGAGCTTTC
TAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCTCCCTGATGCATCCTATGAGTT
TCAACCAGGTGATGTGATGTTGTGACAGGATTGGAGCACTGAAAAATGATGGTTACAGTCA
AAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAACTTGCAATGAACCTCAAGC
TTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTTAGAAGGAAAAACAGATGC
ATGCCAGGGTGACTCTGGAGGACCACTGGTTAGTTCAGATGCTAGAGATATCTGGTACCTTGC
TGGAATAGTGAGCTGGGGAGATGAATGTGCGAAACCAACAAGCCTGGTGTTTATACTAGAGT
TACGGCCTTGCGGGACTGGATTACTTCAAAAACCTGGTATCTAAGAGACAAAAGCCTCATGGAA
CAGATAACATTTTTTTTTGTTTTTGGGTGTGGAGGCCATTTTGTAGAGATACAGAATTGGAGA
AGACTTGCAAAACAGCTAGATTGACTGATCTCAATAAACTGTTTGCTTGATGCATGTATTTT
CTTCCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTGCCAGATCAACTCTGTCATCTGTGA
GCAATAGTTGAAACTTTATGTACATAGAGAAATAGATAATAACAATATTACATTACAGCCTGTA
TTCATTTGTTCTCTAGAAGTTTTGTGAGAATTTTGACTTGTTGACATAAATTTGTAATGCATA
TATACAATTTGAAGCACTCCTTTTCTTCAGTTCCTCAGCTCCTCTCATTTTCAGCAAATATCCA
TTTTCAAGGTGCAGAACAAAGGAGTGAAAGAAAATATAAGAAGAAAAAATCCCTACATTTTA
TTGGCACAGAAAAGTATTAGGTGTTTTTCTTAGTGGAATATTAGAAATGATCATATTCATTAT
GAAAGGTCAAGCAAAGACAGCAGAATACCAATCACTTCATCATTTAGGAAGTATGGGAACTAA
GTAAAGGAAGTCCAGAAAGAAGCCAAGATATATCCTTATTTTCATTTCCAAACAACTACTATG
ATAAATGTGAAGAAGATTCTGTTTTTTGTGACCTATAATAATTATACAACTTCATGCAATG
TACTTGTTCTAAGCAAATTAAAGCAAATATTTATTTAACATTGTTACTGAGGATGTCAACATA
TAACAATAAAATATAAATCACCCA

323/615

FIGURE 320

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871
><subunit 1 of 1, 423 aa, 1 stop
><MW: 47696, pI: 8.96, NX(S/T): 3
MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTNYNSTLSFTTDK
LYAEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICRFH
STEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTLGQS
LRIVGGTEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFITYKNPARWTASFGVTIK
PSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSVPYPYTNVHRVCLPDASYEFQPGDVMFVTG
FGALKNDGYSONHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGDSSGGPLV
SSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI
```

Transmembrane domain:

amino acids 21-40 (type II)

324/615

FIGURE 321

CCGGGCTCCTGGGTGAGGCCGGCAAGTTTGGAGCGTGGTCAGACAATAGGGGCGTGGCTACGG
CTCGCGGAGCGCAACCAACGCTCTAGACCAGACCTGGGCTCGAGACCATAACTGTTTGGCTTT
AACAGTACGTGGGCGGCCGGAATCCGGGAGTCCGGTGACCCGGGCTGTGGTCTAGCATAAAGG
CGGAGCCCAGAAGAAGGGGCGGGGTATGGGAGAAGCCTCCCCACCTGCCCCCGCAAGGCGGCA
TCTGCTGGTCCTGCTGCTGCTCCTCTTACCCTGGTGATCCCCTCCGCTGCAGCTCCTATCCA
TGATGCTGACGCCCAAGAGAGCTCCTTGGGTCTCACAGGCCTCCAGAGCCTACTCCAAGGCTT
CAGCCGACTTTTCTGAAAGGTAACCTGCTTCGGGGCATAGACAGCTTATTCTCTGCCCCCAT
GGACTTCCGGGGCCTCCCTGGGAACCTACCACAAAGAGGAGAACCAGGAGCACCAGCTGGGGAA
CAACACCCCTCTCCAGCCACCTCCAGATCGACAAGATGACCGACAACAAGACAGGAGAGGTGCT
GATCTCCGAGAATGTGGTGGCATCCATTCAACCAGCGGAGGGGAGCTTCGAGGGTGATTTGAA
GGTACCCAGGATGGAGGAGAAGGAGGCCCTGGTACCCATCCAGAAGGCCACGGACAGCTTCCAC
ACAGAACTCCATCCCCGGGTGGCCTTCTGGATCATTAAAGCTGCCACGGCGGAGGTCCCACCAG
GATGCCCTGGAGGGCGGCCACTGGCTCAGCGAGAAGCGACACCGCCTGCAGGCCATCCGGGAT
GGACTCCGCAAGGGGACCCACAAGGACGTCCTAGAAGAGGGGACCGAGAGCTCCTCCCACTCC
AGGCTGTCCCCCGAAAGACCCACTTACTGTACATCCTCAGGCCCTCTCGGCAGCTGTAGGGG
TGGGGACCGGGGAGCACCTGCCTGTAGCCCCATCAGACCCTGCCCCAAGCACCATATGGAAA
TAAAGTTCTTTCTTACATCTAAAAA

325/615

FIGURE 322

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68879
><subunit 1 of 1, 242 aa, 1 stop
><MW: 27007, pI: 8.68, NX(S/T): .2
MGEASPPAPARRHLLVLLLLLSTLVIPSAAAPIHDADAQESSLGLTGLQSLQGF SRLFL
KGNLLRGIDSLFSAPMDFRGLPGNYHKEENQEHQLGNNTLSSHLQIDKMTDNKTGEVLIS
ENVVASIQPAEGSFEGDLKVPRMEEKEALVPIQKATDSFHTELHPRVAFWI IKLPRRRSH
QDALEGGHWLSEKRHRLQAIRDGLRKGTHKDVLEEGTESSSHSRLSPRKTHLLYILRPSR
QL

Important features of the protein:**Signal peptide:**

Amino acids 1-30

N-glycosylation sites:

Amino acids 97-101;112-116

N-myristoylation sites:

Amino acids 80-86;132-138;203-209;216-222

326/615

FIGURE 323

AGAGAAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCCC
TGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCACC GGCC
CAGCGCCGACGATCGCTGCCGTTTTTGCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGCTTC
TCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGCTGCGCTGCCTGCTCTAC
GCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGATGAGG
GACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTCATTTTG
ACTTACTTTCTGTGGTTCATCCGGTCATGATTGCTGTTTGTCTGTTTCTTATCATTGTGGGG
ATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTGCTTCTTGCATGGTACTTTGGAAGT
TTGCTTGTCAATTTTCTGTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAGGAACTTATG
GTTCCAGTACAATGGTCAGATATGGTCACTTTGAAAGCCAGGATGACAAATTATGGATTACCT
AGATATCGGTGGCTTACTCATGCTTGGAAATTTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTA
GTATATTTCACTGACTGGTTGGAAATGACAGAGATGGACTGGCCCCCAGATTCCCTGCTGTGTT
AGAGAATTTCCAGGATGTTCCAAACAGGCCACCAGGAAGATCTCAGTGACCTTTATCAAGAG
GGTTGTGGGAAGAAAATGTATTCCTTTTTTGAGAGGAACCAACAACCTGCAGGTGCTGAGGTTT
CTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGG
GCTCTGTATTATGATAGAAGGGAGCCTGGGACAGACCAATGATGTCCTTGAAGAATGACAAC
TCTCAGCACCTGTCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAA
CACACATCCATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATG
TCACAGAAGAAAACCAAACTTGTTTTATTGGACTTGTGAATTTTGTAGTACATACTATGTG
TTTCAGAAATATGTAGAAATAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA
TGCTTTAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGATGC
CCTTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTACTGAAC
ACAGTTATGTTTTGAGGCAGCATGGTTGATTAGCATTTCCGCATCCATGCAAACGAGTCACA
TATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGTATATAAAGTACT
AATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTACTCAGCGATCTATTC
TTCTGATGCTAAATAAATTATATATCAGAAAACCTTTCAATATTGGTGACTACCTAAATGTGAT
TTTTGCTGGTTACTAAATATTCTTACCCTTAAAAGAGCAAGCTAACACATTGTCTTAAGCT
GATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTGTATAATTCAAGTCGATTTCAAGTTCT
GATAATGTTAAGAATAACCATTATGAAAAGGAAAATTTGTCCTGTATAGCATCATTATTTTAA
GCCTTTCTGTTAATAAAGCTTTACTATTCTGTCCTGGGCTTATATTACACATATAACTGTTA
TTTAAATACTTAACCACTAATTTTGAAAATTACCAGTGTGATACATAGGAATCATTATTCAGA
ATGTAGTCTGGTCTTTAGGAAGTATTAATAAGAAAATTTGCACATAACTTAGTTGATTCAGAA
AGGACTTGATGCTGTTTTTCTCCCAATGAAGACTCTTTTGGACACTAAACACTTTTTAAAA
AGCTTATCTTTGCCTTCTCCAAACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGA
AAATAGTGTCTTTTTCTCCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAG
AGATTCTTTGTTTTATTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTT
TTTACAAGAGTATAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTAT
TTTGTATTATTTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAG
TAA

327/615

FIGURE 324

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880

><subunit 1 of 1, 305 aa, 1 stop

><MW: 35383, pI: 5.99, NX(S/T): 0

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPVV
HPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQWS
DMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREFPGC
SKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWALYYDR
REPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

328/615

FIGURE 325

AGCAGTGCATTGCTGGAGCGAGGAGAAGCTCACGAATCAGCTGCAGGTCTCTGTTTTGAAAAA
GCAGAGATACAGAGGCAGAGGAAAAGGGTGGACTCCTATGTGACCTGTTCTTAGAGCAAGACA
ATCACCATCTGAATTCAGAAAGCCCTGTTTCATGGTTGGGGATATTTTCTCGACTGCATGGAAT
CAGAAAGAAGCAAAAGGATGGGAAATGCCTGCATTCCCCTGAAAAGAATTGCTTATTTTCCTAT
GTCTCTTATCTGCGCTTTTGCTGACTGAGGGGAAGAAAACCAGCGAAGCCAAAATGCCCTGCCG
TGTGTACTTGTACCAAAGATAATGCTTTATGTGAGAATGCCAGATCCATTCCACGCACCGTTC
CTCCTGATGTTATCTCATTATCCTTTGTGAGATCTGGTTTTACTGAAATCTCAGAAGGGAGTT
TTTTATTACGCCATCGCTGCAGCTCTTGTTATTCACATCGAACTCCTTTGATGTGATCAGTG
ATGATGCTTTTATTGGTCTTCCACATCTAGAGTATTTATTCATAGAAAACAACAACATCAAGT
CAATTTCAAGACATACTTTCCGGGGACTAAAGTCATTAATTCACCTTGAGCCTTGCAAACAACA
ATCTCCAGACACTCCCAAAAGATATTTTCAAAGGCCTGGATTCTTTAACAATGTGGACCTGA
GGGGTAATTCATTTAATTGTGACTGTAACTGAAATGGCTAGTGGAATGGCTTGCCACACCA
ATGCAACTGTTGAAGACATCTACTGCGAAGGCCCCCAGAATACAAGAAGCGCAAAATCAATA
GTCTCTCCTCGAAGGATTTGATTGCATCATTACAGAATTTGCAAAGTCTCAAGACCTGCCTT
ATCAATCATTTGTCCATAGACACTTTTTCTTATTTGAATGATGAGTATGTAGTCATCGCTCAGC
CTTTTACTGGAATATGCATTTTCCTTGAATGGGACCATGTGGAAAAGACCTTCCGGAATTATG
ACAACATTACAGGCACATCCACTGTAGTATGCAAGCCTATAGTCATTGAACTCAGCTCTATG
TTATTGTGGCCAGCTGTTTGGTGGCTCTCACATCTATAAGCGAGACAGTTTTGCAATAAAT
TCATAAAAAATCCAGGATATTGAAATTCAAAATCCGAAAACCCAATGACATTGAAACATTCA
AGATTGAAAACAACTGGTACTTTGTTGTTGCTGACAGTTCAAAAGCTGGTTTTACTACCATTTAC
AAATGGAACGGAAACGGATTCTACTCCCATCAATCCTTACACGCGTGGTACAGGGACACTGAT
GTGGAATATCTAGAAATAGTCAGAACACCTCAGACACTCAGAACGCCTCATTTAATTCTGTCT
AGTAGTTCCCAGCGTCTGTAAATTTATCAGTGGAAACAAAGCAACACAATTTACTAACC
ACTGACATTCCTAACATGGAGGATGTGTACGCAGTGAAGCACTTCTCAGTGAAAGGGGACGTG
TACATTTGCTTGACAAGATTCATTGGTGATTCCAAAGTCATGAAATGGGGAGGCTCCTCGTTC
CAGGATATTCAGAGGATGCCATCGCGAGGATCCATGGTGTTCAGCCTCTTCAAATAAATAAT
TACCAATATGCAATTCCTGGAAGTGATTACTCCTTTACTCAAGTGTATAACTGGGATGCAGAG
AAAGCCAAATTTGTGAAATTTTCAAGGAATTAAATGTTTCAAGGCACCAAGATCATTACACATGTG
TCCATTAATAAGCGTAATTTCTTTTTGCTTCCAGTTTTAAGGGAAATACACAGATTTACAAA
CATGTTCATAGTTGACTTAAGCGCATGAGACACCAAAATCTGTGGCTGCCATCAGAAATTTCT
ACAGTACATGACCCGGATGAACTCAATGCATGATGACTCTTCTTATCACACTTGCAAATGAAT
GCCTTTCAAACATTGAGACTGCTAGAACCAAGCACTACCAGTATCTCCATCCTTAAGTGTCCA
GTCCAGTGATGTGGGAAGTTACCTTTTATAAGACAAAATTTAATTGTGTAAGTGTCTTTGCA
GTGAAGATGTGTAATAAGCGTTTAAATGGTATCTGTTACTCCAAAAGAAATATTAATATGTA
CTTTTCCATTTATTTATTCATGTGTACAGAAACAACTGCCAAATAAAATGTTTACATTTTCTT
TCATA

329/615

FIGURE 326

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68882
><subunit 1 of 1, 557 aa, 1 stop
><MW: 63818, pI: 8.61, NX(S/T): 3
MESERSKRMGNACIPLKRIAYFLCLLSALLLTEGKKPAKPKCPAVCTCTKDNALCENARS
IPRTVPPDVISLSFVRSGFTEISEGSFLFTPSLQLLLFSTNSFDVISDDAFIGLPHLEYL
FIENNNIKSISRHTFRGLKSLIHLNANNLQTLPKDIFKGLDSLTVNVDLRGNSFNCDCK
LKWLVEWLGHNTATVEDIYCEGPPEYKKRKINSLSSKDFDCIITEFAKSQDLPLYQSLSID
TFSYLNDEYVVIAQPFTGKCIFLEWDHVEKTERNYDNITGTSTVVCKPIVIETQLYVIVA
QLFGGSHIYKRDSFANKFIKIQDIEILKIRKPNDIETFKIENNWFVVDSSKAGFTTIY
KWNGNGFYSHQSLHAWYRDTDVEYLEIVRTPQTLRTPHLILSSSSQRPVIYQWNKATQLF
TNQTDIPNMEDVYAVKHFSVKGDVYICLTRFIGDSKVMKWGGSSFQDIQRMPSRGSMVFQ
PLQINNYQYAILGSDYSFTQVYNWDAEKAKFVKFQELNVQAPRSFTHVSINKRNFLEASS
FKGNTQIYKHVIVDLA
```

Important features of the protein:**Signal peptide:**

Amino acids 1-34

Transmembrane domain:

Amino acids 281-306

N-glycosylation sites:

Amino acids 192-196;277-281;422-426

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 310-314

Tyrosine kinase phosphorylation sites:

Amino acids 228-235;378-385

N-myristoylation sites:

Amino acids 172-178;493-499

Amidation site:

Amino acids 33-37

330/615

FIGURE 327

CCAAGGCCAGAGCTGTGGACACCTTATCCCACTCATCCTCATCCTCTTCCTCTGATAAAGCCC
CTACCAGTGCTGATAAAGTCTTTCTCGTGAGAGCCTAGAGGCCTTAAAAAAAAAAGTGCTTGA
AAGAGAAGGGGACAAAAGGAACACCAGTATTAAGAGGATTTTCCAGTGTTTCTGGCAGTTGGTC
CAGAAGGATGCCTCCATTTCCTGCTTCTCACCTGCCTCTTCATCACAGGCACCTCCGTGTCACC
CGTGGCCCTAGATCCTTGTTCTGCTTACATCAGCCTGAATGAGCCCTGGAGGAACACTGACCA
CCAGTTGGATGAGTCTCAAGGTCCTCCTCTATGTGACAACCATGTGAATGGGGAGTGGTACCA
CTTCACGGGCATGGCGGGAGATGCCATGCCTACCTTCTGCATACCAGAAAACCACTGTGGAAC
CCACGCACCTGTCTGGCTCAATGGCAGCCACCCCTAGAAAGGCGACGGCATTGTGCAACGCCA
GGCTTGTGCCAGCTTCAATGGGAACCTGCTGTCTCTGGAACACCACGGTGGAAAGTCAAGGCTTG
CCCTGGAGGCTACTATGTGTATCGTCTGACCAAGCCCAGCGTCTGCTTCCACGTCTACTGTGG
TCATTTTTATGACATCTGCGACGAGGACTGCCATGGCAGCTGCTCAGATACCAGCGAGTGCAC
ATGCGCTCCAGGAACCTGTGCTAGGCCCTGACAGGCAGACATGCTTTGATGAAAATGAATGTGA
GCAAAACAACGGTGGCTGCAGTGAGATCTGTGTGAACCTCAAAAACCTACCCTGTGAGTG
TGGGGTTGGCCGTGTGCTAAGAAGTGATGGCAAGACTTGTGAAGACGTTGAAGGATGCCACAA
TAACAATGGTGGCTGCAGCCACTCTTGCCTTGGATCTGAGAAAGGCTACCAGTGTGAATGTCC
CCGGGGCCTGGTGTCTGTCTGAGGATAACCACACTTGCCAAGTCCCTGTGTTGTGCAAATCAAA
TGCCATTGAAGTGAACATCCCCAGGGAGCTGGTTGGTGGCCTGGAGCTCTTCCTGACCAACAC
CTCCTGCCGAGGAGTGTCCAACGGCACCCATGTCAACATCCTCTTCTCTCTCAAGACATGTGG
TACAGTGGTTCGATGTGGTGAATGACAAGATTGTGGCCAGCAACCTCGTGACAGGTCTACCCAA
GCAGACCCCGGGGAGCAGCGGGGACTTCATCATCCGAACCAGCAAGCTGCTGATCCCGGTGAC
CTGCGAGTTTCCACGCCTGTACACCATTCTGAAGGATACGTTCCCAACCTTCGAAACTCCCC
ACTGGAATCATGAGCCGAAATCATGGGATCTTCCCATTCACTCTGGAGATCTTCAAGGACAA
TGAGTTTGAAGAGCCTTACCGGGAAGCTCTGCCCACCCCTCAAGCTTCGTGACTCCCTCTACTT
TGGCATTGAGCCCGTGGTGCACGTGAGCGGCTTGGAAGCTTGGTGGAGAGCTGCTTTGCCAC
CCCCACCTCCAAGATCGACGAGGTCTTGAATACTACCTCATCCGGGATGGCTGTGTTTCAGA
TGACTCGGTAAAGCAGTACACATCCCGGGATCACCTAGCAAAGCACTTCCAGGTCCCTGTCTT
CAAGTTTGTGGGCAAAGACCACAAGGAAGTGTTTCTGCACTGCCGGGTCTTGTCTGTGGAGT
GTTGGACGAGCGTTCCCGCTGTGCCCAGGGTTGCCACCGGCGAATGCGTCGTGGGGCAGGAGG
AGAGGACTCAGCCGGTCTACAGGGCCAGACGCTAACAGGCGGCCCGATCCGCATCGACTGGGA
GGACTAGTTCGTAGCCATACCTCGAGTCCCTGCATTGGACGGCTCTGCTCTTTGGAGCTTCTC
CCCCACCGCCCTCTAAGAACATCTGCCAACAGCTGGGTTTCAGACTTCACACTGTGAGTTCAG
ACTCCCAGCACCAACTCACTCTGATTCTGGTCCATTCACTGGGCACAGGTCACAGCACTGCTG
AACAATGTGGCCTGGGTGGGGTTTCATCTTTCTAGGGTTGAAAATAAACTGTCCACCCAGAA
AGACACTCACCCATTTCCCTCATTTCTTTCCTACACTTAAATACCTCGTGTATGGTGCAATC
TACTGAAATTATGACTTAAATACCCAATGACTCCTTAAATATGTAAATTATAGTTATACCTT
GAAATTTCAATTCAAATGCAGACTAATTATAGGGAATTTGGAAGTGTATCAATAAACAGTAT
ATAATTTT

331/615

FIGURE 328

MPPFLLLTCLFITGTSVSPVALDPCSAYISLNEPWRNTDQHQLDESQGPPLCDNHVNGEWYHFT
GMAGDAMPTFCIPENHCGTHAPVWLNGSHPLEGDGIVQRQACASFNGNCCLWNTTVEVKACPG
GYYVYRLTKPSVCFHVYCGHFYDICDEDEDCHGSCSDTSECTCAPGTVLGPDRQTCFDENECEQN
NGGCSEICVNLKNSYRCECGVGRVLRSDGKTCEDVEGCHNNNGGCSHSCLGSEKGYQCECPRG
LVLSEDNHTCQVPVLCKSNAIEVNI PRELVGGLELFLTNTSCRGVSNNGTHVNILFSLKTCGTV
VDVVNDKIVASNLVTGLPKQTPGSSGDFIIRTSKLLIPVTCEFPRLYTISEGYVPNLRNSPLE
IMSRNHGIFPFTLEIFKDNEFEOPYREALPTLKLRLDSLYFGIEPVVHVSGLESLVESCFATPT
SKIDEVLKYYLIRDGCVSDDSVKQYTSRDHLAKHFQVPVFKFVGKDHKEVFLHCRVLVCGVLD
ERSRCAQGCCHRRMRRGAGGEDSAGLQGQTLTGGPIDWED

Important features of the protein:**Signal peptide:**

amino acids 1-16

N-glycosylation sites.

amino acids 89-93, 116-120, 259-263, 291-295, 299-303

Tyrosine kinase phosphorylation sites.

amino acids 411-418, 443-451

N-myristoylation sites.amino acids 226-232, 233-239, 240-246, 252-258, 296-302, 300-306,
522-528, 531-537**Aspartic acid and asparagine hydroxylation site.**

amino acids 197-209

ZP domain proteins.

amino acids 431-457

Calcium-binding EGF-like proteins.

amino acids 191-212, 232-253

332/615

FIGURE 329

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCCT
GCACTCGGGCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGACC
TGTGTGGGGAGGCCCTCCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAGACC
GGGAGGATCACAGAGCCAGCATGTTACAGGATCCTGACAGTGATCAACCTCTGAACAGCCTCG
ATGTCAAACCCCTGCGCAAACCCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGGATCCCCA
TCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTTGTGGTTGTCTCATCAAGGTGATTC
TGGATAAATACTACTTCTCTGCGGGCAGCCTCTCCACTTCATCCCGAGGAAGCAGCTGTGTG
ACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTCCCCGAAG
GGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTCGGCCA
CAGGGAAGTGGTTCTCTGCCTGTTTTGACAACCTTCACAGAAGCTCTCGCTGAGACAGCCTGTA
GGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGATGTTGTTGAAA
TCACAGAAAACAGCCAGGAGCTTCGCATGCGGAACCTCAAGTGGGCCCTGTCTCTCAGGCCTCCC
TGGTCTCCCTGCACTGTCTTGCTGTGGGAAGAGCCTGAAGACCCCCGTGTGGTGGGTGGGG
AGGAGGCCTCTGTGGATTCTTGGCCTTGGCAGGTCAGCATCCAGTACGACAAACAGCACGTCT
GTGGAGGGAGCATCCTGGACCCCCACTGGGTCTCACGGCAGCCCACTGCTTCAGGAAACATA
CCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAACTGGGCAGCTTCCCATCCCTGG
CTGTGGCCAAGATCATCATCATTGAATTCACCCCATGTACCCCAAAGACAATGACATCGCCC
TCATGAAGCTGCAGTTCCCACTCACTTTCTCAGGCACAGTCAGGCCCATCTGTCTGCCCTTCT
TTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTTGGATGGGGCTTTACGAAGCAGA
ATGGAGGGAAGATGTCTGACATACTGCTGCAGGCGTCAGTCCAGGTCATTGACAGCACACGGT
GCAATGCAGACGATGCGTACCAGGGGAAGTACCGAGAAGATGATGTGTGCAGGCATCCCGG
AAGGGGTGTGGACACCTGCCAGGGTGACAGTGGTGGGCCCTGATGTACCAATCTGACCAGT
GGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCGGGGGCCCGAGCACCCAGGAGTAT
ACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTGTAATGCT
GCTGCCCCCTTTCAGTGCTGGGAGCCGCTTCCTTCTGCCCTGCCACCTGGGGATCCCCAA
AGTCAGACACAGAGCAAGAGTCCCCTTGGGTACACCCCTCTGCCACAGCCTCAGCATTTCTT
GGAGCAGCAAAGGGCCTCAATTCCTGTAAGAGACCCTCGCAGCCCAGAGGCGCCAGAGGAAG
TCAGCAGCCCTAGCTCGGCCACACTTGGTGCTCCAGCATCCCAGGGAGAGACACAGCCCACT
GAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAAGGAACCTTCCCACACTACTGAATGGAAGC
AGGCTGTCTTGTAAAAGCCCAGATCACTGTGGGCTGGAGAGGAGAAGGAAAGGGTCTGCGCCA
GCCCTGTCCGTCTTCACCCATCCCCAAGCCTACTAGAGCAAGAAACCAGTTGTAATATAAAAT
GCACTGCCCTACTGTTGGTATGACTACCGTTACCTACTGTTGTCATTGTTATTACAGCTATGG
CCACTATTATTAAAGAGCTGTGTAACATCTCTGGCAAAAAAAAAA

333/615

FIGURE 330

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47644, pI: 5.18, NX(S/T): 2
MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIIALLSLASIIIVVVLIKVILDKYYFL
CGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSA
CFDNFTEALAEACRQMGYSRAVEIGPDQDLDVVEITENSQELMRNSSGPGCLSGSLVSLHCL
ACGKSLKTPRVVGEEASVDSWPWQVSIQYDKQHVC GGSILDPHWVLTAAHCFRKHTDVFNWK
VRAGSDKLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTP
ATPLWIIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTCT
QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL
```

Transmembrane domain:
amino acids 32-53 (typeII)

334/615

FIGURE 331

AGTGGTTCGATGGGAAGGATCTTTCTCCAAGTGGTTCCTCTTGAGGGGAGCATTTCTGCTGGC
TCCAGGACTTTGGCCATCTATAAAGCTTGGCAATGAGAAATAAGAAAATTCTCAAGGAGGACG
AGCTCTTGAGTGAGACCCAACAAGCTGCTTTTACCAAATTGCAATGGAGCCTTTCGAAATCA
ATGTTCCAAAGCCCCAAGAGGAGAAATGGGGTGAACCTTCTCCCTAGCTGTGGTGGTCATCTACC
TGATCCTGCTCACCGCTGGCGCTGGGCTGCTGGTGGTCCAAGTTCTGAATCTGCAGGCGCGGC
TCCGGGTCTTGAGATGTATTTCTCAATGACACTCTGGCGGCTGAGGACAGCCCGTCCTTCT
CCTTGCTGCAGTCAGCACACCCTGGAGAACACCTGGCTCAGGGTGCATCGAGGCTGCAAGTCC
TGCAGGCCCAACTCACCTGGGTCCGCGTCAGCCATGAGCACTTGCTGCAGCGGGTAGACAACCT
TCACTCAGAACCCAGGGATGTTTCAAGATCAAAGGTGAACAAGGCGCCCCAGGTCTTCAAGGTC
ACAAGGGGGCCATGGGCATGCCTGGTGCCCTGGCCCGCCGGGACCACCTGCTGAGAAGGGAG
CCAAGGGGGCTATGGGACGAGATGGAGCAACAGGCCCCCTCGGGACCCCAAGGCCCCCGGGAG
TCAAGGGAGAGGCGGGCCTCCAAGGACCCCAAGGTGCTCCAGGGGAAGCAAGGAGCCACTGGCA
CCCCAGGACCCCAAGGAGAGAAGGGCAGCAAAGGCGATGGGGGTCTCATTGGCCCAAAGGGG
AAACTGGAATAAGGGAGAGAAAGGAGACCTGGGTCTCCAGGAAGCAAAGGGGACAGGGGCA
TGAAAGGAGATGCAGGGGTCTATGGGGCCTCCTGGAGCCCAGGGGAGTAAAGGTGACTTCGGGA
GGCCAGGCCCACCAGGTTTGGCTGGTTTTCTGGAGCTAAAGGAGATCAAGGACAACCTGGAC
TGCAGGGTGTTCGGGGCCCTCCTGGTGCAGTGGGACACCCAGGTGCCAAGGGTGAGCCTGGCA
GTGCTGGCTCCCCTGGGCGAGCAGGACTTCCAGGGAGCCCCGGGAGTCCAGGAGCCACAGGCC
TGAAAGGAAGCAAAGGGGACACAGGACTTCAAGGACAGCAAGGAAGAAAAGGAGAATCAGGAG
TTCCAGGCCCTGCAGGTGTGAAGGGAGAACAGGGGAGCCCAGGGCTGGCAGGTCCCAAGGGAG
CCCCTGGACAAGCTGGCCAGAAGGGAGACCAGGGAGTGAAAGGATCTTCTGGGGAGCAAGGAG
TAAAGGGAGAAAAGGTGAAAGAGGTGAAAACCTCAGTGTCCGTCAGGATTGTTCGGCAGTAGTA
ACCGAGGCCGGGCTGAAGTTTACTACAGTGGTACCTGGGGGACAATTTGCGATGACGAGTGGC
AAAATTCTGATGCCATTGTCTTCTGCCGCATGCTGGGTACTCCAAAGGAAGGGCCCTGTACA
AAGTGGGAGCTGGCACTGGGCAGATCTGGCTGGATAATGTTTCAAGTGTTCGGGGCACGGAGAGTA
CCCTGTGGAGCTGCACCAAGAATAGCTGGGGCCATCATGACTGCAGCCACGAGGAGGACGCAG
GCGTGGAGTGCAGCGTCTGACCCCGGAAACCCTTTCACTTCTCTGCTCCCGAGGTGTCTCGGG
CTCATATGTGGGAAGGCAGAGGATCTCTGAGGAGTCCCTGGGGACAACCTGAGCAGCCTCTGG
AGAGGGGCCATTAATAAAGCTCAACATCATTGA

335/615

FIGURE 332

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA68886
><subunit 1 of 1, 520 aa, 1 stop
><MW: 52658, pI: 9.16, NX(S/T): 3
MRNKKILKEDELLSETQQAAFHQIAMEPF EINVPKPKRRNGVNFSLAVVVIYLILLTAGAGLL
VVQVLNLQARLRVLEMYFLNDTLAAEDSPSFSLLQSAHPGEHLAQGASRLQVLQAQLTWVRVS
HEHLLQRVDNFTQNPGMFRIKGEQGAPGLQGHKGAMGMPGAPGPPGPPAEKGAKGAMGRDGAT
GPSGPQGPVGKGEAGLQGPQGAPGKQGATGTPGPQGEKGSKGDGGLIGPKGETGTKGEKGD
GLPGSKGDRGMKGDAGVMGPPGAQGSKGDGFRPGPPGLAGFPAGKGDQGPGLQGVPPGAV
GHPGAKGEPGSAGSPGRAGLPGSPGSPGATGLKGSKGDGTLQGGQGRKGESGVPGPAGVKGEQ
GSPGLAGPKGAPGQAGQKGDQGVKGSSGEQGVKGEKGERGENSVSVRIVGSSNRGRAEVYYS
TWGTICDDEWQNSDAIVFCRMLGYSKGRALYKVGAGTGQIWLNDNVQCRGTESTLWSCTKNSWG
HHDCSHEEDAGVECSV

Transmembrane domain:

amino acids 47-66 (type II)

N-glycosylation sites.

amino acids 43-47, 83-87, 136-140

Tyrosine kinase phosphorylation site.

amino acids 432-440

N-myristoylation sites.amino acids 41-47, 178-184, 253-259, 274-280, 340-346, 346-352,
400-406, 441-447, 475-481, 490-496, 515-521**Amidation site.**

amino acids 360-364

Leucine zipper pattern.

amino acids 56-78

Speract receptor repeat

amino acids 422-471, 488-519

Clq domain proteins.

amino acids 151-184, 301-334, 316-349

FIGURE 333

FIGURE 333

GGGCTGTTGATTGTGTGGGGGATTTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCTG
CCTCTGGCATATGCACACACTCACACATTCTGTACACCCGTCACACACACATACCATGTTCT
CCATCCCCCAGGTCCAGCCCTCAGTGCTGTCCCATCCAGCAGGGCTACCTGAAGCTCTGGC
TGCAGCCCTCCCGTCCAGTGGGCAGGCGGCTTCATCCCTCCTTTCTCTCCCAAAGCCCAACTG
CTGTCACTGCATGCTCTGCCAAGGAGGAGGGAAGTGCAGTGACAGCAGGAGTAAGAGTGGGAG
GCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGGTTACGCGAGCCTAGAGAGGGCAGACTA
TCAGGGTGCCGGCGGTGAGAATCCAGGGAGAGGAGCGGAAACAGAAGAGGGGCAGAAGACCG
GGCACTTGTGGGTTGCAGAGCCCCTCAGCCATGTTGGGAGCCAAGCCACACTGGCTACCAGGT
CCCCTACACAGTCCCGGGCTGCCCTTGGTTCTGGTGCTTCTGGCCCTGGGGGCCGGGTGGGCC
CAGGAGGGGTGAGAGCCCGTCTGTCTGGAGGGGAGTGCCTGGTGGTCTGTGAGCCTGGCCGA
GCTGCTGCAGGGGGGCCCGGGGAGCAGCCCTGGGAGAGGCACCCCTGGGCGAGTGGCATT
GCTGCGGTCCGAAGCCACCACCATGAGCCAGCAGGGGAAACCGCAATGGCACCAGTGGGGCC
ATCTACTTCGACCAGGTCTGGTGAACGAGGGCGGTGGCTTTGACCGGGCCTCTGGCTCCTTC
GTAGCCCCCTGTCCGGGGTGTCTACAGCTTCCGGTTCCATGTGGTGAAGGTGTACAACCGCCAA
ACTGTCCAGGTGAGCCTGATGCTGAACACGTGGCCTGTCACTCTCAGCCTTTGCCAATGATCCT
GACGTGACCCGGGAGGCAGCCACCAGCTCTGTGCTACTGCCCTTGACCCCTGGGGACCGAGTG
TCTCTGCGCCTGCGTCCGGGGGAATCTACTGGGTGGTTGGAAATACTCAAGTTTCTCTGGCTTC
CTCATCTTCCCTCTCTTGAGGACCACAAGTCTTTCAAGCACAAGAATCCAGCCCCTGACAACCTT
CTTCTGCCCTCTCTTGCCCCAGAAACAGCAGAGGCAGGAGAGAGACTCCCTCTGGCTCCTATC
CCACCTCTTTGCATGGGACCCTGTGCCAAACACCCAAAGTTAAGAGAAGAGTAGAGCTGTGGC
ATCTCCAGACCAGGCCTTTCCACCCACCCACCCCCAGTTACCCTCCCAGCCACCTGCTGCATC
TGTTCCCTGCCTGCAGCCCTAGGATCAGGGCAAGGTTTGGCAAGAAGGAAGATCTGCACTACTT
TGCGGCCTCTGCTCCTCCGGTTCCCCCACCCAGCTTCTGTCTCAATGCTGATCAGGGACAGG
TGGCGCAGGTGAGCCTGACAGGCCCCCACAGGAGCCAGATGGACAAGCCTCAGCGTACCCTG
CAGGCTTCTTCTGTGAGGAAAGCCAGCATCACGGATCTCAGCCAGCACCGTCAGAAGCTGAG
CCAGCACCGTATGGGCTAGGGTGGGAGGCTCAGCCACAGGCAGAAGGGTGGGAAGGGCCTGGA
GTCTGTGGCTGGTGAAGGAAGGAAGGAGGGTGTATTGTCTAGACTGAACATGGTACACATTCTG
CATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCTGGCTGTCCTTCTATGCTGGATCCCAGAT
GGACTCTGGCCCTTACCTCCCACCTGAGATTAGGGTGAAGTGTGTTTGTCTGGCTGAGAGCA
GAGCTGAGAGCAGGTATACAGAGCTGGAAGTGGACCATGGAAAACATCGATAACCATGCATCC
TCTTGCTTGCCACCTCCTGAAACTGCTCCACCTTTGAAGTTTGAACCTTTAGTCCCTCCACAC
TCTGACTGCTGCCTCCTTCTCCAGCTCTCTCACTGAGTTATCTTCACTGTACCTGTTCCAG
CATATCCCACATATCTCTTCTCTGATCTGTCTGCTTATTTCTCTCTCTTAGGCTTCTCT
ATTACCTGGGATTCCATGATTCATTCTTCTGAGCCCTCTCTGCCAGTATGCTAAACCTCCCT
TCTCTCTTTCTTATCCCGCTGTCCCATTTGCCCCAGCCTGGATGAATCTATCAATAAAACAAC
AGAGAATGGTGGTCAAGTGAAGTATAGTATAGAAATTAAGGAGAAGATGCCTCTGGAGTTTGG
TCGGGTGTTACAGGTACAAGTAGGTATGTTGCAGAGGAAAATAAATATCAAACCTGTATACTAA
AATTAATAA

337/615

FIGURE 334

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180
><subunit 1 of 1, 205 aa, 1 stop
><MW: 21521, pI: 7.07, NX(S/T): 1
MLGAKPHWLPGLPLVLVLLALGAGWAQEGSEPVLLGECLVVCEPGRAAAGGPGGAA
LGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVYSF
RFHVVKVYNRQTVQVSLMLNTWPVISAFANDPDVTREAAATSSVLLPLDPGDRVSLRLRRGNLL
GGWKYSSFSGLIFPL

Signal peptide:
amino acids 1-32

FIGURE 335

[illegible]

339/615

FIGURE 336

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184
><subunit 1 of 1, 388 aa, 1 stop
><MW: 43831, pI: 9.64, NX(S/T): 3
MKTLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRSK
VEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLI AVL YFTWL VFDWNTPKKGRRSQW
VRNWAVWRYFRDYFPIQLVKTHNLLTTRNYIFGYHPHGIMGLGAF CNFSTEATEVSKKFP GIR
PYLATLAGNFRMPVLR EYLM SGGICPVSRDTIDYLLSKNGSGNAIIIVVGGAESLSSMPGKN
AVTLRNRKGFVKLALRHGADLVPIYSFGENEVYKQVIFEEGSWGRWVQKKFQKYIGFAPCIFH
GRGLFSSDTWGLVPYSKPITTVVGE PITIPKLEHPTQQDIDLYHTMYEALVKLFDKHKT KFG
LPETEVLEVN

Important features of the protein:**Transmembrane domain:**

amino acids 76-97

N-glycosylation sites.

amino acids 60-63, 173-176, 228-231

N-myristoylation sites.

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-245, 318-323, 378-383

FIGURE 337

[illegible]

341/615

FIGURE 338

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213
><subunit 1 of 1, 368 aa, 1 stop
><MW: 42550, pI: 9.11, NX(S/T): 1
MGLLAFLKTQFVLHLLVGFVVFVVSGLVINQVQLCTLALWPVSKQLYRRRLNCRLAYSLWSQLVM
LLEWWSCTECTLFDTQATVERFGKEHAVIILNHNFEIDFLCGWTMCERFGVLGSSKVLAKKEL
LYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHRVSM
EVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAADVDTLNFGRGNKNPSLLGILYGKKYEAD
MCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLNFLSWA
TILLSPLFSFVLGVFASGSPLLILTFLGFVGAASFGVRRRLIGESLEPGRWRLQ
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 307-323, 335-352

Tyrosine kinase phosphorylation sites.

amino acids 160-168, 161-169

342/615

FIGURE 339

GATATTCTTTATTTTAAAGAATCTGAAGTACTATGCATCACTCCCTCCAATGTCCTGGGGCAG
CCACCAGGCATATTCATCTTTGTGTGTGTTTTCTTTTGCTTTAGCACTGGGGCACTTCTTGC
TTATTTCTTTGGTAGGAAAGGGGCTCAGTTTGTCTTGTGGGGTTGGTGGCAGGCAGGCCGGCT
TACGCCTGATACGGCCCTGGGTTAGAAGGGAAGGGAAGATAAACTTTATACAAATGGGGATA
GCTGGGGTCTGAGACCTGCTTCCTCAGTAAAATTCTTGGGATCTGCCTATACCTTCTTTTCTC
TAACCTGGCATACCCCTGCTTAAAGCCTCTCAGGGCTTCTCTCTGTTCTTAGGATCAAAGTATT
TAGAGCTACAAGAGCCCTCATGGTCTGGCCCCCTGCCCCCTGGCCAGCTTCATTGTACATGTG
GTGTTCTCTTGTCTGTTCCCTGTAATGTGGTATGCCATGGGGTCTTTGCACAAGCCTTTCCTCTT
TGGCTGGACACTGTTCCCTGCCCCCCCCATACTCTTCCCTACTTAATATGTAGTCATCCTGCAG
ATTTCAATTCTAACATCATTTTCTCCAGGGATCCTGGCCTGACAGAATCTCATCTTGTTTAAT
GCTCTCATAAGACCCTTGTTTCCCTTTTGCAGCACTTGCCACTCAGTTGTATCTTTATGTGC
GTTTGTGGTTGTATGGTTGTGTCTGTTCCCCAGAATGCCAGCTCTGAGCTGCGTGAGGGTC
AAGGGCATTGCTGTGCCTGCCAGGTATAGTGCCTACATGTGGTGGGTGCTCATGTTTTAGAGA
CTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTTCACCAGATGGTGTAGGGCC
CAGCATTTGTAATTCACACGTTGACTGTGCTTGTGAATTATCTGGGGATGCAGGTCTGATTC
AGTAGGCCCAGGTTGGGCATCTCTAACAACTCCCACGTGATGCTGATGCTGGTCCCTATGAAC
TATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGGTGGCTCACACCTATGATCCCA
GCACTTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATTTCAAGACTAGCCTGGCCA
ACATGGTGAACCCCATCTGTACTAAAAATACACAAATTAGCTGGGCATGGTGGCACATGCCT
GTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTGAACCTGGGAGGCGGAGGTTG
CAGTGAGCCGAGATCAGGCCACTGTATTCCAACCAGGGTGACAGAGTGAGACTCTATGTCCAA
AAAAAAAAAAAA

343/615

FIGURE 340

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234

><subunit 1 of 1, 143 aa, 1 stop

><MW: 15624, pI: 9.58, NX(S/T): 0

MHHSLQCPGAATRHHLCVCFSFALALGHFLLISLVGKGLSLSCGVGGRQAGLRRLIRPWVRRE

GKINFYTNGDSWGLRPASSVKFLGSAYTFFSLTWHHTLLKASQGFSFLGSKYLELQEPSWSGP

CPPGQLHCTCGVLLSFL

Important features of the protein:**Signal peptide:**

amino acids 1-28

344/615

FIGURE 341

CGCCATGGCCGGGCTATCCCGCGGGTCCGCGCGCGCACTGCTCGCCGCCCTGCTGGCGTCGACG
CTGTTGGCGCTGCTCGTGTGCGCCGCGCGGGGTCGCGGCGGCCGGGACCACGGGGACTGGGAC
GAGGCCTCCCGGCTGCCGCGCTACCACCCCGCGAGGACGCGGCGCGCGTGGCCCCGCTTCGTG
ACGCACGTCTCCGACTGGGGCGCTCTGGCCACCATCTCCACGCTGGAGGCGGTGCGCGGCCGG
CCCTTCGCCGACGTCCCTCTCGCTCAGCGACGGGCCCCCGGGCGCGGGCAGCGGCGTGCCCTAT
TTCTACCTGAGCCCGCTGCAGCTCTCCGTGAGCAACCTGCAGGAGAATCCATATGCTACACTG
ACCATGACTTTGGCACAGACCAACTTCTGCAAGAAACATGGATTTGATCCACAAAGTCCCCTT
TGTGTTACATAATGCTGTCAGGAAGTGTGACCAAGGTGAATGAAACAGAAATGGATATTGCA
AAGCATTCGTTATTTCATTGACACCCTGAGATGAAAACCTGGCCTTCCAGCCATAATTGGTTC
TTTGCTAAGTTGAATATAACCAATATCTGGGTCTGGACTACTTTGGTGGACCAAAAATCGTG
ACACCAGAAGAATATTATAATGTCACAGTTCAGTGAAGCAGACTGTGGTGAATTTAGCAACAC
TTATGAAGTTTCTTAAAGTGGCTCATACACACTTAAAAGGCTTAATGTTTCTCTGGAAAGCGT
CCCAGAATATTAGCCAGTTTTCTGTC

345/615

FIGURE 342

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71269
><subunit 1 of 1, 220 aa, 1 stop
><MW: 24075, pI: 7.67, NX(S/T): 3
MAGLSRGSARALLAALLASTLLALLVSPARGRGGRDHGDWDEASRLPPLPPREDAARVAR
FVTHVSDWGALATISTLEAVRGRPFADVLSLSDGPPGAGSGVPYFYLSPLQLSVSNLQEN
PYATLTMTLAQTNFCKKHGFDPQSPLCVHIMLSGTVTKVNETEMDIKHSLEFIRHPMKT
WPSSHNWFFAKLNITNIWVLDYFGGPKIVTPEEYYNVTVQ

Important features of the protein:**Transmembrane domain:**

Amino acids 11-29

N-glycosylation sites:

Amino acids 160-164;193-197;216-220

N-myristoylation sites:

Amino acids 3-9;7-13;69-75;97-103

346/615

FIGURE 343

GGCTGGACTGGAACCTCCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGAT
TATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACCTTTTTCAGCAACTAAAAAGCCACAG
GAGTTGAACTGCTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTACATT
AAAATCTGTTTTTTGTTCTTGTAACTAGCCTTTACCTTCCTAACACAGAGGATCTGTCACT
GTGGCTCTGGCCCAAACCTGACCTTCACCTCTGGAACGAGAACAGAGGTTTCTACCCACACCGT
CCCCTCGAAGCCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTCACCAAC
TGTCTCACGTCTGGAGGCACTGACTCGGGCAGTGCAGGTAGCTGAGCCTCTTGGTAGCTGCGG
CTTTCAAGGTGGGCCTTGCCCTGGCCGTAGAAGGGATTGACAAGCCCGAAGATTTCATAGGCG
ATGGCTCCCACTGCCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGGCCAGGACGG
GCCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCCGCCATCTAACCTTTT
CATGTCTGCACATCACCTGATCCATGGGCTAATCTGAACCTCTGTCCCAAGGAACCCAGAGCT
TGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTTTATGTGACAGGA
CTTGCAATTCTCCTGGAACATGAGGGAACGCCGGAGGAAAGCAAAGTGGCAGGGAAGGAACCTG
TGCCAAATTATGGGTGAGAAAAGATGGAGGTGTTGGGTTATCACAAGGCATCGAGTCTCCTGC
ATTCAGTGGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACTCGGGACTCACCTCTG
GGGCCATCAGACAGCCGTTTCCGCCCCGATCCACGTACCAGCTGCTGAAGGGCAACTGCAGGC
CGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCGATCACCAGCCAGGGGCAGCCGTCTG
GGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCCCTCCTTCCCTCTGAGAGGCCCTCCTATGT
CCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGCTAATGGCTCAGTGTGGCCAGGA
GGTCAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCTGTGCGAACACGGAAATGCCTCCAGT
AAGCACAGGCTGCAAAATCCCCAGGCAGGAGTGTGTGGCTCAATTTAAATCATGTTCTAGT
AATTGGAGCTGTCCCCAAGACCAAGGAGCTAGAGCTTGGTTCAAATGATCTCCAAGGGCCCT
TATACCCAGGAGACTTTGATTTGAATTTGAAACCCCAAATCCAAACCTAAGAACCAGGTGCA
TTAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATGCCAACATTTTGGGAGGCCGAGGCG
GGTAGATCACCTGAGGTGAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCCCTGTCTC
TACTAAAAATACAAAAAACTAGCCAGGCATGGTGGTGTGTGCCTGTATCCCAGCTACTCGGG
AGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGTGAAGGAGGCTGAGACAGGAGAATCACT
TCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGAAAAATAAAAAAAGAATTATGGTTATTT
GTAA

347/615

FIGURE 344

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277
><subunit 1 of 1, 109 aa, 1 stop
><MW: 11822, pI: 8.63, NX(S/T): 0
MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTAS
PCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD
```

Signal peptide:
amino acids 1-15

FIGURE 345

ATGA

349/615

FIGURE 346

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286

><subunit 1 of 1, 671 aa, 1 stop

><MW: 74317, pI: 7.61; NX(S/T): 0

MPHAFKPGDLVFAKMKGYPHWPARIDDIADGAVKPPPNKYPIFFFFGTHETAFLGPKDLFPYDK
CKDKYGKPNKRKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDDERDGM
AVTAVTATAASDRMESDSDSDKSSDNSGLKRKTPALKMSVSKRARKASSDLDQASVSPSEEN
SESSSESEKTSQDFTPEKKA AVRAPRRGPLGGRKKKKAPSASDSDSKADSDGAKPEPVAMAR
SASSSSSSSSSSSDSDSVKPKPRGRKPAEKPLPKPRGRKPKPERPPSSSSSSSDSDSDEVDRISE
WKRRDEARRRELEARRRREQEEELRRLREQEKEEKERRRERADRGEAERGSGGSSGDELREDD
EPVKKRGRKGRGRGPPSSSDSEPEAELEREAKKSAKKPQSSSTEPARKPGQKEKRVRPPEEKQQ
AKPVKVERTRKRSSEGFMDRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRCLNALEELG
TLQVTSQILQKNTDVVATLKKIRRYKANKDVMKAAEVYTRLKSRVLGPKIEAVQKVNKAGME
KEKAEKLAGEEELAGEEAPQEKAEDKPSTDLSAPVNGEATSQKGESAEDKEHEEGRDSEEGPR
CGSSEDLHDSVREGPDLDPRGSDRQERERARGDSEALDEES

Signal peptide:

amino acids 1-13

350/615

FIGURE 347

GTTGGTTCTCCTGGATCTTCACCTTACCAACTGCAGATCTTGGGACTCATCAGCCTCAATAATTATATTAAATTA
ACACCATTTGAAAGAGAACATTGTTTTTCATCATGAATGCTAATAAAGATGAAAGACTTAAAGCCAGAAGCCAAGA
TTTTACCTTTTTCTGCTTTTGATGATGCTAAGCATGACCATGTTGTTTCTTCCAGTCACTGGCACTTTGAAGCA
AAATATTCCAAGACTCAAGCTAACCTACAAAGACTTGCTGCTTTCAAATAGCTGTATTCCTTTTTGGGTTTCATC
AGAAGGACTGGATTTTCAAACCTCTTCTCTTAGATGAGGAAAGAGGCAGGCTGCTCTTGGGAGCCAAAGACCACAT
CTTTCTACTCAGTCTGGTTGACTTAAACAAAAATTTTAAAGAGATTTATTGGCCTGCTGCAAAGAACGGGTGGA
ATTATGTAAATTAGCTGGGAAAGATGCCAATACAGAATGTGCAAAATTTTCATCAGAGTACTTCAGCCCTATAACAA
AACTCACATATATGTGTGTGGAAGTGGAGCATTTTCATCCAATATGTGGGTATATTGATCTTGGAGTCTACAAGGA
GGATATTATATTCAAACCTAGACACACATAATTTGGAGTCTGGCAGACTGAAATGTCCTTTTCGATCCTCAGCAGCC
TTTTGCTTCAGTAATGACAGATGAGTACCTCTACTCTGGAACAGCTTCTGATTTCTTGGCAAAGATACTGCATT
CACTCGATCCCTTGGCCTACTCATGACCACCACTACATCAGAAGTACATTTTCAGAGCACTACTGGCTCAATGG
AGCAAAATTTATTGGAATTTCTTCATACCAGACACCTACAATCCAGATGATGATAAAATATATTCTTCTTTTCG
TGAATCATCTCAAGAAGGCAGTACCTCCGATAAAACCATCTTTCTCGAGTTGGAAGAGTTTGTAAAGATGATGT
AGGAGGACAACGCAGCCTGATAAACCAAGTGGACGACTTTTCTTAAGGCCAGACTGATTTGCTCAATTCCTGGAAG
TGATGGGGCAGATACTTACTTTGATGAGCTTCAAGATATTTATTTACTCCCCACAAGAGATGAAAGAAATCCTGT
AGTATATGGAGTCTTTACTACAACCAGCTCCATCTTCAAAGGCTCTGCTGTTGTGTGTATAGCATGGCTGACAT
CAGAGCAGTTTTTAAATGGTCCATATGCTCATAAGGAAAGTGCAGACCATCCTTGGGTGCAGTATGATGGGAGAAT
TCCTTATCCACGGCTGGTACATGTCCAAGCAAAACCTATGACCCACTGATTAAGTCCACCCGAGATTTTCCAGA
TGATGTCATCAGTTTTCATAAAGCGGCACTCTGTGATGTATAAGTCCGTATACCCAGTTGCAGGAGGACCAACGTT
CAAGAGAATCAATGTGGATTACAGACTGACACAGATAGTGGTGGATCATGTTCATTGCAGAAGATGGCCAGTACGA
TGTAATGTTTTCTTGAACAGACATTGGAAGTGTCTCAAAGTTGTCTCAGCATTTCAAAGGAAAGTGAATATGGA
AGAGGTAGTGCTGGAGGAGTTGCAGATATTCAAGCACTCATCAATCATCTTGAACATGGAATGTCTCTGAAGCA
GCAACAATTGTACATTGGTTCCCGAGATGGATTAGTTTCACTCTCCTTGCACAGATGCGACACTTATGGGAAAGC
TTGCGCAGACTGTTGTCTTGCCAGAGACCCCTACTGTGCTGGGATGGAAATGCATGCTCTCGATATGCTCCTAC
TTCTAAAAGGAGAGCTAGACGCCAAGATGTAAATATGGCGACCCAATCACCCAGTCTGGGACATCGAAGACAG
CATTAGTCATGAAACTGCTGATGAAAGGTGATTTTTTGGCATTGAATTTAACTCAACCTTTCTGGAATGTATACC
TAAATCCCAACAAGCAACTATTAAATGGTATATCCAGAGGTGAGGGGATGAGCATCGAGAGGAGTTGAAGCCCGA
TGAAAGAATCATCAAACCGAATATGGGCTACTGATTGCAAGTTTGCAGAAGAAGGATTCTGGGATGTATTACTG
CAAAGCCAGGAGCAGCACTTTTCATCCACACCATAGTGAAGTCACTTTGAATGTATTGAGAATGAACAGATGGA
AAATACCCAGAGGGCAGAGCATGAGGAGGGGAGGTCAAGGATCTATTGGCTGAGTCACGGTTGAGATACAAAGA
CTACATCCAAATCCTTAGCAGCCCAAACCTTCAGCCTCGACCAGTACTGCGAACAGATGTGGCACAGGGAGAAGCG
GAGACAGAGAAACAAGGGGGGGCCAAAGTGAAGCACATGCAGGAAATGAAGAAGAAACGAATCGAAGACATCA
CAGAGACCTGGATGAGCTCCCTAGAGCTGTAGCCACGTTAGTTTTCTACTTAATTTAAAGAAAAGAATTCCTTACC
TATAAAAACATTGCCTTCTGTTTTGTATATCCCTTATAGTAATTCATAAATGCTTCCCATGGAGTTTTGCTAAGG
CACAAGACAATAATCTGAATAAGACAATATGTGATGAATATAAGAAAGGGCAAAAAATTCATTTGAACCAAGTTTT
CCAAGAACAATCTTGACACAAGCAAAGTATAAGAATTATCCTAAAAATAGGGGGTTTACAGTTGTAAATGTTTTA
TGTTTTGAGTTTTTGAATTTTATTGTCATGTTAAATAGTTGAGCTAAGCAAGCCCCGAATTTGATAGTGTATAAGGT
GCTTTATTCCTCGAATGTCCATTAAGCATGGAATTTACCATGCAGTTGTGCTATGTTCTTATGAACAGATATAT
CATTCTATTGAGAACCAGCTACCTTGTGGTAGGGAATAAGAGGTGAGACACAAATTAAGACAACCTCCATTATC
AACAGGAACCTTTCTCAGTGAGCCATTCACTCCTGGAGAATGGTATAGGAATTTGGAGAGGTGCATTATTTCTTTC
TGGCCACTGGGGTTAAATTTAGTGTACTACAACATTGATTTACTGAAGGGCACTAATGTTTCCCCCAGGATTTCT
ATTGACTAGTCAGGAGTAACAGGTTTACAGAGAGAAGTTGGTGCTTAGTTATGTGTTTTTTAGAGTATATACTAA
GCTCTACAGGGACAGAATGCTTAATAAATACTTTAATAAGATATGGGAAAATATTTTAAATAAAACAAGGAAAACA
TAATGATGTATAATGCATCCTGATGGGAAGGCATGCAGATGGGATTTGTTAGAAGACAGAAGGAAAGACAGCCAT
AAATTCCTGGCTTTGGGGAAAACCTCATATCCCCATGAAAAGGAAGAACAATCACAAATAAAGTGAGAGTAATGTAA
TGGAGCTCTTTCACTAGGGTATAAGTAGCTGCCAATTTGTAATTCATCTGTAAAAAAATCTAGATTATAACA
AACTGCTAGCAAATCTGAGGAAACATAAATCTTCTGAAGAATCATAGGAAGAGTAGACATTTTATTTATAACC
AATGATATTTTCACTATATATTTTCTCTTTTAAAAAATATTTATCACTCTGTATATTTTCTTTTTACTGC
CTTTATTTCTCTCTGTATATTGGATTTTGTGATTATTTTGAAGTGAATAGGAGAAAACAATATATAACACACAGA
GAATTAAGAAAATGACATTTTCTGGGAGTGGGGAGTATATATTTGTTGAATAACAGAACGAGTGTAAAATTTTAA
AACGGAAGGGTTAAATTAACCTTTTACATCTTCACTCAACCTTTTCTCATTGCTGAGTTAATCTGTTGTAATT
GTAGTATTGTTTTTGAATTTAACAATAAATAAGCCTGCTACATGT

351/615

FIGURE 348

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883

><subunit 1 of 1, 777 aa, 1 stop

><MW: 89651, pI: 7.97, NX(S/T): 3

MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNIPLRLKLTYSKDLLLSNSCIPFLG
SSEGLDFQTLLLDEERGRLLLGAKEHIFLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDANT
ECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRLKCPFDPPQ
PFASVMTDEYLYSGTASDFLGKDTAFTRSLGPTHDDHYIRTDISEHYWLNKAKFIGTFFIPDT
YNPDDDKIYFFFRESSQEGSTSDKTIILSRVGRVCKNDVGGQSLINKWTTFLKARLICSIPGS
DGADTYFDELQDIYLLPTRDERNPVVYGVFTTTSSIFKGSACVYSMADIRAVENGPIAHKES
ADHRWVQYDGRIPYPRPGTCPSKTYDELIKSTRDFPDDVISFIKRHSVMYKSVYPVAGGPTFK
RINVDYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVSISKEKWNMEEVVLEELQIFKHSS
IILNMEISLQKQQLYIGSRDGLVQLSLHRCDTYKACADCCLARDPYCAWDGNACSRYAPTSTK
RRARRQDVKYGPITQCDIEDSISHETADEKVIIFGIEFNSTFLECIPKSQQATIKWYIQRSG
DEHREELKPDERIIKTEYGLLIRSLQKKDSGMYCKAQEHTFIHTIVKLTNLVINEQMENTQ
RAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRNKGKGPWKHMQEM
KKKRNRRHHRDLDELPRAVAT

Important features of the protein:**Signal peptide:**

amino acids 1-36

N-glycosylation sites.

amino acids 139-142, 607-610, 724-727

Tyrosine kinase phosphorylation site.

amino acids 571-576

Gram-positive cocci surface proteins 'anchoring' hexapeptide.

amino acids 32-37

352/615

FIGURE 349

CCCTGACCTCCCTGAGCCACACTGAGCTGGAAGCCGAGAGGTCATCCTGGAGCATGCCACCGGGGAGCAGA
CAACCTCCCAGGTAAGCTGGGAGCAAGACCTGAAGCTGTTTCTTCAGGAGCCTGGTGTATTTTCCCCACCCAC
CTCAGCAGTTTCAGCCAGCAGGGACTGATCAGGTGTGTGTCTGGAGTGGGAGCAGAAGGCGTGGCTGGCAAGA
GTGGCCTGGAGAAAGAGGTTTCAGCGCTTGACCAGCCGAGCTGCCCGTGAATAAGATCCAGAACCATGGGCATC
GGGTGAGGTGGGGGGGCACAGGTGTCTGTGCACCTTCTTGTCTCAGCAAGAAGAGCTGAGAGAGGGGATCTTGG
AGCCATTGAGGGTGTCTGAGGCTACAGAGGGGAGGGAAGGTATTTTAAGGTAACAGTGTGGCACAATAGTTAA
GAGCACAGTTTTTGGAGCTAGACCGACATAGGTTCAAATTTCTTCTGTTGCTTCTAGTTCTGTAGCCCCAGGT
AAGGGAGTGACTTAACCTCTCTGGAATTCATTTCTCTACTAAAGTAGGGCCAATAATAGCACCCACCTCAT
AGGGAAGATTAAATGACATAATGTATGTGATGCAACTAGCAAAGTACCAGTCCCATAGTAAGTCATGCCCCACAG
TATTTCCACCCACCCCTGTTCTCTGCCTTCCCAACCAGGTACTGCAACGACTGGAGCAGAGGCGGCAGCAGGCTT
CAGAGCGGGAGGCTCCAAGCATAGAACAGAGGTTACAGGAAGTGCAGAGAGCATCCGCGGGGCACAGGTGAGCC
AGGTGAAGGGGGCTGCCCGCTGGCCCTGCTGCAGGGGGCTGGCTTAGATGTGGAGCGCTGGCTGAAGCCAGCCA
TGACCCAGGCCCAGGATGAGGTGGAGCAGGAGCGGCGGCTCAGTGAGGCTCGGCTGTCCCAGAGGGACCTCTCTC
CAACCGCTGAGGATGCTGAGCTTTCTGACTTTGAGGAATGTGAGGAGACGGGAGAGCTCTTTGAGGAGCTGCCC
CCCAAGCCCTGGCCACGAGGGCCCTCCCTGCCCTGCACACGTGGTATTTTCGCTATCAGGCAGGGCGTGAGGATG
AGCTGACAATCACGGAGGGTGAGTGGCTGGAGGTGATAGAGGAGGAGATGCTGACGAATGGGTCAAGGCTCGGA
ACCAGCACGGCGAGGTAGGCTTTGTCCCTGAGCGATATCTCAACTTCCCGGACCTCTCCCTCCCAGAGAGCAGCC
AAGACAGTGACAATCCCTGCGGGGCAGAGCCACAGCATTCCTGGCACAGGCCCTGTACAGCTACACCGGACAGA
GTGCAGAGGAGCTGAGCTTCCCTGAGGGGGCACTCATCCGTCTGCTGCCCGGGCCCAAGATGGAGTAGATGACG
GCTTCTGGAGGGGAGAAATTTGGGGGCGGTGTTGGGGTCTTCCCTCCCTGCTGGTGAAGAGCTGCTTGGCCCCC
CAGGGCCACCTGAACCTCTCTGACCCTGAACAGATGCTGCCGTCCCTTCTCTCCAGCTTCTCCCCACCTGCAC
CTACCTCTGTGTTGGATGGGCCCCCTGCACCTGTCTGCTGGGGACAAAGCCCTGGACTTCCCTGGGTTCCTGG
ACATGATGGCACCTCGACTCAGGCCGATGCGTCCACCACCTCCCCCGCCGGCTAAAGCCCCGGATCCTGGCCACC
CAGATCCCCCTCACCCTGAGGCCAGGGAAGCCTTGACCCCAAGTGATGCTGCTGTCCCTATCTTCAAGCTGTCAGA
CCACACCATCAATGATCCAGAGCAACACAGCCAAAAGCTGGAATCGCCCTTATTTCCACCCCTCACCTCCAAGGGT
GGAACTTGCCCCCTCCCATTTCTAGAGCTGGAACCCACTCCTTTTTTCCATTGTTCTATCATCTCTAGGACC
GGAACCTACTACTTCTCTTCTGTCTGATGACCCCTATCTAGGGTGGTGAAATGCCTGAAATCTCTGGGGCTGGAAACC
ATCCATCAAGGTCTCTAGTAGTTCTGGCCACCTCTTTCCCCACCTGGCTCCATGACCCACCCCACTCTGGATG
CCAGGGTCACTGGGGTGGGCTGGGGAGAGGAACAGGCCTTGGGAATCAGGAGCTGGAGCCAGGATGCGAAGCAG
CTGTAATGGTCTGAGCGGATTTATTGACAATGAATAAAGGGCAGGAAGGCCAGGCCAGGGCCTGGGCTCTTGTG
CTAAGAGGGCAGGGGGCTACGGTGTCTATTGCTTTAGGGGGCCACCACGGGCAGGGGCTGCTCCAGCTGCCAC
GCTCTATCATATGGAGCGAGGTGTTGGGAAGGCGGGGCAGGCAGCCTGTTGCAGGCAGGGGAAGGAGAAGAGAC
TGAGGGGCTGTGACCTCTCCTGAGGCCCCCAGCCTGAGACTGTGCAACTCCAGGTGGAAGTAGAGCTGGTCCCTC
AGCTGGGGGGCAGTCTGTCTCAGTGGAGGGGAGGGCTTTCAGGCCACCCACCCCTGGCCCTGCCAGCTGGTAG
TCCATCAGCACAATGAAGGAGACTTGGAGAAGAGGAAGATAAAGCTGTTGCTTCCCTGTTCAAGCTGTGTCCAGC
TTTTCCCCTGGGGCTCCAGGACCTTCCCTACCTCCACCACCAACCAAGGGATTTATAGCAAAGGCTAAGCCTGC
AGTTTACTCTGGGGGTTGAGGGAGCCGAAAGGCTTAAATAGTTTAAAGTAGGTGATGGGAAGATGAGATTACCTCA
TTTAGGGCTCAGGCAGACTCACCTCACATACTCCCTGCTCCCTGTGGTAGAGACACCTGAGAGAAAGGGGAGGGG
TCAACAATGAGAGACCAGGAGTAGGTCTATCAGTGCCCCCAGAGTAGAGAGCAATAAGAGCCCAGCCAGTGC
AGTCCCGGCTGTGTTTTCTACCTGGTGATCAGAAGTGTCTGGTTGCTTGGCTGCCATTGCTCTTGTAGTGG
GCAGCCCTGGGCTTGGGCCCCCTCCCTCCGGCCCTCAGTGTGGCTCTGCAGAAGCTCTGGGGTCCCTTCAAGTG
CACGAGGGGTAGGCTGCTGTCCCTGAGTCTCCATTCTGTACTGGGGGGCTGGCTAGGACCTGGGGCTGTGGCC
TCTCAGGGGGCAGCCTCTCCATGGCAGGCATCCCTGCCTTGGGCTGCCCTCCCCCAGACCCCTGACCACCCCTG
GGTCTGTCCCCCACCAGAGCCCCAGCTCCTGTCTGTGGGGGAGCCATCACGGTGTTCGTGCAGTCCATAGCGCT
TCTCAATGTGTGTACCCGGAACCTGGGAGGGGAGGGAACACTGGGGTTTAGGACCACAACCTCAGAGGCTGCTTG
GCCCTCCCCTCTGACCAGGGACATCCTGAGTTTGGTGGCTACTTCCCTCTGGCCTAAGGTAGGGGAGGCCTTCTC
AGATTGTGGGCACATTGTGTAGCCTGACTTCTGCTGGAGCTCCAGTCCAGGAGGAAAGAGCCAAGGGCCACTT
TTGGGATCAGGTGCCTGATCACTGGGCCCCCTACCTCAGCCCCCTTTCCCTGGAGCACCTGCCCCACCTGCCCA
CAGAGAACACAGTGGTCTCCCTGTCCGGGGGCGGCTTTTTCTTCTTGGAGCGTCCCTGACGGACAAGTGGAG
GCCTCTTGCTCGGGCTGCAATGGATGCAAGGGGCTGCAGAGCCAGGTGACTGTGTGATGATGGGAGGGGGCTC
CGTCTGCAGGCTGGAGGTGGCATCCCACTGGACAGCAGGAGGAGGGGAGTGAGGGTAACATTTCCATTTCCTT
TCATGTTTTGTTCTTACGTTCTTTCAGCATGCTCCTTAAACCCCAAGAGCCCAATTTCCCAAGCCCCATTT
TTCTTGTCTTTATCTAATAAACTCAATATTAAG

353/615

FIGURE 350

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401
><subunit 1 of 1, 370 aa, 1 stop
><MW: 40685, pI: 4.53, NX(S/T): 0
MQLAKYQSHSKSCPTVFPPTPVLCLPNQVLQRLQRRQQASEREAPSIEQRLQEVRESIRRAQ
VSQVKGAARLALLQGAGLDVERWLKPAQTQAQDEVEQERRLSEARLSQRDLSPTAEDAELSDF
EECEETGELFEPPAPQALATRALPCPAHVVFQYQAGREDELTITEGEWLEVIEEGDADEWKA
RNQHGEVGFVPERYLNFPDLSPSSQSDNPGAEPTAFLAQALYSYTGQSAEELSFPEGAL
IRLLPRAQDGVDDGFWRGEGGRVGVFPSSLVEELLGPPGPPPELSDPEQMLPSPSPPSFSPPA
PTSVLDGPPAPVLPQDKALDFPGFLDMMAPRLRPMRPPPPPPAKAPDPGHPDPLT
```

FIGURE 351A

FIGURE 351A

CACAGGGAGACCCACAGACACATATGCACGAGAGAGACAGAGGAGGAAAGAGACAGAGACAAAGGCACAGCGGAA
GAAGGCAGAGACAGGGCAGGCACAGAAGCGGCCAGACAGAGTCTACAGAGGGAGAGGCCAGAGAAGCTGCAGA
AGACACAGGCAGGGAGAGACAAAGATCCAGGAAAGGAGGGCTCAGGAGGAGAGTTTGGAGAAGCCAGACCCCTGG
GCACCTCTCCCAAGCCCAAGGACTAAGTTTCTCCTATTCTCTTAACGGTCCCTCAGCCCTTCTGAAAACTTTGCC
TCTGACCTTGGCAGGAGTCCAAGCCCTCAGGTACAGAGAGGAGCTTTCCAAGTACAGGTGTGGAGACTTTGGT
GCCCTAGACGGCCTCAGTCCCTCCCAGCTGCATACAGTGCCTAGTCCAGTCCAGACAGGCTCGCATCCCGGGAGGGG
CTTGGCAGGGCGCTGGCTGTGGGGAGCCCAACCTGCCTCCTGCTCCCCATTGTGCCGCTCTCCTGGCTGGTGTG
GCTGCTTCTGCTACTGCTGGCCTCTCTCCTGCCCTCAGCCCGGCTGGCCAGCCCCCTCCCCGGGAGGAGAGAT
CGTGTTTCCAGAGAAGCTCAACGGCAGCGTCTCCTGCTGCTCGGGCGCCCTGCCAGGCTGTTGTGCCGCTTGCA
GGCCTTTGGGGAGAGCGTGTCTACTAGAGCTGGAGCAGGACTCCGGTGTGCAGGTTCGAGGGGCTGACAGTGCAGTA
CTCGGGCAGGGCGCTGAGTGTCTGGGTGGAGCAGAGCCTGGCACTTACCTGACTGGCACCATCAATGGAGATCC
GGAGTCGGTGGCATCTCTGCACTGGGATGGGGGAGCCCTGTTAGGCGTGTGTACAATATCGGGGGGCTGAACTCCA
CCTCCAGCCCCCTGGAGGGAGGCACCCCTAATCTGCTGGGGGACCTGGGGCTCACATCCTACGCCGGAAGAGTCC
TGCCAGCGGTCAAGTCCCATTGTGCAACGTCAAGGCTCCTCTTGGAAGCCCCAGCCCCAGACCCGGAAGAGCCAA
GCGCTTTGCTTCACTGAGTAGATTGTGGAGACACTGGTGGTGCCAGATGACAAGATGGCCGCTATCCACGGTGC
GGGCTAAAGCGCTACCTGTAAACATGATGGCAGCAGCAGCCAAAGCCTTCAAGCACCAGCATCCGCAATCC
TGTACGTTTGGTGGTGACTCGGCTAGTAGTCTGGGGTCAAGGCAGGAGGGGGCCCAAGTGGGGGCCAGTGTGC
CCAGACCTGCGCAGCTTCTGTGCCCTGGCAGCGGGGCCCTCAACACCCCTGAGGACTCGGGCCCTGACCACCTTTGA
CACAGCCATTCTGTTTACCCGTAGGACCTGTGTGGAGTCTCCACTTGCACACGCTGGGTATGGCTGATGTGGG
CACCCTGTGTGATCCCGGCTCGGAGCTGTGCCATTGTGGAGGATGATGGGTCCAGTTCAGCTCAGCCTTCACTGTCTCA
TGAATCGGTGTGATCTTCAACATGTCTCCATGACAACCTCAAGCCATGCATTCAGTTTGAATGGGCCCTTTGAGCAC
CTCTCGCCATGTCTATGGCCCTGTGATGGCTACAGTGTGATCCTGAGGAGCCCTGGTCCCCCTGCAGTGGCCGCTT
CATCACTGACTTCTTGGACAATGGCTATGGGCATGTCTCTTAGACAAACCAGAGGCTCCATTGCATCTGCCTGT
GACTTTCCCTGGCAAGGACTATGATGCTGACCGCCAGTGCCAGCTGACCTTCGGGCCCCGACTCAGCCATTGTCC
ACAGCTGCCGCGGCCCTGTGCTGCCCTCTGGTGTCTTGCCACCTCAATGGCCATGCCATGTGCCAGACCAAACA
CTCGCCCTGGGCCGATGGCACAACCTCGGGGCCGCACAGGCTGCATGGGTGGTTCGCTCCCATCCATGGACCA
GCTCCAGGACTTCAATATTCCACAGGCTGGTGGCTGGGGTCCCTGGGGACCATGGGTGACTGCTCTCGGACCTG
TGGGGGTGGTGTCCAGTTCTCCTCCCGAGACTGCACGAGGCTGTCCCCCGGAATGGTGGCAAGTACTGTGAGGG
CCGCGGTACCCGCTTCCGCTCCTGCAACACTGAGGACTGCCCAACTGGCTCAGCCCTGACCTTCCGCGAGGAGCA
GTGTGCTGCCTACAACCACCGCACCGACCTCTTCAAGAGCTTCCAGGGCCCATGGACTGGGTTCCTCGCTACAC
AGGCGTGGCCCCCAGGACCAAGTGCAAACTCACCTCAGGCGCCGGGCACTGGGCTACTACTATGTGCTGGAGCC
ACGGGTGGTAGATGGGACCCCTGTTTCCCGGACGCTCCTGGTCTGTGTCAGGGCCGATGCATCCATGCTGG
CTGTGATCGCATCATTTGGCTCCAAGAAGAATTGACAAGTGCATGGTGTGCGGAGGGGACGGTTCGTGGTGCAG
CAAGCAGTCAGGCTCCTTCAGGAAATTCAAGTACGGATACAACAATGTGGTCACTATCCCCGCGGGGGCCACCCA
CATTCCTGTCCGGCAGCAGGGAACCCCTGGCCACCGGAGCATCTACTTGGCCCTGAAGCTGCCAGATGGCTCCTA
TGCCCTCAATGGTGAATACACGCTGATGCCCTCCCCACAGATGTGGTACTGCTTGGGCGCTCAGCTTGCCTGCTA
CAGCGGGGCCACTCGAGCTCAGAGACACTGTGAGCCACATGGGCCACTGGCCAGCCTTTGACACTGCAAGTCTT
AGTGGCTGGCAACCCCGAGGACACAGCCTCCGATACAGCTTCTCGTGGCCCGCGGACCCCTTCAACGCCACG
CCCCACTCCCCAGGACTGGCTGCACCGAAGAGCACAGATTCTGGAGATCCTTCGGCGGCGCCCCCTGGGCGGGCAG
GAAATTAACCTCACTATCCCGGCTGCCCTTTCTGGGCACCGGGGCCCTCGGACTTAGCTGGGAGAAAGAGAAGACTT
CTGTTGCTGCCTCATGCTAAGACTCAGTGGGGAGGGGCTGTGGGCGTGAGACCTGCCCTCCTCTCTGCCCTAAT
GCGCAGGCTGGCCCTGCCCTGGTTCCTGCCCTGGGAGGACGTGATGGGTAGTGGATGGAAGGGGCTGACAGAC
AGCCCTCCATCTAAACTGCCCCCTCTGCCCTGCGGGTACAGGAGGGAGGGGGAAGGCAGGGGAGGGCTGGGCC
CAGTTGTATTTATTTAGTATTTATTCACTTTTATTTTAGACACAGGGAAGGGGACAGGACTAGGGTCTGGGGAA
CCTGACCCCTGACCCCTCATAGCCCTCACCTGGGGCTAGGAAATCCAGGCTGGTGGTGTATAGGTATAAGTGGTG
TGTGTATGCGTGTGTGTGTGTGTGAAATGTGTGTGTGCTTATGTATAGGTACAACCTGTTCTGCTTTCCCTC
TTCCTGAATTTTATTTTTTGGGAAAAGAAAAGTCAAGGGTAGGGTGGGCGCTTCAGGGAGTGAGGGATTATCTTTT
TTTTTTTTTCTTTCTTTCTTTCTTTTTTTTTTTGAGACAGAATCTCGCTCTGTGCCCCAGGCTGGAGTGAATG
GCAATCTCGGCTCACTGCACTCTCCGCTCCCGGGTCAAGTGATTCTCATGCTCAGCCTCAGCCTCTGAGTAGCTG
GGATTACAGGCTCCTGCCACCACGCCAGCTAATTTTTGTTTTGTTTTGTTTTGGAGACAGAGTCTCGCTATTGTC
ACCAGGGCTGGAATGATTTTCACTCACTGCAACCTTCGCCACCTGGGTTCAGCAATTCTCCTGCCTCAGCCTCC
CGAGTAGCTGAGATTATAGGCACCTACCACCACGCCCGCTAATTTTTGTATTTTTTAGTAGAGACGGGGTTTCAC
CATGTTGGCCAGGCTGGTCTGCAACTCCTGACCTTAGGTGATTCCTCAGCTTTCATCTCCCAAAGTCTGCTGGGAT
ACAGGCGTGAGCCACCGTGCCTGGCCACGCCCAACTAATTTTTGTATTTTTTAGTAGACAGGGTTTCACTAGT
TGGCCAGGCTGCTCTTGAACCTCTGACCTCAGGTAATCGACCTGCCTCGGCCCTCCCAAAGTGTGGGATTACAGG

TTTTTAAATTGAATTCTACTATT

356/615

FIGURE 352

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492

><subunit 1 of 1, 837 aa, 1 stop

><MW: 90167, pI: 8.39, NX(S/T): 1

MSQTGSHPGRGLAGRWLWGAQPCLLLPIVPLSWLVWLLLLLLASLLPSARLASPLPREEEIVF
PEKLNGSVLPGSGAPARLLCRLQAFGETLLLELEQDSGVQVEGLTVQYLGQAPELLGGAEPGT
YLTGTINGDPESVASLHWDGGALLGVLQYRGAELHLQPLEGGTPNSAGGPGAHLRRKSPASG
QGPMC NVKAPLGSPSPRRRAKRFASLSRFVETLVVADDKMAAFHGAGLKRYLLTMMAAAKA
FKHPSIRNPVSLVVTRLVILSGEEGPQVGPSAAQTLRSFCAWQRGINTPEDSGPDHFDTAIL
FTRQDL CGVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAHELGHVFNMLHDNSKPCI
SLNGPLSTSRHVMAVMAHVDPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHLPVTFPGK
DYDADRQCQLTFGPDSRHCPQLPPPCAALWCSGHLNGHAMCQTKHSPWADGTPCGPAQACMGG
RCLHMDQLQDFNIPQAGGWGPWGPWGDCSRTC GGGVQFSSRDCTRPVPRNGGKYCEGRRTFR
SCNTEDCPTGSALTFREEQCAAYNHRTDLFKSFPGMDWVPRYTGVAPQDQCKLTCQARALGY
YYVLEPRVVDGTPCSPDSSSVQVQGRCIHAGCDRIIGSKKKFDKCMVCGDGS GCSKQSGSFR
KFRYGYNNVVTIPAGATHILVRQQGNPGHRSIYLALKLPDGSYALNGEYTLMPSPSTDVVLPGA
VSLRYSGATAASETLSGHGPLAQPLTLQVLVAGNPQDTRLRYSFEVPRPTPSTPRPTPDWLH
RRAQILEILRRRPWAGRK

Important features of the protein:**Signal peptide:**

amino acids 1-48

N-glycosylation site.

amino acids 68-71

Glycosaminoglycan attachment site

amino acids 188-191, 772-775

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 182-185

Tyrosine kinase phosphorylation site.

amino acids 730-736

N-myristoylation sites.amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-
172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-
582, 679-684, 682-687, 763-768**Amidation sites.**

amino acids 560-563, 834-837

Leucine zipper pattern.

amino acids 17-38, 24-45

Neutral zinc metalloproteinases, zinc-binding region signature.

amino acids 358-367

357/615

FIGURE 353

GCGGAACTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCCGAGGGCCCAGGGAGCTGCCC
GGCTGGCCTAGGCAGGCAGCCGCACCATGGCCAGCACGGCCGTGCAGCTTCTGGGCTTCCTGC
TCAGCTTCCTGGGCATGGTGGGCACGTTGATCACCACCATCCTGCCGCACTGGCGGAGGACAG
CGCACGTGGGCACCAACATCCTCACGGCCGTGTCCTACCTGAAAGGGCTCTGGATGGAGTGTG
TGTGGCACAGCACAGGCATCTACCAGTGCCAGATCTACCGATCCCTGCTGGCGCTGCCCCAAG
ACCTCCAGGCTGCCCCGCGCCCTCATGGTCATCTCCTGCCTGCTCTCGGGCATAGCCTGCGCCT
GCGCCGTCATCGGGATGAAGTGCACGCGCTGCGCCAAGGGCACACCCGCCAAGACCACCTTTG
CCATCCTCGGCGGCACCCCTCTTCATCCTGGCCGGCCTCCTGTGCATGGTGGCCGTCTCCTGGA
CCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCCAGCGGCATGAAGTTTGAGA
TTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGTGGCACCCCTGC
TTTGCCTGTCCTGCCAGGACGAGGCACCCTACAGGCCCTACCAGGCCCCGCCAGGGCCACCA
CGACCACTGCAAACACCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAGACAATCGGGCCC
CCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTGTGAGTCCCCACAG
CCTGCTTCTCCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTCAATGGAGGCAGGGG
TTCCAGCACAAAGTTTACTTCTGGGCAATTTTTGTATCCAAGGAAATAATGTGAATGCGAGGA
AATGTCTTTAGAGCACAGGGACAGAGGGGGAATAAGAGGAGGAGAAAGCTCTCTATACCAA
GACTGAAAAAAAAAATCCTGTCTGTTTTTGTATTTATTATATATATTTATGTGGGTGATTTGA
TAACAAGTTTAATATAAAGTGAAGTTGGGAGTTTGGTCAGTGGGGTTGGTTTGTGATCCAGGAA
TAAACCTTGCGGATGTGGCTGTTTATGAAAAAAAAAAAAA

358/615

FIGURE 354

MASTAVQLLGFLLSFLGMVGTLLITTLPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIYQ
CQIYRSLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAKGTTPAKTTFAILGGTLFI
LAGLLCMVAVSWTTNDVVQNFYNPLLPSPGMKFEIGQALYLGFISSSLIGGTLLCLSCQDEA
PYRPHYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGYRLNDYV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-103, 115-141, 160-182

359/615

FIGURE 355

GAGCTCCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCGC
AGGCGGCAGGGCGGGCGGCCAGGATCATGTCACACCACCATGCCAAGTGGTGGCGTTCCTCC
TGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCCAGG
ACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGCGTGA
GGCAGAGTTCAGGCTTCACCGAATGCAGGGCCCTATTTACCATCCTGGGACTTCCAGCCATGC
TGCAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGTCCTGGGTGCCATTGGCCTCCTGGTAT
CCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCCAACATGA
CACTGACCTCCGGGATCATGTTTATTGTCTCAGGTCTTTGTGCAATTGCTGGAGTGTCTGTGT
TTGCCAACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCGGCATGGGTG
GGATGGTGCAGACTGTTTACAGACCAGGTACACATTTGGTGCGGCTCTGTTCTGGGCTGGGTG
CTGGAGGCCCTCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGGCTGGCACCAG
AAGAAACCAACTACAAAGCCGTTTCTTATCATGCCTCAGGCCACAGTGTTCCTTACAAAGCCTG
GAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAACACCAAAAACAAGAAGATATACGATGGAG
GTGCCCCGACAGAGGACGAGGTACAATCTTATCCTTCCAAGCACGACTATGTGTAAATGCTCTA
AGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCACCCAAAAACAAGGAGATCCCA
TCTAGATTTCTTCTTGCTTTGACTCACAGCTGGAAGTTAGAAAAGCCTCGATTTTCTCTTTG
GAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCCACCATAAAACAGCTGAG
TTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTATTTCTTTTTTAAATATAA
CTTTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCACATTTTGATGATTTAGACAG
ACTCCCCCTCTTCTCCTAGTCAATAAACCCATTGATGATCTATTTCCCAGCTTATCCCCAAG
AAAACTTTTGAAAGGAAAGAGTAGACCCAAAGATGTTATTTTCTGCTGTTGAATTTGTCTC
CCCACCCCAACTTGGCTAGTAATAAACACTTACTGAAGAAGAAGCAATAAGAGAAAGATATT
TGTAATCTCTCCAGCCCATGATCTCGGTTTTCTTACACTGTGATCTTAAAGTTACCAAACCA
AAGTCATTTTCAGTTTGAGGCAACCAAACCTTTCTACTGCTGTTGACATCTTCTTATTACAGC
AACACCATTCTAGGAGTTTCTGAGCTCTCCACTGGAGTCCTCTTTCTGTCGCGGGTCAGAAA
TTGTCCCTAGATGAATGAGAAAATTATTTTTTTTAAATTAAGTCCTAAATATAGTTAAATATA
ATAATGTTTTAGTAAAATGATACACTATCTCTGTGAAATAGCCTCACCCCTACATGTGGATAG
AAGGAAATGAAAAAATAATTGCTTTGACATTGTCTATATGGTACTTTGTAAAGTCATGCTTAA
GTACAAATTCCATGAAAAGCTCACACCTGTAATCCTAGCACTTTGGGAGGCTGAGGAGGAAGG
ATCACTTGAGCCCAGAAGTTCGAGACTAGCCTGGGCAACATGGAGAAGCCCTGTCTCTACAAA
ATACAGAGAGAAAAAATCAGCCAGTCATGGTGGCATAACCTGTAGTCCCAGCATTCGGGGAG
GCTGAGGTGGGAGGATCACTTGAGCCCAGGGAGGTTGGGGCTGCAGTGAGCCATGATCACACC
ACTGCACTCCAGCCAGGTGACATAGCGAGATCCTGTCTAAAAAATAAAAAATAAATAATGGA
ACACAGCAAGTCCTAGGAAGTAGGTTAAAACTAATTCTTTAA

360/615

FIGURE 356

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734

><subunit 1 of 1, 261 aa, 1 stop

><MW: 27856, pI: 8.50, NX(S/T): 1

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFAQYEGLRSCVRQSSGFTEC
RPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIMFI
VSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGMVQTVQTRYTFGAALFVGWVAGGLTLIGG
VMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTEDEVQ
SYPSKHDYV

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

361/615

FIGURE 357

GGAAAACTGTTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCGG
AGTCCAGCTGGCTAAAACTCATCCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTGGG
CTGTTTCTTGGTGGTGTGGAATGGTGGGCACAGTGGCTGTCACTGTCATGCCTCAGTGGAGA
GTGTGGGCCCTTCATTGAAAACAACATCGTGGTTTTTAAAACTTCTGGGAAGGACTGTGGATG
AATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGGCTCTT
TCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCCTTCTTGGCT
TTCATGATGGCCATCCTTGGCATGAAATGCACCAGGTGCACGGGGGACAATGAGAAGGTGAAG
GCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGCTCATCCCT
GTGAGCTGGGTGGCCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAATGTTGCCCAA
AAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGCTGATTGTTGGA
GGAGCTCTGTTCTGCTGCGTTTTTGTGCAACGAAAAGAGCAGTAGCTACAGATACTCGATA
CCTTCCCATCGCACAAACCAAAAAAGTTATCACACCGGAAAGAAGTCACCGAGCGTCTACTCC
AGAAGTCAGTATGTGTAGTTGTGTATGTTTTTTAACTTTACTATAAAGCCATGCAATGACA
AAAATCTATATTACTTTCTCAAATGGACCCCAAGAACTTTGATTTACTGTTCTTAATGCTC
CTAATCTTAATTACAGGAACGTGTCATCAGCTATTTATGATTCTATAAGCTATTTTCAGCAGAA
TGAGATATTAAACCAATGCTTTGATTGTTCTAGAAAGTATAGTAATTTGTTTTCTAAGGTGG
TTCAAGCATCTACTCTTTTATCATTACTTCAAATGACATTGCTAAAGACTGCATTATTTT
ACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAGTGTAACATTTATATCTCA
CATAGAGACATGCTTATATGGTTTTATTTAAATGAAATGCCAGTCCATTACACTGAATAAAT
AGAACTCAACTATTGCTTTTCAGGGAAATCATGGATAGGGTTGAAGAAGGTTACTATTAATTG
TTTAAAAACAGCTTAGGGATTAATGTCTCCATTTATAATGAAGATTAATAATGAAGGCTTTAA
TCAGCATTGTAAAGGAAATGAATGGCTTTCTGATATGCTGTTTTTTAGCCTAGGAGTTAGAA
ATCCTAACTTCTTTATCCTCTTCTCCCAGAGGCTTTTTTTTTCTTGTGTATTAAATTAACATT
TTTAAACCGCAGATATTTTGTCAAGGGGCTTTGCATTCAAACCTGCTTTTCCAGGGCTATACTC
AGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATGGTTTTAGGAAAGTGAAAATATTTTT
GTTTTTGTATTTGAAGAAGAATGATGCATTTTGACAAGAAATCATATATGTATGGATATATTT
TAATAAGTATTTGAGTACAGACTTTGAGGTTTCATCAATATAAATAAAGAGCAGAAAAATAT
GTCTTGGTTTTCAATTGCTTACCAAAAAACAACAACAAAAAAGTTGTCCTTTGAGAACTTC
ACCTGCTCCTATGTGGGTACCTGAGTCAAATTTGTCATTTTGTCTGTGAAAAATAAATTTT
CTTCTTGTACCATTTCTGTTTAGTTTTACTAAAATCTGTAAATACTGTATTTTTCTGTTTATT
CCAAATTTGATGAACTGACAATCCAATTTGAAAGTTTGTGTCGACGTCTGTCTAGCTTAAAT
GAATGTGTTCTATTTGCTTTATACATTTATATTAATAAATGTACATTTTCTAATT

362/615

FIGURE 358

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735

><subunit 1 of 1, 225 aa, 1 stop

><MW: 24845, pI: 9.07, NX(S/T): 0

MATHALEIAGLFLGGVGMVGTVAVTVMQWRVSAFIENNIIVVFENFWEGLWMNCVRQANIRMQ
CKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGIIF
IITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVFCCN
EKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

363/615

FIGURE 359

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCCTCGCCCTCCTGCTCGCGCCCC
GCCGCCATGGCTGCCTCCCCGCGCGGCCTGCTGTCCTGGCCCTGACCGGGCTGGCGCTGCTC
CTGCTCCTGTGCTGGGGCCCAGGTGGCATAAGTGGAAATAAACTCAAGCTGATGCTTCAAAAA
CGAGAAGCACCTGTTCCAATAAGACTAAAGTGGCCGTTGATGAGAATAAAGCCAAAGAATTC
CTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCCCGAGGTGCAGCAG
TGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATCACCTAT
TGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCACTATGAT
GAAGACTCTGCAATTGGTCCCCGGAGCCCCCTACGGCTTTAGGCATGGAGCCAGCGTCAACTAC
GATGACTACTTAACCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATTCTCTTCATGT
ATCTCCTAATGCCTTACACTACTTGGTTTCTGATTTGCTCTATTTTCAGCAGATCTTTTCTACC
TACTTTGTGTGATCAAAAAAGAAGAGTTAAAACAACACATGTAAATGCCTTTTGATATTTTCAT
GGGAATGCCTCTCATTTAAAAATAGAAATAAAGCATTTTGTAAAAAGA

364/615

FIGURE 360

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742

><subunit 1 of 1, 148 aa, 1 stop

><MW: 17183, pI: 8.77, NX(S/T): 0

MAASPARPAVLALTGLALLLLCWGPGGISGNKCLKMLQKREAPVPTKTKVAVDENKAKEFLG
SLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRNGHEYYGDIYQRHYDED
SAIGPRSPYGFRHGASVNYDDY

Signal peptide:

amino acids 1-30

365/615

FIGURE 361

GAGATTGGAAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAGA
TTCCCCAGGCTCTCAGAGAAGATCAGCAGAAAGTCTGCAAGACCCTAAGAACCATCAGCCCTC
AGCTGCACCTCCTCCCCTCCAAGGATGACAAAGGCGCTACTCATCTATTTGGTCAGCAGCTTT
CTTGCCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCCAGGTGCTGCAGCTGGAG
GACTTGATGGGTTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCTGGCTTTTGTGGAAAGC
AAGTTCAACATATCAAAGATAAATGAAAATGCGGATGGAAGCTTTGACTATGGCCTCTTCCAG
ATCAACAGCCACTACTGGTGCAACGATTATAAGAGTTACTCGGAAAACCTTTGCCACGTAGAC
TGTCAGATCTGCTGAATCCCAACCTTCTTGACGGCATCCACTGCGCAAAAAGGATTGTGTCC
GGAGCACGGGGGATGAACAACTGGGTAGAATGGAGGTTGCACTGTTTCAAGCCGGCCACTCTCC
TACTGGCTGACAGGATGCCGCCTGAGATTGAAACAGGGTGCGGGTGACCGTGGAGTCATTCCA
AGACTCCTGTCCTCACTCAGGGATTCTTCATTTCTTCTCCTACTGCCTCCACTTCATGTTAT
TTTCTTCCCTTCCCATTACAACTAAAACAGACCAGAGCCCCAGGAATAAATGGTTTTCTTGG
CTTCCTCCTTACTCCCATCTGGACCCAGTCCCCTGGTTCCTGTCTGTTATTTGTAAACTGAGG
ACCACAATAAAGAAATCTTTATATTTATCG

366/615

FIGURE 362

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746

><subunit 1 of 1, 148 aa, 1 stop

><MW: 16896, pI: 6.05, NX(S/T): 1

MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKIN
ENADGSFDYGLFQINSHYWCNDYKSYSENLCNVDCQDLLNPNNLAGIHC AKRIVSGARGMNNW
VEWRLHCSGRPLSYWLTGCRLR

Signal peptide:

amino acids 1-18

367/615

FIGURE 363

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTCAGCCCTGCTTGACTGAGAACCCAC
CAGCTCATCCCAGACACCTCATAGCAACCTATTTATACAAAGGGGGAAAGAAACACCTGAGCA
GAATGGAATCATTATTTTTTTTCCCAAGGAGAAAACCGGGGTAAAGGGAGGGGAAGCAATTCAAT
TTGAAGTCCCTGTGAATGGGCTTTTTCAGAAGGCAATTAAAGAAATCCACTCAGAGAGGACTTGG
GGTGAAACTTGGGTCTGTGGTTTTCTGATTGTAAGTGAAGCAGGTCTTGCACACGCTGTTG
GCAAAATGTCAGGACCAGGTTAAGTGACTGGCAGAAAACTTCCAGGTGGAACAAGCAACCCAT
GTTCTGCTGCAAGCTTGAAGGAGCCTGGAGCGGGAGAAAGCTAACTTGAACATGACCTGTTGC
ATTTGGCAAGTTCTAGCAAC**ATG**CTCCTAAGGAAGCGATACAGGCACAGACCATGCAGACTCC
AGTTCCCTCCTGCTGCTCCTGATGCTGGGATGCGTCTGATGATGGTGGCGATGTTGCACCCTC
CCCACCACACCCTGCACCAGACTGTCACAGCCCAAGCCAGCAAGCACAGCCCTGAAGCCAGGT
ACCGCCTGGACTTTGGGGAATCCCAGGATTGGGTACTGGAAGCTGAGGATGAGGGTGAAGAGT
ACAGCCCTCTGGAGGGCCTGCCACCCTTTATCTCACTGCGGGAGGATCAGCTGCTGGTGGCCG
TGGCCTTACCCCAGGCCAGAAGGAACCAGAGCCAGGGCAGGAGAGGTGGGAGCTACCGCCTCA
TCAAGCAGCCAAGGAGGCAGGATAAGGAAGCCCCAAAGAGGGACTGGGGGGCTGATGAGGACG
GGGAGGTGTCTGAAGAAGAGGAGTTGACCCCGTTACGCCTGGACCCACGTGGCCTCCAGGAGG
CACTCAGTGCCCGCATCCCCCTCCAGAGGGCTCTGCCCGAGGTGCGGCACCCACTGTGTCTGC
AGCAGCACCCCTCAGGACAGCCTGCCCCACAGCCAGCGTCATCCTCTGTTTCCATGATGAGGCCT
GGTCCACTCTCCTGCGGACTGTACACAGCATCCTCGACACAGTGCCCAGGGCCTTCCTGAAGG
AGATCATCCTCGTGGACGACCTCAGCCAGCAAGGACAACCTCAAGTCTGCTCTCAGCGAATATG
TGGCCAGGCTGGAGGGGGTGAAGTTACTCAGGAGCAACAAGAGGCTGGGTGCCATCAGGGCCC
GGATGCTGGGGGCCACCAGAGCCACCGGGGATGTGCTCGTCTTCATGGATGCCCACTGCGAGT
GCCACCCAGGCTGGCTGGAGCCCCCTCCTCAGCAGAAATAGCTGGTGACAGGAGCCGAGTGGTAT
CTCCGGTGATAGATGTGATTGACTGGAAGACTTTCCAGTATTACCCCTCAAAGGACCTGCAGC
GTGGGGTGTGGACTGGAAGCTGGATTTCCACTGGGAACCTTTGCCAGAGCATGTGAGGAAGG
CCCTCCAGTCCCCCATAAGCCCCATCAGGAGCCCTGTGGTGCCCGGAGAGGTGGTGGCCATGG
ACAGACATTACTTCCAAAACACTGGAGCGTATGACTCTCTTATGTGCTGCGTGGCAGGTGGTGA
ACCTCGAACTGTCTTTCAAGGCCTGGCTCTGTGGTGGCTCTGTTGAAATCCTTCCCTGCTCTC
GGGTAGGACACATCTACCAAAATCAGGATTCCCATTTCCCCCTCGACCAGGAGGCCACCCTGA
GGAACAGGGTTCGCATTGCTGAGACCTGGCTGGGGTCATTCAAAGAAACCTTCTACAAGCATA
GCCCAGAGGCCCTTCTCCTTGAGCAAGGCTGAGAAGCCAGACTGCATGGAACGCTTGCAGCTGC
AAAGGAGACTGGGTTGTGCGACATTCCACTGGTTTCTGGCTAATGTCTACCCTGAGCTGTACC
CATCTGAACCCAGGCCAGTTTCTCTGGAAAGCTCCACAACACTGGACTTGGGCTCTGTGCAG
ACTGCCAGGCAGAAGGGGACATCCTGGGCTGTCCCATGGTGTGGCTCCTTGCAGTGACAGCC
GGCAGCAACAGTACCTGCAGCACACCAGCAGGAAGGAGATTCACTTTGGCAGCCACAGCACC
TGTGCTTTGCTGTGAGGCAGGAGCAGGTGATTCTTCAGAACTGCACGGAGGAAGGCCTGGCCA
TCCACCAGCAGCACTGGGACTTCCAGGAGAATGGGATGATTGTCCACATTCTTTCTGGGAAAT
GCATGGAAGCTGTGGTGCAAGAAAACAATAAAGATTTGTACCTGCGTCCGTGTGATGGAAAAG
CCCGCCAGCAGTGGCGATTTGACCAGATAAATGCTGTGGATGAACGAT**TGA**ATGTCAATGTCAG
AAGGAAAAGAGAATTTTGGCCATCAAAATCCAGCTCCAAGTGAACGTAAAGAGCTTATATATT
TCATGAAGCTGATCCTTTTGTGTGTGTGCTCCTTGTGTTAGGAGAGAAAAAGCTCTATGAAA
GAATATAGGAAGTTTCTCCTTTTCACACCTTATTTTATTGACTGCTGGCTGCTTA

368/615

FIGURE 364

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760

><subunit 1 of 1, 639 aa, 1 stop

><MW: 73063, pI: 6.84, NX(S/T): 2

MLLRKRYRHRPCRLQFLLLLLLMLGCVLMMVAMLHPPHHTLHQT VTAQASKHSPEARYRLDFGE
SQDWVLEAEDEGE EYSPL EGLPPFISLREDQLLVAVALPQARRNQSQGRRGGSYRLIKQPRRQ
DKEAPKRDWGADEDEGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHPQDS
LPTASVILCFHDEAWSTLLRTVHSILDTPRAFLKEIILVDDLSQQGQLKSALSEYVARLEGV
KLLRSNKRLGAIRARMLGATRATGDVLVFMDAHCECHPGWLEPLLSRIAGDRSRVVSPVIDVI
DWKTFQYYPSKDLQRGVLDWKLDHFHWEPLPEHVRKALQSPISPIRSPVVPGEVVAMDRHYFQN
TGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGHYQND SHSPLDQEATLRNRVRIA
ETWLG SFKETFYKHSPEAFSLSKAEKPDCMERLQLQRR LGCRT FHWFLANVYPELYPSEPRPS
FSGKLHNTGLGLCADCQAEGDILGCPMVLAPCSDSRQQQYLQHTSRKEIHFGSPQHLCFAVRQ
EQVILQNCTEEGLAIHQHWFQENGMIVHILSGKCMEAVVQENNKDLYLRPCDGKARQQWRF
DQINAVDER

Signal peptide:

amino acids 1-28

369/615

FIGURE 365

GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCGG
AGCCAGACGCTGACCACGTTCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCCGGC
AGCCGGGAGCCATGCGACCCAGGGCCCCGCGCCTCCCCGCAGCGGCTCCGCGGCCTCCTGC
TGCTCCTGCTGCTGCAGCTGCCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAGCAA
AGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAG
CAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTGGGATCC
CAGGTCGGGATGGATTCAAAGGAGAAAAGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTCCT
GGACACCCAACTACAAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAA
TTGCGGAGTGACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTTCAGTGGCT
CACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTACATTCAATGGAGCTG
AATGTTTCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGA
ATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTG
GATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTTCAGATTACCCAAAAGGAGATGCTTCTA
CTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAATTAAATGCTTTAATTTT
CATTTGCTACCTCTTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAG
TTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTC
CACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAGTGTTTCAATATTTTTTT
TAGTTGGTTAGAATACTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTG
TGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTTAAAAAATATAAAAGCTACCAATCTTTG
TACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA

370/615

FIGURE 366

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGVP
GRDGSPGANVIPGTPGIPGRDGFKEGKECLRESFEESWTPNYKQCSWSSLNYGIDLKIAEC
TFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYLDQGSPEMNSTI
NIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

371/615

FIGURE 367

GTAAACCAGCGCAGTCCTCCGTGCGTCCCGCCCGCCGCTGCCCTCACTCCCGGCCAGGATGGC
ATCCTGTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGTTCTGGCCCTGCGGTGCT
CACAGACGATGTTCCACAGGAGCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCCGTC
GGGAGAAGGCCCGTGAGAGCACCAGCCCCGGCCGGGAGCCCGTGGACACCGGTCCCCCAGC
CCCCACCGTCGCGCCAGGACCCGAGGACAGCACC GCGCAGGAGCGGCTGGACCAGGGCGGCGG
GTCGCTGGGGCCCGGCGCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTGCGTGGT
GCTGGCGCTCGTGGTTCGTGCGCTGAGAAAGTTTTCTGCCTCCTGAAGCGAATAAAGGGGCCG
CGCCCGGCCGCGGCGCGACTCGGCAAAAAAAAAAAAAA

372/615

FIGURE 368

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398
><subunit 1 of 1, 121 aa, 1 stop
><MW: 12073, pI: 4.11, NX(S/T): 0
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVESTSPGREPVDGTP
PAPTVPAGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 91-110

Glycosaminoglycan attachment site.

amino acids 44-47

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 116-119

N-myristoylation site.

amino acids 91-96

373/615

FIGURE 369

GGCCGTTGGTTGGTGCGCGGCTGAAGGGTGTGGCGCGAGCAGCGTCGTTGGTTGGCCGGCGGC
GGGCCGGGACGGGCATGGCCCTGCTGCTGTGCCTGGTGTGCCTGACGGCGGCGCTGGCCCACG
GCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGAACT
TCAAGTCCTGGTGGGTGGGCGACATCCCCGTGTGAGGGGCGCTGCTCACCGACTGGAGCGACG
ACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATCACCCGGGAGAAGCTGGACCAAG
TGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCCCCGGGT
ATTTCCCCAACGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAACGCCATCA
TCGAAAGGCACCTGGCACCAGGCAGCTGGGGAGGAGGGCAGCTCTCCAGGGAGGGACCCAGCC
TAGCACCTGAAGGATCAATGCCATCACCCCGCGGGGACCTCCCCTAAGTAGCCCCCAGAGGCG
CTGGGAGTGTTGCCACCGCCCTCCCCTGAAGTTTGCTCCATCTCACGCTGGGGGTCAACCTGG
GGACCCCTTCCCTCCGGGCCATGGACACACATACATGAAAACCAGGCCGCATCGACTGTCAGC
ACCGCTGTGGCATCTTCCAGTACGAGACCATCTCCTGCAACAACCTGCACAGACTCGCACGTGCG
CCTGCTTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCCGTGCCAGGGCCCCTAC
TGTCCTTGGGGTCCCAGGCTCTCCTTGGAGGGGGCTCCCCGCCTTCCACCTGGCTGTCATCGG
GTAGGGCGGGGCGTGGGTTTCAGGGGCGCACCACTTCCAAGCCTGTGTCCACAGGTCTTCGG
CGCAGTGGAAGTCAGCTGTCCAGGGCCTCCTGAACTACATAAATAACTGGCACAAGTAAGTCC
CCTCCTCAAACCAACACAGGCAGTGTGTGTATGTGAGCACCTCGTGGGTGAGTATGTGTGGGG
CACAGGCTGGCTCCCTCAGCTCCACGTCTAGAGGGGCTCCCGAGGAGGTGGAACCTCAACC
CAGCTCTGCGCAGGAGGCGGCTGCAGTCCTTTTCTCCCTCAAAGGTCTCCGACCCTCAGCTGG
AGGCGGGCATCTTTCTTAAAGGGTCCCCATAGGGTCTGGTTCCACCCCATCCAGGTCTGTGG
TCAGAGCCTGGGAGGGTTCCCTACGATGGTTAGGGGTGCCCCATGGAGGGGCTGACTGCCCA
CATTGCCTTTCAGACAGGACACGAGCATGAGGTAAGGCCGCCCTGACCTGGACTTCAGGGGGA
GGGGGTAAAGGGAGAGAGGAGGGGGGCTAGGGGGTCTCTAGATCAGTGGGGGCACTGCAGGT
GGGGCTCTCCCTATACCTGGGACACCTGCTGGATGTCACCTCTGCAACCACACCCATGTGGTG
GTTTCATGAACAGACCACGCTCCTCTGCCTTCTCCTGGCCTGGGACACACAGAGCCACCCCGG
CCTTGTGAGTGACCCAGAGAAGGGAGGCCCTCGGGAGAAGGGGTGCTCGTAAGCCAACACCAGC
GTGCCGCGGCCCTGCACACCCTTCGGACATCCCAGGCACGAGGGTGTGCTGGATGTGGCCACAC
ATAGGACCACACGTCCCAGCTGGGAGGAGAGGCCTGGGGCCCCCAGGGAGGGAGGCAGGGGGT
GGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCCCCGAGCCTGGTATCGCCAGCCTTAAGGT
GTCTGGAGCCCCCACACTTGGCCAACCTGACCTTGGAAGATGCTGCTGAGTGTCTCAAGCAGC
ACTGACAGCAGCTGGGCCTGCCCCAGGGCAACGTGGGGGCGGAGACTCAGCTGGACAGCCCCT
GCCTGTCACTCTGGAGCTGGGCTGCTGCTGCCTCAGGACCCCCTCTCCGACCCCGGACAGAGC
TGAGCTGGCCAGGGCCAGGAGGGCGGGAGGGAGGGAATGGGGGTGGGCTGTGCGCAGCATCAG
CGCCTGGGCAGGTCCGCAGAGCTGCGGGATGTGATTAAAGTCCCTGATGTTTCTC

374/615

FIGURE 370

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399

><subunit 1 of 1, 157 aa, 1 stop

><MW: 17681, pI: 7.65, NX(S/T): 1

MALLLCCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMKE
LHLAIPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIIERHL
APGSWGGGQLSREGPSLAPEGSMPSPRGDLP

Signal peptide:

amino acids 1-15

375/615

FIGURE 371

GCCGGCTGTGCAGAGACGCCATGTACCGGCTCCTGTCAGCAGTGACTGCCCCGGGCTGCCGCCC
CCGGGGGCTTGGCCTCAAGCTGCGGACGACGCGGGGTCCATCAGCGCGCCGGGCTGCCGCCTC
TCGGCCACGGCTGGGTGCGGGGCTCGGGCTGGGGCTGGGGCTGGCGCTCGGGGTGAAGCTGG
CAGGTGGGCTGAGGGGCGCGGCCCCGGCGCAGTCCCCCGCGGCCCCGACCCTGAGGCGTCGC
CTCTGGCCGAGCCGCCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGCAGACCCGGCGCCGC
CCTGCTCCAGGTGCTTCGCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGATCAAGG
ATGAGGTGGGCGCACCGGGCATAGTGGTTGGAGTTTCTGTAGATGGAAAAGAAGTCTGGTCAG
AAGGTTTAGGTTATGCTGATGTTGAGAACCGTGTACCATGTAAACCAGAGACAGTTATGCGAA
TTGCTAGCATCAGCAAAAGTCTCACCATGGTTGCTCTTGCCAAATTGTGGGAAGCAGGGAAAC
TGGATCTTGATATTCCAGTACAACATTATGTTCCCGAATTCCCAGAAAAAGAATATGAAGGTG
AAAAGGTTTCTGTCACAACAAGATTACTGATTTCCCATTTAAGTGGAATTCGTCATTATGAAA
AGGACATAAAAAAGGTGAAAGAAGAGAAAGCTTATAAGCCTTGAAGATGATGAAAGAGAATG
TTGCATTTGAGCAAGAAAAAGAAGGCAAAAGTAATGAAAAGAATGATTTTACTAAATTTAAAA
CAGAGCAGGAGAATGAAGCCAAATGCCGGAATTCAAACCTGGCAAGAAAAAGAATGATTTTG
AACAAGGCGAATTATATTTGAGAGAAAAGTTTGAAAATTC AATTGAATCCCTAAGATTATTTA
AAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTTGTATTCAACTTTTGGCTATACCC
TACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAAATATTTGGACTATATGCAGAAAATAT
TCCATGACTTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGCCAGTGATTTACAATAGAG
CAAGGTAAATGAATACCTTCTGCTGTGTCTAGCTATATCGCATCTTAACACTATTTTATTAAT
TAAAAGTCAAATTTTCTTTGTTTCCATTCCAAAATCAACCTGCCACATTTTGGGAGCTTTTCT
ACATGTCTGTTTTCTCATCTGTAAAGTGAAGGAAGTAAACATGTTTATAAAGTAAAAAA

376/615

FIGURE 372

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41221, pI: 8.54, NX(S/T): 0

MYRLLSAVTARAAAPGGLASSCGRRGVHQAGLPPLGHGWVGGLGLGLGLALGVKLAGGLRGA
APAQSPAAPDPEASPLAEPPQEQSLAPWSPQTPAPPCSRCFARAIESSRDLLHRIKDEVGAPG
IVVGVSVDGKEVWSEGLGYADVENRVPCKPETVMRIASISKSLTMVALAKLWEAGKLDLDIPV
QHYVPEFPEKEYEGEKVSVTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAFEQEK
EGKSNEKNDFTKFKTEQENEAKCRNSKPGKKKNDFEQGELYLREKFENSIESLRLFKNDPLFF
KPGSQFLYSTFGYTLLAAIVERASGCKYLDYMQKIFHDLMLTTVQEENEPVIYNRAR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 39-60

377/615

FIGURE 373

GACTACGGGGAGAGAGAGAGAGACCAGGACAGCTGCTGAGACCTCTAAGAAGTCCAGATACTAA
GAGCAAAGATGTTTTCAAACCTGGGGGCCCTCATTGTCTTCTACGGGCTGTTAGCCCAGACCATGG
CCCAGTTTGGAGGCCCTGCCCCGTGCCCTGGACCAGACCCTGCCCTTGAATGTGAATCCAGCCCTG
CCCTTGAGTCCCACAGGTCTTGCAGGAAGCTTGACAAATGCCCTCAGCAATGGCCTGCTGTCT
GGGGGCCTGTTGGGCATTCTGGAAAACCTTCCGCTCCTGGACATCCTGAAGCCTGGAGGAGGT
ACTTCTGGTGGCCTCCTTGGGGGACTGCTTGGAAAAGTGACGTGAGTGATTCTTGGCCTGAAC
AACATCATTGACATAAAGGTCAGTACCCCCAGCTGCTGGAACTTGGCCTTGTGCAGAGCCCT
GATGGCCACCGTCTCTATGTCACCATCCCTCTCGGCATAAAGCTCCAAGTGAATACGCCCCTG
GTCGGTGCAAGTCTGTTGAGGCTGGCTGTGAAGCTGGACATCACTGCAGAAATCTTAGCTGTG
AGAGATAAGCAGGAGAGGATCCACCTGGTCCTTGGTGACTGCACCCATTCCCCTGGAAGCCTG
CAAATTTCTCTGCTTGATGGACTTGGCCCCCTCCCCATTCAAGGTCTTCTGGACAGCCTCACA
GGGATCTTGAATAAAGTCCTGCCTGAGTTGGTTCAGGGCAACGTGTGCCCTCTGGTCAATGAG
GTTCTCAGAGGCTTGGACATCACCTGGTGCATGACATTGTTAACATGCTGATCCACGGACTA
CAGTTTGTTCATCAAGGTCTTAAGCCTTCCAGGAAGGGGCTGGCCTCTGCTGAGCTGCTTCCCAG
TGCTCACAGATGGCTGGCCCATGTGCTGGAAGATGACACAGTTGCCTTCTCTCCGAGGAACCT
GCCCCCTCTCCTTTCCACCAGGCGTGTGTAACATCCCATGTGCCTCACCTAATAAAATGGCT
CTTCTTATGCA

378/615

FIGURE 374

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76533
><subunit 1 of 1, 256 aa, 1 stop
><MW: 26713, pI: 5.62, NX(S/T): 0
MFQTGGLIVFYGLLAQTMAQFGGLPVFLDQTLPLNVNPALPLSPTGLAGSLTNALSNGLL
SGGLLGILENLPLLDILKPGGGTSGGLLGGLLGKVTSVIPGLNNIIDIKVTDLPQLLELGL
VQSPDGHRLYVTIPLGIKLQVNTPLVGASLLRLAVKLDITAEILAVRDKQERIHVLVGLDC
THSPGSLQISLLDGLGPLPIQGLLDSL TGILNKVLPVLVQGNVCPLVNEVLRGLDITLVH
DIVNMLIHGLQFVIKV

Important features of the protein:**Signal peptide:**

Amino acids 1-19

Transmembrane domain:

Amino acids 79-97

N-myristoylation sites:

Amino acids 46-52;49-55;58-64;62-68;66-72;80-86;81-87;
82-88;85-91;86-92;89-95;202-208;233-239

379/615

FIGURE 375

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCCTAAGTTGACTGTCCTTT
AAATATGTCAAGATCCAGACTTTTCAGTGTACCTCAGCGATCTCAACGATAGGGATCTTGTG
TTTGCCGCTATTCCAGTTGGTGCTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGTA
TTATAATGACCAACACCCTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTTGGTGGC
AGCTCTTCTCTGTGGAGCTGTGGTCCTCTGCCTCCAGTGCTGGCTGAGGAGACCCCGAATTGA
TTCTCACAGGCGCACCATGGCAGTTTTTGCTGTTGGAGACTTGGACTCTATTTATGGGACAGA
AGCAGCTGTGAGTCCAACCTGTTGGAATTCACCTTCAAACCTCAAACCCCTGACCTATATCCTGT
TCCTGCTCCATGTTTTGGCCCTTTAGGCTCCCCACCTCCATATGAAGAAATTGTAAAAACAAC
CTGATTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATTCAAAACATCAA
ATTTAGGAATAGTTATTTTCAGTTGTTGGAAATGTCCAGAGATCTATTCATATAGTCTGAGGAA
GGACAATTCGACAAAAGAATGGATGTTGGAAAAAATTTGGTCATGGAGATGTTTAAATAGTA
AAGTAGCAGGCTTTTGATGTGTCACTGCTGTATCATACTTTTATGCTACACAACCAAATTAAT
GCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTTTCCATCACATTTA
GGACTCCACTGCAGTATACAGCACACCATTTTCTGCTTTAAACTCTTTCCTAGCATGGGGTCC
ATAAAAATTATTATAATTTAACAATAGCCCAAGCCGAGAATCCAACATGTCCAGAACCAGAAC
CAGAAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAAGAAAGTTTGGAGTTG
AAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCTCAGCAAAAACAAGAGGT
TTTATGCCCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGAAGGAGATTGCTGAAGATA
TAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTTCCCCTTTTACAGTAATGAATGT
GGCCTCCATAGTCCATAGTGTCTCTGGAGCCTCAGGGCTTGGCATTATTGTCAGCATCATG
CTAAGAACCTTCGGCATAGGTATCTGTTCCCATGAGGACTGCAGAAGTAGCAATGAGACATCT
TCAAGTGGCATTTTGGCAGTGGCCATCAGCAGGGGGACAGACAAAAACATCCATCACAGATGA
CATATGATCTTCAGCTGACAAATTTGTTGAACAAAACAATAAACATCAATAGATATCTAAAAA

380/615

FIGURE 376

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303

><subunit 1 of 1, 146 aa, 1 stop

><MW: 16116, pI: 4.99, NX(S/T): 0

MSRSRLFSVTSIAISTIGILCLPLFQLVLSDLPCEEDEMVCVNYNDQHPNGWYIWILLLLVLVAA
LLCGAVVLCLQCWLRRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYPVP
APCFGPLGSPPPYEEIVKTT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 52-70

381/615

FIGURE 377

CGCGGATCGGACCCAAGCAGGTTCGGCGGCGGGCGGCAGGAGAGCGGCCGGGCGTCAGCTCCTCG
ACCCCCGTGTCGGGCTAGTCCAGCGAGGCGGACGGGCGGCGTGGGCCCC**ATG**GCCAGGCCCGGC
ATGGAGCGGTGGCGCGACCGGCTGGCGCTGGTGACGGGGGCTCGGGGGGCATCGGCGCGGCC
GTGGCCCCGGGCCCTGGTCCAGCAGGGACTGAAGGTGGTGGGCTGCGCCCGCACTGTGGGCAAC
ATCGAGGAGCTGGCTGCTGAATGTAAGAGTGCAGGCTACCCCGGGACTTTGATCCCCTACAGA
TGTGACCTATCAAATGAAGAGGACATCCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGC
GGTGTAGACATCTGCATCAACAATGCTGGCTTGGCCCGGCCTGACACCCTGCTCTCAGGCAGC
ACCAGTGGTTGGAAGGACATGTTCAATGTGAACGTGCTGGCCCTCAGCATCTGCACACGGGAA
GCCTACCAGTCCATGAAGGAGCGGAATGTGGACGATGGGCACATCATTAACATCAATAGCATG
TCTGGCCACCGAGTGTTACCCCTGTCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTC
ACTGCGCTGACAGAGGGACTGAGGCAAGAGCTTCGGGAGGCCAGACCCACATCCGAGCCACG
TGCATCTCTCCAGGTGTGGTGGAGACACAATTCGCCCTTCAAACCTCCACGACAAGGACCCTGAG
AAGGCAGCTGCCACCTATGAGCAAATGAAGTGTCTCAAACCCGAGGATGTGGCCGAGGCTGTT
ATCTACGTCCTCAGCACCCCCGCACACATCCAGATTGGAGACATCCAGATGAGGCCCCACGGAG
CAGGTGACCT**TAG**TGACTGTGGGAGCTCCTCCTTCCCTCCCCACCCTTCATGGCTTGCCTCCTG
CCTCTGGATTTTAGGTGTTGATTTCTGGATCACGGGATACCACTTCCTGTCCACACCCCGACC
AGGGGCTAGAAAATTTGTTTGAGATTTTTATATCATCTTGTCAAATTGCTTCAGTTGTAAATG
TGAAAATGGGCTGGGGAAAGGAGGTGGTGTCCCTAATTGTTTTACTTGTTAACTTGTTCTTG
TGCCCTGGGCACTTGGCCTTTGTCTGCTCTCAGTGTCTTCCCTTTGACATGGGAAAGGAGTT
GTGGCCAAAATCCCCATCTTCTTGACCTCAACGTCTGTGGCTCAGGGCTGGGGTGGCAGAGG
GAGGCCTTACCTTATATCTGTGTTGTTATCCAGGGCTCCAGACTTCCTCCTCTGCCTGCCCC
ACTGCACCTCTCCCCCTTATCTATCTCCTTCTCGGCTCCCCAGCCCAGTCTTGCTTCTTGT
CCCCTCCTGGGGTCATCCCTCCACTCTGACTCTGACTATGGCAGCAGAACACCAGGGCCTGGC
CCAGTGGATTCATGGTGATCATTAAGAAAGAAATCGCAACCAAAAAAAAAAAAA

382/615

FIGURE 378

MARPGMERWRDRLALVTGASGGIGA AAVARALVQQGLKVVG CARTVGNIEELAAECKSAGYPGT
LIPYRCDLSNEEDILSMFSAIRSQHSGVDICINNAGLARPD TLLSGSTSGWKDMFNVNVLALS
ICTREAYQSMKERNVDDGHIININSMGHRVLP LSVTHFY SATKYAVTALTEGLRQELREAQT
HIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVLSTPAHIQIGDIQ
MRPTEQVT

Important features of the protein:**Signal peptide:**

amino acids 1-17

N-myristoylation sites.amino acids 18-24, 21-27, 22-28, 24-30, 40-46, 90-96, 109-115,
199-205**Short-chain alcohol dehydrogenase.**

amino acids 30-42, 104-114

383/615

FIGURE 379

GAGCGGAGTAAAATCTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACCGGCGTT
TCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGACGCAGCTGACGCCCGCTTATTAGC
TCTCGCTGCGTCGCCCCGGCTCAGAAGCTCCGTGGCGGGCGGCGACCGTGACGAGAAGCCACG
GCCAGCTCAGTTCTCTTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCCCTTTTAAACTCCCT
CTTCAAACTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATACAACCTTGCTGAAGATGAA
GAATATACAATATTGAGGATATTTTTTTCTTTTTTTTTTCAAGTCTTGATTTGTGGCTTACCT
CAAGTTACCATTTTTTCAGTCAAGTCTGTTTGTGTTGCTTCTTCAGAAATGTTTTTTACAATCTC
AAGAAAAATATGTCCAGAAATTGAGTTTACTGTTGCTTGTATTTGGACTCATTTGGGGATT
GATGTTACTGCACTATACTTTTCAACAACCAAGACATCAAAGCAGTGTCAGTTACGTGAGCA
AATACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAATAAGAACACAGTGGA
TGTCGAGAACGGTGCTTCTATGGCAGGATATGCGGATCTGAAAAGAACAATTGCTGTCCTTCT
GGATGACATTTTGCAACGATTGGTGAAGCTGGAGAACAAGTTGACTATATTGTTGTGAATGG
CTCAGCAGCCAACACCACCAATGGTACTAGTGGGAATTTGGTGCCAGTAACCACAAATAAAAG
AACGAATGTCTCGGGCAGTATCAGATAGCAGTTGAAAATCACCTTGTGCTGCTCCATCCACTG
TGGATTATATCCTATGGCAGAAAAGCTTTATAATTGCTGGCTTAGGACAGAGCAATACTTTAC
AATAAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTTCATGGAACCTAATTCTGTACATA
AAAATTTTAAAGTTATTTGTTTGCTTTTCAGGCAAGTCTGTTCAATGCTGTACTATGTCCTTAA
AGAGAATTTGGTAACTTGGTTGATGTGGTAAGCAGATAGGTGAGTTTTGTATAAATCTTTTGT
GTTTGAGATCAAGCTGAAATGAAAACACTGAAAACATGGATTTCATTTCTATAACACATTTAT
TAAAGTATATAACACGTTTTTTGGACAAGTGAAGAATGTTAATCATTCTGTCATTTGTTCTC
AATAGATGTAAGTGTAGACTACGGCTATTTGAAAAATGTGCTTATTGTACTATATTTTGT
ATTCGAATTATGAGCAGAGAAAGGAAATATAATGTTGAAAATAATGTTTTGAAATCATGACCC
AAAGAATGTATTGATTTGCACTATCCTTCAGAATAACTGAAGGTTAATTATTGTATATTTTAA
AAAATTACACTTATAAGAGTATAATCCTTGAAATGGGTAGCAGCCACTGTCCATTACCTATCGT
AAACATTGGGGCAATTTAATAACAGCATTAAAATAGTTGTAAACTCTAATCTTATACTTATTG
AAGAATAAAAGATATTTTTATGATGAGAGTAACAATAAAGTATTCATGATTTTTTCACATACAT
GAATGTTCATTTAAAGTTTAAATCCTTTGAGTGTCTATGCTATCAGGAAAGCACATTATTTCC
ATATTTGGGTAAATTTTGCTTTTATTATATTTGGTCTAGGAGGAAGGGACTTTGGAGAATGGAA
CTCTTGAGGACTTTAGCCAGGTGTATATAATAAAGGTACTTTTGTGCTGCATTAAATTTGCTTG
GAAAGTGTTAACATTATATTATATAAGAGTATCCTTTATGAAATTTTGAATTTGTATAACAGA
TGCATTAGATATTCATTTTATATAATGGCCACTTAAATAAGAACATTTAAATATAAACTAT
GAAGATTGACTATCTTTTCAGGAAAAAGCTGTATATAGCACAGGGAACCCTAATCTTGGGTA
ATTCTAGTATAAAACAAATTATACTTTTATTTAAATTTCCCTTGTAGCAAATCTAATTGCCAC
ATGGTGCCCTATATTTCATAGTATTTATTCTCTATAGTAACTGCTTAAGTGCAGCTAGCTTCT
AGATTTAGACTATATAGAATTTAGATATTGTATTGTTTCGTCATTATAATATGCTACCACATGT
AGCAATAATTACAATATTTTATTAAATAAATATGTGAAATATTGTTTCATGAAAGACAGATT
TCCAAATCTCTCTTCTCTCTGTACTGTCTACCTTTATGTGAAGAAATTAATTATATGCCA
TTGCCAGGT

384/615

FIGURE 380

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648

><subunit 1 of 1, 140 aa, 1 stop

><MW: 15668, pI: 10.14, NX(S/T): 5

MFFTISRKNMSQKLSLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE
NKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNLVP
VTTNKRTNVSGSIR

Important features of the protein:**Signal peptide:**

amino acids 1-26

385/615

FIGURE 381

AAC TTCTAC **ATG**GGCCTCCTGCTGCTGGTGCTCTTCCTCAGCCTCCTGCCGGTGGCCTACACC
ATCATGTCCCTCCCACCCCTCCTTTGACTGCGGGCCGTT CAGGTGCAGAGTCTCAGTTGCCCGG
GAGCACCTCCCCTCCCGAGGCAGTCTGCTCAGAGGGCCTCGGCCCAGAATTCCAGTTCTGGTT
TCATGCCAGCCTGTAAAAGGCCATGGAAC TTTGGGTGAATCACCGATGCCATTTAAGAGGGTT
TTCTGCCAGGATGGAAATGTTAGGTCGTTCTGTGTCTGCGCTGTT CATTT CAGTAGCCACCAG
CCACCTGTGGCCGTTGAGTGCTTGAAA **TGAG**GAAGTGAAGAAATTAATTTCTCATGTATTTTT
CTCATTTATTTATTAATTTTTTAACTGATAGTTGTACATATTTGGGGGTACATGTGATATTTGG
ATACATGTATACAATATATAATGATCAAATCAGGGTAACTGGGATATCCATCACATCAAACAT
TTATTTTTTTATTCTTTT TAGACAGAGTCTCACTCTGTCACCCAGGCTGGAGTGCAGTGGTGCC
ATCTCAGCTTACTGCAACCTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCTCCACCTCCCAA
GTAGCTGGGACTACAGGCATGCACCACAATGCCCAACTAATTTTTGTATTTTTTAGTAGAGACG
GGGTTTTGCCATGTTGCCCAGGCTGGCCTTGAACTCCTGGCCTCAAACAATCCACTTGCCTCG
GCCTCCCAAAGTGTTATGATTACAGGCGTGAGCCACCGTGCCTGGCCTAAACATTTATCTTTT
CTTTGTGTTGGGAAC TTTGAAATTATACAATGAATTATTGTTAACTGTCATCTCCCTGCTGTG
CTATGGAACACTGGGACTTCTTCCCTCTATCTAACTGTATATTTGTACCAGTTAACCAACCGT
ACTTCATCCCCACTCCTCTCTATCCTTCCCAACCTCTGATCACCTCATTCTACTCTCTACCTC
CATGAGATCCACTTTTTTTAGCTCCCATGTGAGTAAGAAAATGCAATATTTGTCTTTCTGTG
CCTGGCTTATTTCACTTAACATAATGACTTCCTGTTCCATCCATGTTGCTGCAAATGACAGGA
TTTCGTTCTTAATTTCAATTAAATAAACCACACATGGCAAAAA

386/615

FIGURE 382

MGLLLLVLFLSLLPVAYTIMSLPPSFDCGPFRCRVSVAREHLPSRGSLLRGPRPRI PVLVSCQ
PVKGHGTLGESPMPEKRVFCQDGNVRSFCVCAVHFSSHQPPVAVECLK

Important features of the protein:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 86-92

Zinc carboxypeptidases, zinc-binding region 2 signature.

amino acids 68-79

387/615

FIGURE 383

TTCTGAAGTAACGGAAGCTACCTTGTATAAAGACCTCAACACTGCTGACCATGATCAGCGCAG
CCTGGAGCATCTTCCTCATCGGGACTAAAATTGGGCTGTTCTTCAAGTAGCACCTCTATCAG
TTATGGCTAAATCCTGTCCATCTGTGTGTCGCTGCGATGCGGGTTTCATTTACTGTAATGATC
GCTTTCTGACATCCATTCCAACAGGAATACCAGAGGATGCTACAACCTCTCTACCTTCAGAACA
ACCAAATAAATAATGCTGGGATTCTTTCAGATTTGAAAACTTGCTGAAAGTAGAAAGAATAT
ACCTATACCACAACAGTTTATGATGAATTTCTACCAACCTCCCAAAGTATGTAAAAGAGTTAC
ATTTGCAAGAAAATAACATAAGGACTATCACTTATGATTCACTTTCAAAAATTCCCTATCTGG
AAGAATTACATTTAGATGACAACCTCTGTCTCTGCAGTTAGCATAGAAGAGGGAGCATTCCGAG
ACAGCAACTATCTCCGACTGCTTTTCTGTCCCGTAATCACCTTAGCACAATTCCCTGGGGTT
TGCCCAGGACTATAGAAGAACTACGCTTGGATGATAATCGCATATCCACTATTTTCATCACCAT
CTCTTCAAGGTCTCACTAGTCTAAAACGCCTGGTTCTAGATGGAAACCTGTTGAACAATCATG
GTTTAGGTGACAAAGTTTTCTTCAACCTAGTTAATTTGACAGAGCTGTCCCTGGTGCGGAATT
CCCTGACTGCTGCACCAGTAAACCTTCCAGGCACAAACCTGAGGAAGCTTTATCTTCAAGATA
ACCACATCAATCGGGTGCCCCCAAATGCTTTTTCTTATCTAAGGCAGCTCTATCGACTGGATA
TGTCCAATAATAACCTAAGTAATTTACCTCAGGGTATCTTTGATGATTTGGACAATATAACAC
AACTGATTCTTCGCAACAATCCCTGGTATTGCGGGTGCAAGATGAAATGGGTACGTGACTGGT
TACAATCACTACCTGTGAAGGTCAACGTGCGTGGGCTCATGTGCCAAGCCCCAGAAAAGGTTTC
GTGGGATGGCTATTAAGGATCTCAATGCAGAACTGTTTGATTGTAAGGACAGTGGGATTGTAA
GCACCATTGAGATAACCACTGCAATACCCAACACAGTGTATCCTGCCCAAGGACAGTGGCCAG
CTCCAGTGACCAAACAGCCAGATATTAAGAACCCAAGCTCACTAAGGATCAACAAACCACAG
GGAGTCCCTCAAGAAAAACAATTACAATTACTGTGAAGTCTGTACCTCTGATACCATTCTATA
TCTCTTGGAACCTTGCTCTACCTATGACTGCTTTGAGACTCAGCTGGCTTAAACTGGGCCATA
GCCCCGCATTTGGATCTATAACAGAAACAATTGTAACAGGGGAACGCAGTGAGTACTTGGTCA
CAGCCCTGGAGCCTGATTCACCCTATAAAGTATGCATGGTTCCCATGGAAACCAGCAACCTCT
ACCTATTTGATGAAACTCCTGTTTGTATTGAGACTGAAACTGCACCCCTTCGAATGTACAACC
CTACAACCACCCTCAATCGAGAGCAAGAGAAAGAACCTTACAAAAACCCCAATTTACCTTTGG
CTGCCATCATTTGGTGGGGCTGTGGCCCTGGTTACCATTGCCCTTCTTGCTTTAGTGTGTGGT
ATGTTCATAGGAATGGATCGCTCTTCTCAAGGAACCTGTGCATATAGCAAAGGGAGGAGAAGAA
AGGATGACTATGCAGAAGCTGGCACTAAGAAGGACAACCTCTATCCTGGAAATCAGGGAAACTT
CTTTTCAGATGTTACCAATAAGCAATGAACCCATCTCGAAGGAGGAGTTTGTAAATACACACCA
TATTTCCCTCCTAATGGAATGAATCTGTACAAAACAATCACAGTGAAAGCAGTAGTAACCGAA
GCTACAGAGACAGTGGTATTCCAGACTCAGATCACTCACACTCATGATGCTGAAGGACTCACA
GCAGACTTGTGTTTTGGGTTTTTTAAACCTAAGGGAGGTGATGGT

388/615

FIGURE 384

MISAAWSIFLIGTKIGLFLQVAPLSVMAKSCPSVCRCDAGFIYCNDREFLTSTIPTGIPEDATTL
YLQNNQINNAGIPSDLKNLLKVERIYLYHNSLDEFPTNLPKYVKELHLQENNIRTITYDSLK
IPYLEELHLLDDNSVSAVSIEEGAFRDSNYLRLLFLSRNHLSTIPWGLPRTIEELRLDDNRIST
ISSPSLQGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLTAAAPVNLPGTNLRKL
YLQDNHINRVPPNAFSYLRQLYRLDMSNNNLSNLPQGIFDDLDNITQLILRNNPWYCGCKMKW
VRDWLQSLPVKVNVVRGLMCQAPEKVRGMAIKDLNAELFDCKDSGIVSTIQITTAIPNTVYPÄQ
GQWPAPVTKQPDIKNPKLTKDQQTGSPSRKTITITVKSVTSDTIHISWKLALPMTALRLSWL
KLGHSPAFGSITETIVTGERSEYLVTALEPDSPYKVCMPMETSNNLYLFDETPVCITETETAPL
RMYNPTTTLNREQEKEPYKNPNLPLAAIIGGAVALVTIALLALVCWYVHRNGSLFSRNCAYSK
GRRRKDDYAEAGTKKDNSILEIRETSFQMLPISNEPISKEEFVIHTIFPPNGMNLYKNNHSES
SSNRSYRDSGIPDSDHSHS

Important features of the protein:**Signal peptide:**

amino acids 1-28

Transmembrane domain:

amino acids 531-552

N-glycosylation sites.

amino acids 226-229, 282-285, 296-299, 555-558, 626-629, 633-636

Tyrosine kinase phosphorylation site.

amino acids 515-522

N-myristoylation sites.amino acids 12-17, 172-177, 208-213, 359-364, 534-539, 556-561,
640-645**Amidation site.**

amino acids 567-570

Leucine zipper pattern.

amino acids 159-180

Phospholipase A2 aspartic acid active site.

amino acids 34-44

389/615

FIGURE 385

CCGTCATCCCCCTGCAGCCACCCTTCCAGAGTCCTTTGCCAGGCCACCCAGGCTTCTTGG
CAGCCCTGCCGGGCCACTTGTCTTCATGCTGCCAGGGGAGGTGGGAAGGAGGTGGGAGGAG
GGCGTGCAGAGGCAGTCTGGGCTTGGCCAGAGCTCAGGGTGCTGAGCGTGTGACCAGCAGTGA
GCAGAGGCCGGCCATGGCCAGCCTGGGGCTGCTGCTCCTGCTCTTACTGACAGCACTGCCACC
GCTGTGGTCTCCTCACTGCCTGGGCTGGACACTGCTGAAAGTAAAGCCACCATTGCAGACCT
GATCCTGTCTGCGCTGGAGAGAGCCACCGTCTTCTAGAACAGAGGCTGCCTGAAATCAACCT
GGATGGCATGGTGGGGGTCCGAGTGCTGGAAGAGCAGCTAAAAAGTGTCCGGGAGAAGTGGGC
CCAGGAGCCCCCTGCTGCAGCCGCTGAGCCTGCGCGTGGGGATGCTGGGGGAGAAGCTGGAGGC
TGCCATCCAGAGATCCCTCCACTACCTCAAGCTGAGTGATCCCAAGTACCTAAGAGAGTTCCA
GCTGACCCTCCAGCCCCGGTTTTGGAAAGCTCCACATGCCTGGATCCACACTGATGCCTCCTT
GGTGTACCCACGTTTCGGGCCCCAGGACTCATTCTCAGAGGAGAGAAGTGACGTGTGCCTGGT
GCAGCTGCTGGGAACCGGGACGGACAGCAGCGAGCCCTGCGGCCTCTCAGACCTCTGCAGGAG
CCTCATGACCAAGCCCCGGCTGCTCAGGCTACTGCCTGTCCACCAACTGCTCTTCTTCTCTG
GGCCAGAATGAGGGGATGCACACAGGGACCACTCCAACAGAGCCAGGACTATATCAACCTCTT
CTGCGCCAACATGATGGACTTGAACCGCAGAGCTGAGGCCATCGGATACGCCTACCCTACCCG
GGACATCTTCATGGAAAACATCATGTTCTGTGGAATGGGCGGCTTCTCCGACTTCTACAAGCT
CCGGTGGCTGGAGGCCATTCTCAGCTGGCAGAAACAGCAGGAAGGATGCTTCGGGGAGCCTGA
TGCTGAAGATGAAGAATTATCTAAAGCTATTCAATATCAGCAGCATTTTTTCGAGGAGAGTGAA
GAGGCGAGAAAAACAATTTCCAGATTCTCGCTCTGTTGCTCAGGCTGGAGTACAGTGGCGCAA
TCTCGGCTCACTGCAACCTTTGCCTCCTGGGTTCAAGCAATTCTCTTGCCCTCATCTCCCGAG
TAGCTGGGACTACAGGAGCGTGCCACCATACTGGCTAATTTTTTATATTTTTTTAGTAGAGAC
AGGGTTTTCATCATGTTGCTCATGCTGGTCTCGAACTCCTGATCTCAAGAGATCCGCCCCACCTC
AGGCTCCCAAAGTGTGGGATTATAGGTTGTGAGCCACCGTGTCTGGCTGAAAAGCACTTTCAAA
GAGACTGTGTTGAATAAAAGGGCCAAGGTTCTTGCCACCCAGCACTCATGGGGGCTCTCTCCCC
TAGATGGCTGCTCCTCCCACAACACAGCCACAGCAGTGGCAGCCCTGGGTGGCTTCTTATACA
TCCTGGCAGAATACCCCCCAGCAAACAGAGAGCCACACCCATCCACACCGCCACCACCAAGCA
GCCGCTGAGACGGACGGTTCATGCCAGCTGCCTGGAGGAGGAACAGACCCCTTTAGTCTCA
TCCCTTAGATCCTGGAGGGCACGGATCACATCCTGGGAAGAAGGCATCTGGAGGATAAGCAAA
GCCACCCCGACACCCAATCTTGAAGCCCTGAGTAGGCAGGGCCAGGGTAGGTGGGGGCCGGG
AGGGACCCAGGTGTGAACGGATGAATAAAGTTCAACTGCAACTGAAAAAAAAA

390/615

FIGURE 386

MSARGRWEGGGRRACRGSGLLARAQGAERTVSSEQRPAMASLGLLLLLLLLTALPPLWSSSLPG
LDTAESKATIADLILSALERATVFLEQRLPEINLDGMVGVRVLEEQLKSVREKWAQEPLLQPL
SLRVGMLGEKLEAAIQRSYLHKLSDPKYLREFQLTLQPGFWKLPHAWIHTDASLVYPTFGPQ
DSFSEERSDVCLVQLLGTGTDSSSEPCGLSDLCRSLMTKPGCSGYCLSHQLLFFLWARMRGCTQ
GPLQQSQDYINLFCANMMDLNRRAEAIGYAYPTRDIFMENIMFCGMGGFSDFYKLRWLEAILS
WQKQQEGCFGEFDAEDEELSKAIQYQQHFSRRVKRREKQFPDSRSVAQAGVQWRNLGSLQPLP
PGFKQFSCILLPSSWDYRSVPPYLANFYIFLVETGFHHVAHAGLELLISRPPTSGSQSVGL

Important features of the protein:**Signal peptide:**

amino acids 1-26

Transmembrane domain:

amino acids 39-56

Tyrosine kinase phosphorylation sites.

amino acids 149-156, 274-282

N-myristoylation sites.

amino acids 10-16, 20-26, 63-69, 208-214

Amidation site.

amino acids 10-14

Glycoprotein hormones beta chain signature 1.

amino acids 230-237

391/615

FIGURE 387

GGTCTGAGTGCAGAGCTGCTGTCATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGC
TGCTGCTGCTATCGGGGATGTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGG
GAGGGAGTGGGGTCGGCATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGG
TGAAGCCTCAGGACTGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTT
TCCTTAAGACAGATGGGAGTTTTGTGGTTCATGATATAACCTTCTGGATCTTATGTAGTGGAAG
TTGTATCTCCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGA
GAGCAAGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAA
TGAAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTTC
TAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCTAAAG
TGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATGCTGAATT
CCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCAAAATCATCTG
GCAAACTAGCAGCGGCAGCAGTAAACAGGCAAAAGTGGGGCTGGCAAAAGGAGGTAGTCAG
GCCGTCCAGAGCTGGCATTTCACAAACACGGCAACACTGGGTGGCATCCAAGTCTTGGA
CCGTGTGAAGCAACTACTATAAACTTGAGTCATCCCGACGTTGATCTCTTACAACGTGTGTATGTT
AACTTTTTAGCACATGTTTTGTACTTGGTACACGAGAAAACCCAGCTTTCATCTTTTGTCTGT
ATGAGGTCAATATTGATGTCAGTGAATTAATTACAGTGTCTATAGAAAATGCCATTAATAAA
TTATATGAACTACTATACATTATGTATATTAATTAAACATCTTAATCCAGAAATCAAAAAA
AAAAAAAAAAAAAAAAAAAAA

392/615

FIGURE 388

MAAALWGFFPVLLLLLLLLSGDVQSSEVPGAAAEGSGSGVGIGDRFKIEGRAVVPGVKPDWIS
AARVLVDGEEHVGFLLKTDGSFVVHDIPSGSYVVEVVS PAYRFD PVRVDITSKGKMRARYVNYI
KTSEVVR LPYP LQMKSSGPPSYFIKRESWGWTDFLMNPMVMMVLPLLI FVLLPKVVNTSDPD
MRREMEQSMNMLNSNHELDPDVSEFMTRLFSSKSSSGKSSSGSSKTGKSGAGKRR

Important features of the protein:**Signal sequence:**

amino acids 1-23

Transmembrane domain:

amino acids 161-182

N-glycosylation site.

amino acids 184-187

Glycosaminoglycan attachment sites.

amino acids 37-40, 236-239

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 151-154

N-myristoylation sites.

amino acids 33-38, 36-41, 38-44, 229-234

Amidation site.

amino acids 238-241

ATP/GTP-binding site motif A (P-loop).

amino acids 229-236

393/615

FIGURE 389

GTCGTGTGCTTGGAGGAAGCCGCGGAACCCCCAGCGTCCGTCCTCCATGGCGTGGAGCCTTGGGAG
CTGGCTGGGTGGCTGCCTGCTGGTGTGTCAGCATTGGGAATGGTACCACCTCCCGAAAATGTCAG
AATGAATTCTGTTAATTTCAAGAACATTCTACAGTGGGAGTCACCTGCTTTTGCCAAAGGGAA
CCTGACTTTCACAGCTCAGTACCTAAGTTATAGGATATTCCAAGATAAATGCATGAATACTAC
CTTGACGGAATGTGATTTCTCAAGTCTTTCCAAGTATGGTGACCACACCTTGAGAGTCAGGGC
TGAATTTGCAGATGAGCATTCAGACTGGGTAAACATCACCTTCTGTCTGTGGATGACACCAT
TATTGGACCCCCCTGGAATGCAAGTAGAAGTACTTGCTGATTCTTTACATATGCGTTTCTTAGC
CCCTAAAATTGAGAATGAATACGAACTTGGAATGAAGAATGTGTATAACTCATGGACTTA
TAATGTGCAATACTGGAAAAACGGTACTGATGAAAAGTTTCAAATTACTCCCCAGTATGACTT
TGAGGTCCTCAGAAACCTGGAGCCATGGACAACCTTATTGTGTTCAAGTTCGAGGGTTTCTTCC
TGATCGGAACAAAGCTGGGGAATGGAGTGAGCCTGTCTGTGAGCAAACAACCCATGACGAAAC
GGTCCCCCTCCTGGATGGTGGCCGTATCCTCATGGCCTCGGTCTTCATGGTCTGCCTGGCACT
CCTCGGCTGCTTCTCCTTGCTGTGGTGCCTTTACAAGAAGACAAAGTACGCCTTCTCCCCCTAG
GAATTCTCTTCCACAGCACCTGAAAGAGTTTTTGGGCCATCCTCATCATAACACACTTCTGTT
TTTCTCCTTTCCATTGTCGGATGAGAATGATGTTTTTGACAAGCTAAGTGTGATTGCAGAAGA
CTCTGAGAGCGGCAAGCAGAATCCTGGTGACAGCTGCAGCCTCGGGACCCCGCTGGGCAGGG
GCCCCAAAGCTAGGCTCTGAGAAGGAAACACACTCGGCTGGGCACAGTGACGTACTCCATCTC
ACATCTGCCTCAGTGAGGGATCAGGGCAGCAAACAAGGGCCAAGACCATCTGAGCCAGCCCCA
CATCTAGAACTCCAGACCTGGACTTAGCCACCAGAGAGCTACATTTTAAAGGCTGTCTTGGCA
AAAATACTCCATTTGGGAACCTCACTGCCTTATAAAGGCTTTCATGATGTTTTTCAGAAGTTGGC
CACTGAGAGTGTAATTTTCAGCCTTTTATATCACTAAAATAAGATCATGTTTTAATTGTGAGA
AACAGGGCCGAGCACAGTGGCTCACGCCTGTAATACCAGCACCTTAGAGGTCGAGGCAGGCGG
ATCACTTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAATATGGTGAAACCCAGTCTCTACTAA
AAATACAAAAATTAGCTAGGCATGATGGCGCATGCCTATAATCCCAGCTACTCGAGTGCCTGA
GGCAGGAGAATTGCATGAACCCGGGAGGAGGAGGAGGAGGTTGCAGTGAGCCGAGATAGCGGC
ACTGCACTCCAGCCTGGGTGACAAAGTGAGACTCCATCTCAAAAAAAAAAAAAAAAAAATTGTG
AGAAACAGAAATACTTAAAATGAGGAATAAGAATGGAGATGTTACATCTGGTAGATGTAACAT
TCTACCAGATTATGGATGGACTGATCTGAAAATCGACCTCAACTCAAGGGTGGTCAGCTCAAT
GCTACACAGAGCACGGACTTTTGGATTCTTTGCAGTACTTTGAATTTATTTTCTACCTATAT
ATGTTTTATATGCTGCTGGTGTCCATTAAAGTTTTACTCTGTGTTGC

394/615

FIGURE 390

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83551
><subunit 1 of 1, 325 aa, 1 stop
><MW: 37011, pI: 5.09, NX(S/T): 4
MAWSLGSWLGGCLLVSALGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQYLSYRIFQ
DKCMNTTLTECDFSSLSKYGDHTLRVRAEFADHSDWVNITFCPVDDTIIGPPGMQVEVLADS
LHMRFLAPKIENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDFEVLRLNLEPWTTYCV
QVRGFLPDRNKAGEWSEPVCETTHDETVPSSWMVAVILMASVFMVCLALLGCFSLLWCVYKKT
KYAFSPRNSLPQHLKEFLGHPHNTLLFFSFPLSDENDVFDKLSVIAEDSESGKQNP GDSCSL
GTPPGQGPQS

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 222-245

N-glycosylation sites.

amino acids 49-53, 68-72, 102-106, 161-165

N-myristoylation sites.

amino acids 6-12, 316-322

395/615

FIGURE 391

CTGTGCAGCTCGAGGCTCCAGAGGCACACTCCAGAGAGAGCCAAGGTTCTGACGCGATGAGGA
AGCACCTGAGCTGGTGGTGGCTGGCCACTGTCTGCATGCTGCTCTTCAGCCACCTCTCTGCGG
TCCAGACGAGGGGCATCAAGCACAGAATCAAGTGGAACCGGAAGGCCCTGCCCAGCACTGCCC
AGATCACTGAGGGCCAGGTGGCTGAGAACCGCCCGGGAGCCTTCATCAAGCAAGGCCGCAAGC
TCGACATTGACTTCGGAGCCGAGGGCAACAGGTACTACGAGGCCAACTACTGGCAGTTCCCCG
ATGGCATCCACTACAACGGCTGCTCTGAGGCTAATGTGACCAAGGAGGCATTTGTCACCGGCT
GCATCAATGCCACCCAGGCGGCGAACCAGGGGGAGTTCCAGAAGCCAGACAACAAGCTCCACC
AGCAGGTGCTCTGGCGGCTGGTCCAGGAGCTCTGCTCCCTCAAGCATTGCGAGTTTTGGTTGG
AGAGGGGCGCAGGACTTCGGGTCACCATGCACCAGCCAGTGCTCCTCTGCCTTCTGGCTTTGA
TCTGGCTCATGGTGAAATTAAGCTTGCCAGGAGGCTGGCAGTACAGAGCGCAGCAGCGAGCAAA
TCCTGGCAAGTGACCCAGCTCTTCTCCCCCAAACCCACGCGTGTTCTGAAGGTGCCAGGAGC
GGCGATGCACTCGCACTGCAAATGCCGCTCCCACGTATGCGCCCTGGTATGTGCCTGCGTTCT
GATAGATGGGGGACTGTGGCTTCTCCGTCCTCCATTCTCAGCCCCTAGCAGAGCGTCTGGCA
CACTAGATTAGTAGTAAATGCTTGATGAGAAGAACACATCAGGCACTGCGCCACCTGCTTCAC
AGTACTTCCCAACAACCTCTTAGAGGTAGGTGTATTCCCGTTTTACAGATAAGGAACTGAGGC
CCAGAGAGCTGAAGTACTGCACCCAGCATCACCAGCTAGAAAGTGGCAGAGCCAGGATTCAAC
CCTGGCTTGTCTAACCCAGGTTTTCTGCTCTGTCCAATTCCAGAGCTGTCTGGTGATCACTT
TATGTCTCACAGGGACCCACATCCAACATGTATCTCTAATGAAATTGTGAAAGCTCCATGTT
TAGAAATAAATGAAAACACCTGA

396/615

FIGURE 392

MRKHL S W W L A T V C M L L F S H L S A V Q T R G I K H R I K W N R K A L P S T A Q I T E A Q V A E N R P G A F I K Q G
R K L D I D F G A E G N R Y Y E A N Y W Q F P D G I H Y N G C S E A N V T K E A F V T G C I N A T Q A A N Q G E F Q K P D N K
L H Q Q V L W R L V Q E L C S L K H C E F W L E R G A G L R V T M H Q P V L L C L L A L I W L M V K

Important features of the protein:**Signal peptide:**

amino acids 1-26

Transmembrane domain:

amino acids 157-171

N-glycosylation sites.

amino acids 98-102, 110-114

Tyrosine kinase phosphorylation site.

amino acids 76-83

N-myristoylation sites.

amino acids 71-77, 88-94, 93-99, 107-113, 154-160

Amidation site.

amino acids 62-66

397/615

FIGURE 393

TGAAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCCTCTGATTGGTGAA
TGGTGAAGGTGCCTGTCTAACTTTTCTGTAAAAAGAACCAGCTGCCTCCAGGCAGCCAGCCCT
CAAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTTCGCCAA
TTTAACACCAAGAAGAATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTGAGAG
ATGAATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCTTCTGCCCTCCTTTG
CTGGCGACAGCCTCTCAAATGCAGATGGTTGTGCTCCCTTGCCTGGGTTTTACCCTGCTTCTC
TGGAGCCAGGTATCAGGGGCCAGGGCCAAGAATTCCACTTTGGGCCCTGCCAAGTGAAGGGG
GTTGTTCCCCAGAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAGCTCAGGAT
AACATCACGAGTGCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCTCGGATGCTGAGAGC
TGTTACCTTGTCCACACCCTGCTGGAGTTCTACTTGAAAACGTGTTTTCAAAAACCACCACAAT
AGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCAACAACCTTTGTTCTCATC
GTGTCACAACCTGCAACCCAGTCAAGAAAATGAGATGTTTTCCATCAGAGACAGTGCACACAGG
CGGTTTCTGCTATTCCGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGCTCTGACCAAAGCC
CTTGGGGAAGTGACATTCTTCTGACCTGGATGCAGAAATTCTACAAGCTCT**TGA**ATGTCTAGA
CCAGGACCTCCCTCCCCCTGGCACTGGTTTGTTCCTGTGTCATTTCAAACAGTCTCCCTTCC
TATGCTGTTCACTGGACACTTCACGCCCTTGGCCATGGGTCCCATTCTTGGCCCAGGATTATT
GTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAGGTGCCTCTGGATGCTGT
GAAGAGTCTACAGAGAAGATTCTTGTATTTATTACAACCTCTATTTAATTAATGTCAGTATTTT
AACTGAAGTTCTATTTATTTGTGAGACTGTAAGTTACATGAAGGCAGCAGAATATTGTGCCCC
ATGCTTCTTTACCCCTCACAATCCTTGCCACAGTGTGGGGCAGTGGATGGGTGCTTAGTAAGT
ACTTAATAAACTGTGGTGCTTTTTTTGGCCTGTCTTTGGATTGTTAAAAAACAGAGAGGGATG
CTTGGATGTAAACTGAACTTCAGAGCATGAAAATCACACTGTCTTCTGATATCTGCAGGGAC
AGAGCATTGGGGTGGGGGTAAAGGTGCATCTGTTTGAAAAGTAAACGATAAAATGTGGATTAAA
GTGCCCAGCACAAAGCAGATCCTCAATAAACATTTTCAATTTCCCACCCACACTCGCCAGCTCAC
CCCATCATCCCTTTCCCTTGGTGCCCTCCTTTTTTTTTTATCCTAGTCATTCTTCCCTAATCT
TCCACTTGAGTGTCAAGCTGACCTTGCTGATGGTGACATTGCACCTGGATGTACTATCCAATC
TGTGATGACATTCCCTGCTAATAAAAGACAACATAACTCCAAAAAAAAAAAAAAAAAAAAA
AAAA

398/615

FIGURE 394

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002

><subunit 1 of 1, 206 aa, 1 stop

><MW: 23799, pI: 9.12, NX(S/T): 3

MNFQQRLQSLWTLARPCPPLLATASQMOMVVLPCLGFTLLLSQVSGAQGQEFHFGPCQVKG

VVPQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLEVHTLLEFYLKTVFKNHHN

RTVEVRTLKSFSTLANNEVLIVSQLQPSQENEMFSIRDSAHRRFLLFRAFKQLDVEAALTKA

LGEVDILLTWMQKFYKL

Signal sequence:

amino acids 1-42

N-glycosylation sites.

amino acids 85-89, 99-103, 126-130

399/615

FIGURE 395

GCCTTGGCCTCCCAAAGGGCTGGGATTATAGGCGTGACCACCATGTCTGGTCCAGAGTCTCAT
TTCCTGATGATTTATAGACTCAAAGAAAACTATGTTTCAGAAGCTCTCTTCTCTTCTGGCCTC
CTCTCTGTCTTCTTTCCCTCTTTCTTCTTATTTTAATTAGTAGCATCTACTCAGAGTCATGCA
AGCTGGAAATCTTTCATTTTGCTTGTGTCAGTGGGGTAGGTCAGTCTTAGTTTTTATTTTT
TGAAATTTCAACTTTCAGATTCAGGGGGTACATGTGAAGGTTTGTTTTATGAGTATATTGCAT
GATGCTGAGGTTTGGGGT

400/615

FIGURE 396

MFRSSLLFWPPLCLLSLFLILISSIYSECKLEIFHFACQWGRSLSLSFYFLKFQLSDSGGT
CEGLFYEYIA

Important features of the protein:

Signal peptide:

amino acids 1-25

N-myristoylation site.

amino acids 62-68

401/615

FIGURE 397

CATGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCCTG
TGTCTCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAATGT
CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTT
CATATATGGGCAAAAGAAATGGCTGAATAAATCAGAATGCAGAAATATCAATAGAACCTACTG
TGATCTTTCTGCTGAAACTTCTGACTACGAACACCAGTATTATGCCAAAGTTAAGGCCATTTG
GGGAACAAAAGTGTTCCAAATGGGCTGAAAGTGGACGGTTCTATCCTTTTTTAGAAACACAAAT
TGGCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTCCTGACAGCTCC
AGAGAAGTGAAGAGAAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAATATACTCCAATCT
GAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCCCAGTGTGTGACCAA
CCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGTACACGTGGAGTCCTT
CGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTGCCAGGACTTTGAAAGA
TCAATCATCAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTTGCCCATATCTATTACCGT
GTTTCTTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCACGTGGCAAAGAGAAACA
CCCAGCAAATTTGATTTTGATTTATGGAAATGAATTTGACAAAAGATTCTTTGTGCCTGCTGA
AAAAATCGTGATTAACTTTATCACCTCAATATCTCGGATGATTCTAAAATTTCTCATCAGGA
TATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGCCAGCGGGAA
CCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAGGGTATGCTTCGCATTTGATGGA
AATTTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCTCTCAGCCAGCAAGAGTCCCTCAG
CAGAACAATACCCCCGGATAAAACAGTCATTGAATATGAATATGATGTCAGAACCACTGACAT
TTGTGCGGGGCCTGAAGAGCAGGAGCTCAGTTTGCAGGAGGAGGTGTCCACACAAGGAACATT
ATTGGAGTCGCAGGCAGCGTTGGCAGTCTTGGGCCCGCAAACGTTACAGTACTCATACACCCC
TCAGCTCCAAGACTTAGACCCCCTGGCGCAGGAGCACACAGACTCGGAGGAGGGGCCGGAGGA
AGAGCCATCGACGACCCCTGGTCGACTGGGATCCCCAAACTGGCAGGCTGTGTATTTCCTTCGCT
GTCCAGCTTCGACCAGGATTCAGAGGGCTGCGAGCCTTCTGAGGGGGATGGGCTCGGAGAGGA
GGGTCTTCTATCTAGACTCTATGAGGAGCCGGCTCCAGACAGGCCACCAGGAGAAAATGAAAC
CTATCTCATGCAATTCATGGAGGAATGGGGGTATATGTGCAGATGGAAAAC**TGAT**GCCAACA
CTTCCTTTTGCCTTTTGTTCCTGTGCAACAAGTGAGTCACCCCTTTGATCCCAGCCATAAA
GTACCTGGGATGAAAGAAGTTTTTTCAGTTTGTGAGTGCTGTGAGAA

402/615

FIGURE 398

MPLPPLL LLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYF
IYGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLETQI
GPPEVALTTDEKSISSVLTAPKWKRNPELDPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTN
HTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQCARTLKDQSSEFKAKIIFWYVLPISITV
FLFSVMGYSIYRYIHVGKEKHPANLILYGNFEDKREFFVPAEKIVINFITLNISSDDSKISHQD
MSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKHLGYASHLMEIFCDSEENTEGTSLTQQESLS
RTIPDPKTVIEYEYDVRTTDCAGPEEQELSLQEEVSTQGTLLSQAAALAVLGPQTLQYSYTP
QLQDLDP LAQEHTDSEEGPEEEPSTTLVDWDPQTGRLCIPSLSSFDQDSEGCEPSEGDGLGEE
GLLSRLYEPPAPDRPPGENETYLMQFMEEWGLYVQMEN

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 240-260

N-glycosylation sites.amino acids 31-34, 72-75, 80-83, 171-174, 180-183, 189-192,
304-307, 523-526**Tyrosine kinase phosphorylation site.**

amino acids 385-392, 518-526

N-myristoylation sites.

amino acids 53-58, 106-111, 368-373, 492-497

Tissue factor

amino acids 1-278

403/615

FIGURE 399

CCGGCGATGTCGCTCGTGCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAG
CCGACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTA
ATCCCCGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACACTAGTGTTGCAACAGGGGAC
TATTCAATTTTGTATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTTGAAG
GCCACCAAGATTTGTGTGACGGGCAAAAGCAACTTCCAGTCCTACAGCTGTGTGAGGTGCAAT
TACACAGAGGCCTTCCAGACTCAGACCAGACCCTCTGGTGTTAAATGGACATTTTCCTACATC
GGCTTCCCTGTAGAGCTGAACACAGTCTATTTTCATTGGGGCCCATAATATTCCTAATGCAAAT
ATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGACCACATA
ATGAAATATAAAAAAAGTGTGTCAAGGCCGGAAGCCTGTGGGATCCGAACATCACTGCTTGT
AAGAAGAATGAGGAGACAGTAGAAGTGAACCTCACAACTCCCTGGGAAACAGATACATG
GCTCTTATCCAACACAGCACTATCATCGGGTTTTCTCAGGTGTTTGAGCCACACCAGAAGAAA
CAAACGCGAGCTTCAGTGGTGATTCCAGTGACTGGGGATAGTGAAGGTGCTACGGTGACAGCTG
ACTCCATATTTTCCTACTTGTGGCAGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGC
CCACAAACAGGCGTCCCTTTCCCTCTGGATAACAACAAAAGCAAGCCGGGAGGCTGGCTGCCT
CTCCTCCTGCTGTCTCTGCTGGTGGCCACATGGGTGCTGGTGGCAGGGATCTATCTAATGTGG
AGGCACGAAAGGATCAAGAAGACTTCCTTTTCTACCACCACACTACTGCCCCCATTAAGGTT
CTTGTGGTTTACCCATCTGAAATATGTTTCCATCACACAATTTGTTACTTCACTGAATTTCTT
CAAAACCATTCAGAAAGTGAGGTCATCCTTGAAAAGTGGCAGAAAAAGAAAATAGCAGAGATG
GGTCCAGTGCAGTGGCTTGCCACTCAAAAGAAGGCAGCAGACAAAGTCGTCTTCTTCTTCC
AATGACGTCAACAGTGTGTGCGATGGTACCTGTGGCAAGAGCGAGGGCAGTCCCAGTGAGAAC
TCTCAAGACCTCTTCCCCCTTGCCCTTAACCTTTTCTGCAGTGATCTAAGAAGCCAGATTCAT
CTGCACAAATACGTGGTGGTCTACTTTAGAGAGATTGATACAAAAGACGATTACAATGCTCTC
AGTGTCTGCCCCAAGTACCACCTCATGAAGGATGCCACTGCTTTCTGTGCAGAACTTCTCCAT
GTCAAGCAGCAGGTGTCAGCAGGAAAAAGATCACAAAGCCTGCCACGATGGCTGCTGCTCCTTG
TAG

404/615

FIGURE 400

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLIPGDLRDLRVEPVTTSVATGDYS
ILMNVSWVLRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGF
PVELNTVYFIGAHNIPNANMNEDGPSMSVNFTSPGCLDHIMKYKKKCVKAGSLWDPNITACKK
NEETVEVNFTTTPLGNRYMALIQHSTIIGFSQVFEPHQKKQTRASVVIPVTGDSEGATVQLTP
YFPTCGSDCIRHKGTVVLCPTGVPFPLDNNKSKPGGWLPLLLLSLLVATWVLVAGIYLMWRH
ERIKKTSFSTTTLLPPIKVLVVYPSEICFHHTICYFTEFLQNHCRSEVILEKWQKKKIAEMGP
VQWLATQKKAADKVVFLLSNDVNSVCDGTCGKSEGSPSENSQDLFPLAFNLFCSDLRSQIHLH
KYVVVYFREIDTKDDYNALSVC PKYHLMKDATAFCAELLHV KQQVSAGKRSQACHDGCCSL

Important features of the protein:**Signal peptide:**

amino acids 1-14

Transmembrane domain:

amino acids 290-309

N-glycosylation sites.amino acids 67 - 71, 103 - 107, 156 - 160, 183 - 187, 197 - 201
and 283 - 287**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 228 - 232 and 319 - 323

Casein kinase II phosphorylation sites.

amino acids 178 - 182, 402 - 406, 414 - 418 and 453 - 457

N-myristoylation site.

amino acids 116-122

Amidation site.

amino acids 488-452

405/615

FIGURE 401

GGGAACAGGGAACATATCAGCCCGTCGGCCTCCGGGCCCTGCATTCTCTAGCC**ATG**GACCG
GGACCTTTTGCGGCAGTCGCTAAATTGCCACGGGTCGTCTTTGCTCTCTCTACTTCGGAG
CGAACAGCAGGACAATCCACACTTCCGTAGCCTCCTGGGGTCGGCCGCCGAGCCAGCCCG
GGGCCCCGCCGCCCAGCACCCGTTGCAGGGCAGAAAAGAGAAGAGAGTTGACAACATCGA
GATACAGAAATTCATCTCCAAAAAGCGGATCTGCTTTTGCACCTTTCCTGGAAATCAGA
TGCACCTGCAACTTCTGAAATTAATGAAGACAGTGAAGATCATTATGCAATCATGCCACC
TTTAGAGCAATTCATGGAGATACCTAGTATGGATCGGAGAGAGCTGTTTTTCCGAGATAT
TGAGCGTGTTGATATAGTGATTGGAAGAATTAGTTCTATTTCGGGAATTCGGTTTTTTCAT
GGTGTGATCTGTTTAGGAAGTGGTATCATGAGAGATATAGCCCACTTAGAAATCACAGC
TCTTTGTCCCTTAAGAGATGTGCCTTCTCACAGTAACCATGGGGATCCTTTATCATATTA
CCAAACTGGTGACATCATTCGAGCTGGAATCAAGGATATTGACAGATACCATGAAAAGCT
AGCAGTATCTCTGTATAGCTCTTCTCTCCACCACACCTATCTGGTATTAAATTAGGTGT
AATTAGCTCTGAAGAGCTTCCTTTATACTACAGGAGAAGTGTTGAGCTAAATAGCAATTC
TTTGGAGTCCTATGAAAATGTCATGCAGAGTTCCTTGGGATTTGTTAATCCAGGAGTAGT
TGAATTCCTTCTAGAAAACTAGGAATAGATGAATCTAATCCACCATCTTTAATGAGAGG
CCTACAAAGCAAAAATTTCTCTGAAGATGATTTTGCTTCTGCATTGAGAAAAAACAATC
CGCATCTTGGGCTTTAAAATGTGTGAAGATCGGAGTTGACTATTTTAAAGTTGGACGCCA
TGTGGATGCTATGAATGAATACAATAAAGCTTTGGAAATAGACAAACAAAACGTGGAAGC
TTTGGTAGCTCGTGGAGCATTATATGCGACAAAAGGAAGTTTGAACAAAGCAATAGAAGA
TTTTGAGCTTGCATTAGAAAACGTCCAACCTCACAGAAATGCAAGAAAAATACCTCTGCCA
GACACTTGTAGAGAGAGGAGGACAGTTAGAAGAAGAAGAAAAGTTTTTAAATGCTGAAAG
TTACTATAAGAAAGCCTTGGCTTTGGATGAGACTTTTAAAGATGCAGAGGATGCTTTGCA
GAACTTCATAAATATATGCAGAAATCTTTGGAATTAAGAGAAAAACAAGCTGAAAAGGA
AGAAAAGCAGAAAACAAAAGAAAATAGAAACAAGTGCAGAAAAGTTGCGTAAGCTCTTAAA
AGAAGAGAAGAGGCTAAAGAAGAAAAGAAGAAAATCAACTTCTTCTTCAAGTGTTTCTTC
TGCTGATGAATCAGTGTCTTCATCATCATCCTCTTCTCTTCTGGTCACAAAAGGCATAA
GAAACATAAGAGGAACCGTTCAGAGTCTTCTCGCAGTTCCAGAAGGCATTCATCTAGGGC
ATCCTCAAATCAGATAGATCAGAATAGGAAAGATGAGTGCTACCCAGTTCCAGCTAATAC
TTCAGCATCTTTTCTTAACCATAAACAAGAAGTGGAGAACTACTGGGGAAGCAGGATAG
GTTACAGTATGAAAAGACACAGATAAAAGAGAAAGATAGATGCCCTCTCTCTTCATCTTC
ACTTGAAATACCGGATGATTTTGGAGTGACTCCTATTTATTTAAAAAGTTAACTATAAA
ACAGCCTCAGGCAGGTCTTCAGGAGATATTCCAGAAGAGGGCATTGTTATCATAGATGA
CAGCTCCATTCATGTTACTGACCCTGAAGACCTTCAAGTGGGACAAGATATGGAGGTGGA
AGACAGTGGTATTGATGATCCTGACCACGGG**TAG**GCTTAGGTTTATGTGTGTGTATGTGT
CTTAGTTTTTAACAAAAAAATTA AAAAGTAAAAAACTAAAAATAGAAAAATGCTTAGAG
AATAAGGATATAAAGAATATTTTTGTGCAGTTGAACAATGAGTGCTTAAGCTAAATGTCA
TCACAAAAGAGTAAAAAAATTTTACAAAATTA AAAATGTTTAAAGTTAAAAAGCTCTAGG
AAGCTAAGGTCAATTTATTATTGGAGAAATAAAAATATTTTTATGAATTTACTGT

406/615

FIGURE 402

MDRDLLRQSLNCHGSSLLSLLRSEQQDNPHFRSLLGSAAEPARGPPPQHPLQGRKEKRVD
NIEIQKFISKADLLFALSWKSDAPATSEINEDSEDHYAIMPPLEQFMEIPSMRRELFF
RDIERGDIVIGRISSIREFGFFMVLIICLGSGIMRDIAHLEITALCPLRDVPSHSNHGDPL
SYYQTGDIIRAGIKDIDRYHEKLAVSLYSSSLPPHLSGIKLGVISSEELPLYRRSVELN
SNSLESYENVMQSSSLGFVNPGVVEFLLEKLGIDESNPPSLMRGLQSKNFSEDDFASALRK
KQSASWALKCVKIGVDYFKVGRHVDAMNEYNKALEIDKQNEALVARGALYATKGSINKA
IEDFELALENCPTHNRNARKYLCQTLVERGGQLEEEEEKFLNAESYYKKALALDETFKDAED
ALQKLHKYMQKSLELREKQAEKEEKQKTKKIETSAEKLRLKLLKEEKRLKKRRKSTSSSS
VSSADESVSSSSSSSSSGHKRHKHKKRNRSESSRRHSSSRASSNQIDQNRKDECYPVP
ANTSASFLNHKQEVKLLGKQDRLOQYEKTOIKEKDRCPLSSSSLEIPDDFGVYSYLFKKL
TIKQPQAGPSGDIPEEGIVIIDDSSIHVTDPEDLQVGQDMEVEDSGIDDPDHG

Important features of the protein:**Signal peptide:**

Amino acids 1-23

Transmembrane domain:

Amino acids 138-155

N-glycosylation sites:

Amino acids 288-292; 508-512; 542-546

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 300-304; 472-476; 473-477; 517-521; 598-602

N-myristoylation sites:

Amino acids 218-224; 222-228; 271-277; 348-354

Amidation site:

Amino acids 52-56

Cell attachment sequence:

Amino acids 125-128

407/615

FIGURE 403

CCGAGGCGGGAGGAGCCCCGAGGGGGCGCGAGCCCCGCATGAATCATTGTAGTCAATCATTTTC
CAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTTCCGAAGTCCAGCTCAGAATA
GGAAAATAACTTGGGATTTTATATTGGAAGACATGGATCCTTGCTGCCAACGAGATCAGCATTT
ATGACAAACTTTCAGAGACTGTTGATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTCAG
AGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAAAGAATGAACCTCAGAGACCCCCC
CGCAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCTTGCTCA
CTGCCTACTTTGTGATTCAACCTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTCTGGAGCTC
ACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTTGCCCATTGCCAAGAAGTACA
TGTCAGAAAATAAGGGAGTTCCTCTGCATGGGGGTGATGAAGACAGACCCTTTCAGACTTTG
ACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCTGCCAACTGCACTG
GCTGTGCCCAGAAACACCTGAAGGTGATGCTCCTGGAAGACGCCCCAAGGAAATTTGAGAGGC
TCCATCCACTGGTGATCAAGACGGGAAAGCCCCTGTTGGAGGAAGAGATTACAGCATTTTTTGT
GCCAGTACCCTGAGGCGACAGAAGGCTTCTCTGAAGGGTTTTTCGCCAAGTGGTGGCGCTGCT
TTCCTGAGCGGTGGTTCCCATTTCCTTATCCATGGAGGAGACCTCTGAACAGATCACAAATGT
TACGTGAGCTTTTTCTGTTTTCACTCACCTGCCATTTCCAAAAGATGCCTCTTTAAACAAGT
GCTCCTTTCTTCACCCAGAACCTGTTGTGGGGAGTAAGATGCATAAGATGCCTGACCTATTTA
TCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTCCAGTGCCGAAGACATTGTC
AGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTCGACACCACCCACTGGAAGG
TCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCATCTGCGATGGAACCGCTTTCTCAGAAC
TGTAGGAAATAGAACTGTGCACAGGAACAGCTTCCAGAGCCGAAAACCAGGTTGAAAGGGGAA
AAATAAAAACAAAAACGATGAAACTGCAAAAA

408/615

FIGURE 404

MDLAANEISIIYDKLSETVDLVRQTGHQCGMSEKAIEKFIRQLLEKNEPQRPPQYPLLIVVYK
VLATLGLILLTAYFVIQPFSPPLAPEPVLSGAHTWRSLIHHIRLMSLPKAKKYMSENKGVPLHG
GDEDRPFPDFDPWWTNDCEQNESEPI PANCTGCAQKHLKVMLLEDAPRKFERLHPLVIKTGKP
LLEEEIQHFLLCQYPEATEGEFSEGFFAKWWRCFPERWFPPYPWRRPLNRSQMLRELFVFTHL
PFPKDASLNKCSFLHPEPVVGSKMHKMPDLFIIGSGEAMLQLIPPFQCRRHCSVAMPIEPGD
IGYVDTTHWKVYVIARGVQPLVICDGTAFSEL

409/615

FIGURE 405

TGCCGGGCTGCGGGGCGCCTTGACTCTCCCTCCACCCTGCCTCCTCGGGCTCCACTCGTCTGCCCCCTGGACTCCC
GTCTCCTCCTGTCTCCGGCTTCCCAGAGCTCCCTCCTTATGGCAGCAGCTTCCCGCGTCTCCGGGCGCAGCTTCT
CAGCGGACGACCCTCTCGCTCCGGGGCTGAGCCAGTCCCTGGATGTTGCTGAAACTCTCGAGATCATGCGGGG
TTTGGCTGCTGCTTCCCGCCGGGTGCCACTGCCACCGCCGCCCTCTGCTGCCGCCGTCGCGGGGATGCTCAG
TAGCCCGCTGCCCGGCCCGCGATCCTGTGTTCTCGGAAGCCGTTTGCTGCTGCAGAGTTGCACGAAC TAGTC
ATGGTGCTGTGGGAGTCCCGCGGCAGTGCCAGCTGGACACTTTGCGAGGGCTTTTGCTGGCTGCTGCTGCTG
CCCGTCATGCTACTCATCGTAGCCCGCCCGGTGAAGCTCGTGCTTTCCCTACCTCCTTAAGTGACTGCCAAACG
CCCACCGGCTGGAATTGCTCTGGTTATGATGACAGAGAAAATGATCTCTTCTCTGTGACACCAACACCTGTAA
TTTGATGGGGAATGTTTAAGAATTGGAGACACTGTGACTTGCGTCTGTCAAGTCAAGTGCAACAATGACTATGTG
CCTGTGTGTGGCTCCAATGGGGAGAGCTACCAGAATGAGTGTTACCTGCGACAGGCTGCATGCAAACAGCAGAGT
GAGATACTTGTGGTGTGAGAAGGATCATGTGCCACAGATGCAGGATCAGGATCTGGAGATGGAGTCCATGAAGGC
TCTGGAGAACTAGTCAAAAGGAGACATCCACCTGTGATATTTGCCAGTTTGGTGCAGAATGTGACGAAGATGCC
GAGGATGTCTGGTGTGTGTGTAATATTGACTGTTCTCAAACCAACTTCAATCCCCTCTGCGCTTCTGATGGGAAA
TCTTATGATAATGCATGCCAAATCAAAGAAGCATCGTGTGAGAAACAGGAGAAAATTGAAGTCATGTCTTTGGGT
CGATGTCAAGATAACACAACACTACAATACTAAGTCTGAAGATGGGCATTATGCAAGAACAGATTATGCAGAGAAT
GCTAACAAATTAGAAGAAAGTGCCAGAGAACACCACATACCTTGTCCGGAACATTACAATGGCTTCTGCATGCAT
GGGAAGTGTGAGCATTTCTATCAATATGCAGGAGCCATCTGCAGGTGTGATGCTGGTTATACTGGACAACACTGT
GAAAAAAGGACTACAGTGTCTATACGTTGTTCCCGGTCCTGTACGATTTCAAGTATGTCTTAATCGCAGCTGTG
ATTGGAACAATTCAGATTGCTGTCTGTGTGGTGGTCCCTCTGCATCACAAGGAAATGCCCCAGAAGCAACAGA
ATTCACAGACAGAAGCAAAATACAGGGCACTACAGTTCAGACAATACAACAAGAGCGTCCACGAGGTTAATCTAA
AGGGAGCATGTTTCACAGTGGCTGGACTACCGAGAGCTTGGACTACACAATACAGTATTATAGACAAAAGAATAA
GACAAGAGATCTACACATGTTGCCTTGCAATTTGTGGTAATCTACACCAATGAAAACATGTACTACAGCTATATTT
GATTATGTATGGATATATTTGAAATAGTATACATGTCTTGATGTTTTTCTGTAATGTAAATAAACTATTTATA
TCACACAATATAGTTTTTTCTTTCCCATGTATTTGTTATATATAATAATACTCAGTGATGAG

410/615

FIGURE 406

MVLWESPRQCSSWTLCEGFCWLLLLPVMLLIVARPVKLAAFPTSLSDCQTPTGWNC SGY
DDRENDLFLCDTNTCKFDGECLRIGDTVTCVCQFKCNDYVPVCGSNGESYQNECYLRQ
AACKQQSEILVSEGS CATDAGSGSGDGVHEGSGETSQKETSTCDICQFGAECDEDAED
VWCVCNIDCSQTNFNPLCASDGKSYDNACQIKEASCQKQEKIEVMSLGRCQDNTTTT TK
SEDGHYARTDYAENANKLEESAREHHIPCPEHYNGFCMHGKCEHSINMQEPSCRC DAGY
TGQHCEKKDYSVLYVVPGPVRFQYVLIAAVIGTIQIAVICVVVLCITRKCPRSNRIHRQ
KQNTGHYSSDNTTRASTRLI

411/615

FIGURE 407

CTCGCAGCCGAGCGCGGCCGGGGAAGGGCTCTCCTTCCAGCGCCGAGCACTGGGCCCCCTGGCAG
ACGCCCCAAGATTGTTGTGAGGAGTCTAGCCAGTTGGTGAGCGCTGTAATCTGAACCAGCTGT
GTCCAGACTGAGGCCCCATTTGCATTGTTTAACTACTTAGAAAATGAAGTGTTCAATTTTTAA
CATTCCTCCTCCAATTGGTTTAAATGCTGAATTACTGAAGAGGGCTAAGCAAACCAGGTGCTT
GCGCTGAGGGCTCTGCAGTGGCTGGGAGGACCCCGCGCTCTCCCCGTGTCTCTCCACGACT
CGCTCGGCCCTCTGGAATAAAACACCCGCGAGCCCCGAGGGCCCAGAGGAGGCCGACGTGCC
CGAGCTCCTCCGGGGGTCCCGCCCGAGCTTTCTTCTCGCCTTCGCATCTCCTCCTCGCGCG
TCTTGACATGCCAGGAATAAAAAGGATACTCACTGTTACCATTCTGGCTCTCTGTCTTCCAA
GCCCTGGGAATGCACAGGCACAGTGACGAATGGCTTTGACCTGGATCGCCAGTCAGGACAGT
GTTTAGATATTGATGAATGCCGAACCATCCCCGAGGCCTGCCGAGGAGACATGATGTGTGTTA
ACCAAAATGGCGGGTATTTATGCATTCCCCGGACAAACCTGTGTATCGAGGGCCCTACTCGA
ACCCCTACTCGACCCCCCTACTCAGGTCCGTACCCAGCAGCTGCCCCACCACTCTCAGCTCCAA
ACTATCCCACGATCTCCAGGCCTCTTATATGCCGCTTTGGATACCAGATGGATGAAAGCAACC
AATGTGTGGATGTGGACGAGTGTGCAACAGATTCCCACCAGTGCAACCCACCCAGATCTGCA
TCAATACTGAAGCGGGTACACCTGCTCCTGCACCGACGGATATTGGCTTCTGGAAGGCCAGT
GCTTAGACATTGATGAATGTCGCTATGGTTACTGCCAGCAGCTCTGTGCGAATGTTCTTGGAT
CCTATTCTGTACATGCAACCCTGGTTTTACCCTCAATGAGGATGGAAGGTCTTGCCAAGATG
TGAACGAGTGTGCCACCGAGAACCCTGCGTGCAACCTGCGTCAACACCTACGGCTCTCTCA
TCTGCCGCTGTGACCCAGGATATGAACTTGAGGAAGATGGCGTTTATTGCAGTGATATGGACG
AGTGCAGCTTCTCTGAGTTCCTCTGCCAACATGAGTGTGTGAACCAGCCCGGCACATACTTCT
GCTCCTGCCCTCCAGGCTACATCCTGCTGGATGACAACCGAAGCTGCCAAGACATCAACGAAT
GTGAGCACAGGAACCACACGTGCAACCTGCAGCAGACGTGCTACAATTTACAAGGGGGCTTCA
AATGCATCGACCCCATCCGCTGTGAGGAGCCTTATCTGAGGATCAGTGATAACCGCTGTATGT
GTCCTGCTGAGAACCCTGGCTGCAGAGACCAGCCCTTTACCATCTTGTACCGGGACATGGACG
TGGTGTGAGGACGCTCCGTTCCCGCTGACATCTTCCAAATGCAAGCCACGACCCGCTACCCTG
GGGCTATTACATTTTCCAGATCAAATCTGGGAATGAGGGCAGAGAATTTTACATGCGGCAAA
CGGGCCCCATCAGTGCCACCCTGGTGATGACACGCCCCATCAAAGGGCCCCGGGAAATCCAGC
TGGACTTGGAATGATCACTGTCAACACTGTCATCAACTTCAGAGGCAGCTCCGTGATCCGAC
TGCGGATATATGTGTGCGAGTACCCATTCTGAGCCTCGGGCTGGAGCCTCCGACGCTGCCTCT
CATTGGCACCAGGGACAGGAGAAGAGAGGAAATAACAGAGAGAATGAGAGCGACACAGACGT
TAGGCATTTCTGTGAACGTTTCCCCGAAGAGTCAGCCCCGACTTCCTGACTCTCACCTGTA
CTATTGCAGACCTGTCACCCCTGCAGGACTTGCCACCCCCAGTTCCTATGACACAGTTATCAAA
AAGTATTATCATTGCTCCCTGATAGAAGATTGTTGGTGAATTTTCAAGGCCTTCAGTTTATT
TCCACTATTTTCAAAGAAAATAGATTAGGTTTGGGGGGTCTGAGTCTATGTTCAAAGACTGT
GAACAGCTTGCTGTCACTTCTTACCTCTTCCACTCCTTCTCTCACTGTGTTACTGCTTTGCA
AAGACCCGGGAGCTGGCGGGGAACCCTGGGAGTAGCTAGTTTGTCTTTTGCCTACACAGAGAA
GGCTATGTAAACAAACCACAGCAGGATCGAAGGGTTTTAGAGAATGTGTTTCAAACCATGC
CTGGTATTTTCAACCATAAAAGAAGTTTCAGTTGTCCTTAAATTTGTATAACGGTTTAATTCT
GTCTTGTTTCAATTTTGAATTTTTTAAAAAATATGTCGTAGAATTCTTCGAAAGGCCTTCAGA
CACATGCTATGTTCTGTCTTCCCAAACCCAGTCTCCTCTCCATTTTAGCCAGTGTTTTCTTT
GAGGACCCCTTAATCTTGCTTTCTTTAGAATTTTTACCCAATTGGATTGGAATGCAGAGGTCT
CCAACTGATTAAATATTTGAAGAGA

412/615

FIGURE 408

MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQN
GGYLCIPRTNPVYRGYPYSPYSTPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDENQCV
DVDECATDSHQCNPTQICINTEGGYTCSTDGWLLLEGQCLDIDECRYGYCQQLCANVPGSYS
CTCNPGFITLNEGRSCQDVNECATENPCVQTCVNTYGSILCRCDPGYELEEDGVHCSDMDECS
FSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCI
DPIRCEEPYLRI SDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAY
YIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRI
YVSQYPF

Important features of the protein:**Signal peptide:**

amino acids 1-25

N-glycosylation sites.

amino acids 283-287, 296-300

N-myristoylation sites.amino acids 21-27, 64-70, 149-155, 186-192, 226-232, 242-248,
267-273, 310-316**Aspartic acid and asparagine hydroxylation sites.**

amino acids 144-156, 181-193, 262-274

Cell attachment sequence.

amino acids 54-57

Calcium-binding EGF-like.

amino acids 131-166, 172-205, 211-245, 251-286

413/615

FIGURE 409

CCCACGCGTCCGCGGACGCGTGGGTGCGACTAGTTCTAGATCGCGAGCGGCCGCCGCGGCTCA
GGGAGGAGCACCGACTGCGCCGCACCCTGAGAGATGGTTGGTGCCATGTGGAAGGTGATTGTT
TCGCTGGTCCTGTTGATGCCTGGCCCCCTGTGATGGGCTGTTTCGCTCCCTATACAGAAGTGTT
TCCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTTCTCACCCCTTACATTGAAGCTGGG
AAGATCCAAAAAGGAAGAGAATTGAGTTTGGTCGGCCCTTTCCCAGGACTGAACATGAAGAGT
TATGCCGGCTTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTTCTGGTTCTTCCCA
GCTCAGATACAGCCAGAAGATGCCCCAGTAGTTCTCTGGCTACAGGGTGGGCCGGGAGGTTCA
TCCATGTTTGGACTCTTTGTGGAACATGGGCCCTTATGTTGTCAAGTAACATGACCTTGCGT
GACAGAGACTTCCCCTGGACCACAACGCTCTCCATGCTTTACATTGACAATCCAGTGGGCACA
GGCTTCAGTTTTTACTGATGATACCCACGGATATGCAGTCAATGAGGACGATGTAGCACGGGAT
TTATACAGTGCACCTAATTCAGTTTTTCCAGATATTTCTGAATATAAAAAATAATGACTTTTAT
GTCAGTGGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTCATCCATTCCCTC
AACCCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGATGGATATTCTGAT
CCCGAATCAATTATAGGGGGCTATGCAGAATTCCTGTACCAAATTGGCTTGTGGATGAGAAG
CAAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATCAGGAAGCAGAACTGG
TTTGAGGCCCTTTGAAATACTGGATAAACTACTAGATGGCGACTTAACAAGTGATCCTTCTTAC
TTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTTTGCGGTGCACGGAACCTGAGGAT
CAGCTTTACTATGTGAAATTTTTGTCACTCCCAGAGGTGAGACAAGCCATCCACGTGGGGAAT
CAGACTTTTAATGATGGAACATAGTTGAAAAGTACTTGCGAGAAGATACAGTACAGTCAGTT
AAGCCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGATCTACAATGGCCAACCTGGAC
ATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTTGATGGGCATGGACTGGAAAGGATCCCAG
GAATACAAGAAGGCAGAAAAAAAAGTTTGGAAGATCTTTAAATCTGACAGTGAAGTGGCTGGT
TACATCCGGCAAGCGGGTGAAGTTCCATCAGGTAATTATTCGAGGTGGAGGACATATTTTACCC
TATGACCAGCCTCTGAGAGCTTTTGACATGATTAATCGATTCAATTTATGAAAAGGATGGGAT
CCTTATGTTGGATAAACTACCTTCCCAAAAAGAGAACATCAGAGGTTTTTCATTGCTGAAAAGAA
AATCGTAAAAACAGAAAATGTCATAGGAATAAAAAAATTATCTTTTCATATCTGCAAGATTTT
TTTCATCAATAAAAAATTATCCTTGAAACAAGTGAGCTTTTGTGTTTTGGGGGGAGATGTTTACT
ACAAAATTAACATGAGTACATGAGTAAGAATTACATTATTTAACTTAAAGGATGAAAGGTATG
GATGATGTGACACTGAGACAAGATGTATAAATGAAATTTTAGGGTCTTGAATAGGAAGTTTAA
ATTTCTTCTAAGAGTAAGTGAAAAGTGCAGTTGTAACAAACAAAGCTGTAACATCTTTTCTG
CCAATAACAGAAGTTTGGCATGCCGTGAAGGTGTTTGGAAATATTATTGGATAAGAATAGCTC
AATTATCCCAAATAAATGGATGAAGCTATAATAGTTTTTGGGAAAAGATTCTCAAATGTATAA
AGTCTTAGAACAAAAGAATTCTTTGAAATAAAAAATATTATATATAAAAGTAAAAA

414/615

FIGURE 410

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGDGQPLFLTPYIEAGKIQKGRELSLV
GPFPGLNKMSYAGFLT VNKTYSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEHGP
YVVT SNMTLRDRDFPWTTL SMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALI QFFQI
FPEYKNNDFYVTGESYAGKYVPAIAHLIHS LN PVREVKINLNGIAIGDGYS DPESIIGGYAEF
LYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGDLTSDPSYFQNV TGCSNYY
NFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNQTFNDGTIVEKYLREDTVQSVKPWLTEIMNNY
KVLIYNGQLDIIVAAALTERSLMGMDWKG SQEYKKA EKKVWKIFKSDSEVAGYIRQAGDFHQV
IIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

Signal sequence:
amino acids 1-22

N-glycosylation site.
amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.
amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.
amino acids 423-432

N-myristoylation site.
amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.
amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.
amino acids 375-391

415/615

FIGURE 411

GCAAGCCAAGGCGCTGTTTGAGAAGGTGAAGAAGTTCGGACCCATGTGGAGGAGGGGGACATTGTGTACCGCCT
CTACATGCGGCAGACCATCATCAAGGTGATCAAGTTCATCCTCATCATCTGCTACACCGTCTACTACGTGCACAA
CATCAAGTTCGACGTGGACTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCCCACCC
CCTGGCCACACTCTTCAAGATCCTGGCGTCTTCTACATCAGCCTAGTCATCTTCTACGGCCTCATCTGCATGTA
CACACTGTGGTGGATGCTACGGCGCTCCCTCAAGAAGTACTCGTTTGAGTCGATCCGTGAGGAGAGCAGCTACAG
CGACATCCCCGACGTCAAGAACGACTTCGCCTTCATGCTGCACCTCATTGACCAATACGACCCGCTCTACTCCAA
GCGCTTCGCCGTCTTCTGTGCGAGGTGAGTGAGAACAAGCTGCGGCAGCTGAACCTCAACAACGAGTGGACGCT
GGACAAGCTCCGGCAGCGGCTCACCAAGAACGCGCAGGACAAGCTGGAGCTGCACCTGTTTCATGCTCAGTGGCAT
CCCTGACACTGTGTTTGACCTGGTGGAGCTGGAGTCCCTCAAGCTGGAGCTGATCCCCGACGTGACCATCCCCGCC
CAGCATTGCCAGCTCACGGGCCCTCAAGGAGCTGTGGCTTACCACACAGCGGCAAGATTGAAGCGCTGCGCT
GGCCTTCCTGCGGAGAACCTGCGGGCGCTGCACATCAAGTTCACCGACATCAAGGAGATCCCGCTGTGGATCTA
TAGCCTGAAGACACTGGAGGAGCTGCACCTGACGGGCAACCTGAGCGCGGAGAACCAACCGCTACATCGTCATCGA
CGGGCTGCGGGAGCTCAAACGCCCTCAAGGTGCTGCGGCTCAAGAGCAACCTAAGCAAGCTGCCACAGGTGGTCAC
AGATGTGGGCGTGACCTGCAGAAGCTGTCCATCAACAATGAGGGCACCAGCTCATCGTCTCAACAGCCTCAA
GAAGATGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGCGACCTGGAGCGCATCCCCACTCCATCTTCAGCCT
CCACAACCTGCAGGAGATTGACCTCAAGGACAACAACCTCAAGACCATCGAGGAGATCATCAGCTTCCAGCACCT
GCACCGCCTCACCTGCCTTAAGCTGTGGTACAACCACATCGCCTACATCCCCATCCAGATCGGCAACCTCACCAA
CCTGGAGCGCTTCTACCTGAACGCAACAAGATCGAGAAGATCCCCACCCAGCTCTTCTACTGCCGCAAGCTGCG
CTACCTGGACCTCAGCCACAACAACCTGACCTTCCCTGCCGACATCGGCCTCCTGCAGAACCTCCAGAACCT
AGCCATCACGGCCAAACCGGATCGAGACGCTCCCTCCGGAGCTCTTCCAGTGCCGGAAGCTGCGGSCCTGCACCT
GGGCAACAACGTGCTGCACTGCTGCTCCCTCCAGGGTGGGCGAGCTGACCAACCTGACGCAGATCGAGCTGCGGGG
CAACCGGCTGGAGTGCTGCTGTGGAGCTGGGCGAGTGCCCACTGCTCAAGCGCAGCGGCTTGGTGGTGGAGGA
GGACCTGTTCAACACACTGCCACCGAGGTGAAGGAGCGGCTGTGGAGGGCTGACAAGGAGCAGGCTGAGCGAG
GCCGGCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCTCAGGCCCGGAGGGGCGAGGCTAGCTTCTCCCAG
AACTCCCGGACAGCCAGGACAGCCTCGCGGCTGGGCAGGAGCCTGGGGCCGCTTGTGAGTCAGGCCAGAGCGAGA
GGACAGTATCTGTGGGCTGCCCCCTTTCTCCCTGAGACTCACGTCCCCAGGGCAAGTGCTTGTGGAGGAG
AGCAAGTCTCAAGAGCGCAGTATTTGGATAATCAGGGTCTCCTCCCTGGAGGCCAGCTTGCCCCAGGGGCTGAG
CTGCCACCAGAGGTCTGGGACCTCACTTTAGTTCTTGGTATTTATTTTCTCCATCTCCCACCTCCTTCATCC
AGATAACTTATACATTCCCAAGAAAGTTCAGCCCAGATGGAAGGTGTTTCAGGGAAAGGTGGGCTGCCTTTTCCCC
TTGTCCTTATTTAGCGATGCCGCCGGGCATTTAACACCCACCTGGACTTCAGCAGAGTGGTCCGGGGCGAACCCAG
CCATGGGACGGTCACCCAGCAGTGCCGGGCTGGGCTCTGCGGTGCGGTCCACGGGAGAGCAGGCTCCAGCTGGA
AAGGCCAGGCTGGAGCTTGCTCTTTCAGTTTTTGTGGCAGTTTTAGTTTTTGTTTTTTTTTTTTAAATCAAA
AAACAATTTTTTTTAAAAAAAGCTTTGAAAATGGATGGTTGGGTATTAAGGAGAAAAAAACTTAAAAAA
AAAAGACACTAACGGCCAGTGAGTTGGAGTCTCAGGGCAGGGTGGCAGTTTCCCTTGAGCAAAGCAGCCAGACGT
TGAAGTGTGTTTCCCTTCCCTGGGCGCAGGGTGCAGGGTGTCTCCGGATCTGGTGTGACCTTGGTCCAGGAGTT
CTATTTGTTTCCCTGGGAGGGAGGTTTTTTTGTGTTTTTGGGTTTTTTTGGTGTCTTGTGTTTTCTTCTCCTCC
ATGTGTCTTGGCAGGCACTCATTTCTGTGGCTGTGCGCCAGAGGGAATGTTCTGGAGCTGCCAAGGAGGGAGGAG
ACTCGGGTTGGCTAATCCCCGATGAACGGTGCTCCATTCGCACCTCCCCTCCTCGTGCCTGCCCTGCCCTCTCCA
CGCACAGTGTAAAGAGCCAAGAGGAGCCACTTCGCCAGACTTTGTTTCCCCACCTCCTGCGGCATGGGTGTGT
CCAGTGCCACCGCTGGCCTCCGCTGCTTCCATCAGCCCTGTGCGCACCTGGTCTTTCATGAAGAGCAGACACTTA
GAGGCTGGTGGGAATGGGGAGGTGCGCCCTGGGAGGGCAGGCGTTGGTTCCAAGCCGTTCCCGTCCCTGGCGC
CTGGAGTGACACAGCCAGTGGCACCTGGTGGCTGGAAGCCAACCTGCTTTAGATCACTCGGGTCCCCACCTT
AGAAGGGTCCCCGCTTAGATCAATCACGTGGACACTAAGGCAGGTTTTAGAGTCTTGTCTTAATGATTATGT
CCATCCGTCTGCCGTCCATTTGTGTTTTCTGCGTCTGTCATTGGATATAATCCTCAGAAATAATGCACACTAG
CCTCTGACAACCATGAAGCAAAAATCCGTTACATGTGGGTCTGAACCTGTAGACTCGGTACAGTATCAAATAAA
ATCTATAACAGAAAAA

416/615

FIGURE 412

MRQTIKVIKFILIIICYTVYYVHNIKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYIS
LVIFYGLICMYTLWWMRLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSKRF
AVFLSEVSENKLRQLNLNNEWTLDKLRQRLTKNAQDKLELHLFMLSGIPDPTVFDLVELEVLKL
ELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFIRENLRALHIKFTDIKEIPLWIYSLK
TLEELHLTGNLSEAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSINNEGT
KLIVLNSLKKMANLTELELIRCDLERIPHSIFSLHNLQEIIDLKDNNLKTIEEIIISFOHLHRLT
CLKLWYNHAIYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKRLRYLDLSHNNLTFLPADIG
LLQNLQNLAITANRIETLPPELFQCRKLRLHLGNNVLQSLPSRVGELTNLTQIELRGNRLEC
LPVELGECPLLKRSGLVVEEDLNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497**N-myristoylation site.**

amino acids 173-179, 261-267, 395-401, 441-447

417/615

FIGURE 413

GAATCATCCACGCACCTGCAGCTCTGCTGAGAGAGTGAAGCCGTGGGGGTTTTGAGCTCATC
TTCATCATTTCATATGAGGAAATAAGTGGTAAAATCCTTGGAATACAATGAGACTCATCAGAA
ACATTTACATATTTTGTAGTATTGTTATGACAGCAGAGGGTGATGCTCCAGAGCTGCCAGAAG
AAAGGGAACCTGATGACCAACTGCTCCAACATGTCTCTAAGAAAGGTTCCCGCAGACTTGACCC
CAGCCACAACGACACTGGATTTATCCTATAACCTCCTTTTTCAACTCCAGAGTTTCAGATTTTC
ATTCTGTCTCCAACTGAGAGTTTTGATTCTATGCCATAACAGAATTCAACAGCTGGATCTCA
AAACCTTTGAATTCAACAAGGAGTTAAGATATTTAGATTTGTCTAATAACAGACTGAAGAGTG
TAACTTGGTATTTACTGGCAGGTCTCAGGTATTTAGATCTTTCTTTAATGACTTTGACACCA
TGCCATCTGTGAGGAAGCTGGCAACATGTCACACCTGGAAATCCTAGGTTTGAGTGGGGCAA
AAATACAAAAATCAGATTTCCAGAAAATTTGCTCATCTGATCTAAATACTGTCTCTTAGGAT
TCAGAACTCTTCCTCATTATGAAGAAGGTAGCCTGCCCATCTTAAACACAACAAAATGCACA
TTGTTTTACCAATGGACACAATTTCTGGGTTCTTTTGCCTGATGGAATCAAGACTTCAAAAA
TATTAGAAATGACAAATATAGATGGCAAAAGCCAATTTGTAAGTTATGAAATGCAACGAAATC
TTAGTTTGAATAATGCTAAGACATCGGTTCTATTGCTTAATAAAGTTGATTTACTCTGGGACG
ACCTTTTCTTATCTTACAATTTGTTTGGCATATCATCAGTGGAACACTTTTCAGATCCGAAATG
TGACTTTTGGTGGTAAGGCTTATCTTGACCACAATTCATTTGACTACTCAATACTGTAATGA
GAACTATAAAATTTGGAGCATGTACATTTTCAGAGTGTTTTACATTCAACAGGATAAAATCTATT
TGCTTTTGACCAAAATGGACATAGAAAACCTGACAATATCAAATGCACAAATGCCACACATGC
TTTTCCCGAATTATCCTACGAAATTTCCAATATTTAAATTTTGCCAATAATATCTTAACAGAG
AGTTGTTTAAAGAAGTATCCAACCTGCCTCACTTGAAAACCTCTCATTTTGAATGGCAATAAAC
TGGAGACACTTTCTTTAGTAAGTTGCTTTGCTAACAACACACCCTTGGAACACTTGGATCTGA
GTCAAAATCTATTACAACATAAAATGATGAAAATTGCTCATGGCCAGAACTGTGGTCAATA
TGAATCTGTACATAAATAAATTTGTCTGATTCTGTCTTCAAGTGCTTGCCAAAAGTATTCAAA
TACTTGACCTAATAATAACCAAACTGCAAACTGACCTAAAGAGACTATTCTAGATTCATACA
TACGAGAATAAATATTGCATTTAATTTTCTAACTGATCTCCCTGGATGCAGTCATTTTCAGTA
GACTTTTCAGTTCTGAACATTGAAATGAACTTTCATTCTCAGCCCATCTCTGGATTTTGTTCAGA
GCTGCCAGGAAGTTAAACTCTAAATGCGGGAAGAAATCCATTCCGGTGTACCTGTGAATTAA
AAAATTTTCATTTCAGCTTGAAACATATTTCAGAGGTCATGATGGTTGGATGGTCAGATTCATACA
CCTGTGAATACCTTTTAAACCTAAGGGGAAGTGGTTAAAAGACGTTTCATCTCCACGAATTAT
CTTGCAACACAGCTCTGTTGATTGTCACCATTGTGGTTATTATGCTAGTTCTGGGGTTGGCTG
TGGCCTTCTGCTGTCTCCACTTTGATCTGCCCTGGTATCTCAGGATGCTAGGTCAATGCACAC
AAACATGGCAGAGGTTAGGAAAACAACCAAGAACAACCTCAAGAGAAATGTCCGATTGCCAG
CATTTATTTTCATACAGTGAACATGATTCTCTGTGGGTGAAGAATGAATTGATCCCCAATCTAG
AGAAGGAAGATGGTTCTATCTTGATTTGCCTTTATGAAAGCTACTTTGACCCTGGCAAAAGCA
TTAGTGAAAATATTGTAAGCTTCATTGAGAAAAGCTATAAGTCCATCTTTGTTTTGTCTCCCA
ACTTTGTCCAGAAATGAGTGGTGCCATTATGAATTCTACTTTGCCACCACAATCTCTTCCATG
AAAATTTCTGATCATATAATTCTTATCTTACTGGAACCCATTCCATTCTATTGCAATTCACCA
GGTATCATAAACTGAAAGCTCTCCTGGAAAAAAGCATACTTGGAATGGCCCAAGGATAGGC
GTAAATGTGGGCTTTTCTGGGCAACCTTCGAGCTGCTATTAATGTTAATGTATTAGCCACCA
GAGAAATGTATGAAGTGCAGACATTACAGAGTTAAATGAAGAGTCTCGAGGTTCTACAATCT
CTCTGATGAGAACAGATTGTCTATAAAATCCCACAGTCCTTGGAAGTTGGGGACCACATACA
CTGTTGGGATGTACATTGATACAACCTTTATGATGGCAATTTGACAATATTTATTAAAAATAAA
AAATGGTTATTTCCCTTCATATCAGTTTCTAGAAGGATTTCTAAGAATGTATCCTATAGAAACA
CCTTCACAAGTTTATAAGGGCTTATGGAAAAGGTGTTTCATCCAGGATGTTTTATAATCATG
AAAAATGTGCCAGGTGCAGTGGCTCACTTTGTAATCCCAGCACTATGGGAGGCCAAGGTGG
GTGACCCACGAGGTCAAGAGATGGAGACCATCCTGGCCAACATGGTGAAACCTGTCTCTACT
AAAAATACAAAAATTAGCTGGGCGTGATGGTGCACGCTGTAGTCCCAGCTACTTGGGAGGCT
GAGGCAGGAGAATCGCTTGAACCCGGGAGGTGGCAGTTGCAGTGAGCTGAGATCGAGCCACTG
CACTCCAGCCTGGTGACAGAGCGAGACTCCATCTCAAAAAAAGAAAAAAGAAAAA
ATGGAAAAACATCCTCATGGCCACAAAAATAAGGTCTAATTCAATAAATTATAGTACATTAATGT
AATATAATATTACATGCCACTAAAAAGAATAAGGTAGCTGTATATTTCTTGGTATGGAAAAA
CATATTAATATGTTATAAACTATTAGGTTGGTGCAAACTAATTGTGGTTTTTGGCATTGAAA
TGGCATTGAAATAAAAGTGTAAAGAAATCTATACCAGATGTAGTAACAGTGGTTTGGGTCTGG
GAGGTTGGATTACAGGGAGCATTTGATTTCTATGTTGTGTATTTCTATAATGTTTGAATTGTT
TAGAATGAATCTGTATTTCTTTTATAAGTAGAAAAAATAAAGATAGTTTTTACAGCCT

418/615

FIGURE 414 .

MRLIRNIYIFCSIVMTAEGDAPELPEERELMTNCSNMSLRKVPADLTPATTTLDLSYNLLFQL
QSSDFHSVSKLRVLILCHNRIQQDLKTFFFNKELRYLDLSNNRLKSVTWYLLAGLRYLDLSF
NDFDTMPICEEAGNMSHLEILGLSGAKIQKSDFKIAHLHLNTVFLGFRTPHYEEGSLPILN
TTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLLLLNKV
DLLWDDLFLLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFRVFYIQ
QDKIYLLLTkMDIENLTISNAQMPHMLFPNYPTKFQYLNfANNILTDELfKRTIQLPHLKTLI
LNGNKLETLSLVSCFANNTPLEHLDLSQNLLQHKNdENCsWPETVVNMNLSYNKLSDSVFRCL
PKSIQILDlnnnQIQTVPKETIHLMALRELNIafNfLTDLPgCSHFsrLSVLNIEMNFILSPS
LDFVQSCQEVKTLNAGRNPFrCTCELKNfIQLEtySEVMmVGWSDSYTCEYPLNLRGTRLKDV
HLHELSCNTALLIVTIVVIMLVGLAVAFcCLHFDLPWYLRMLGQCTQTWHRVRKTTQEQLKR
NVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSISENIVSFIEKSYKSI
FVLSPNFVQNEWCHYEFYFAHHNLFHENSdHIILILLEPIPFYCIPTRYHKLKALLEKKAYLE
WPKDRRKCGLFWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLMRTDCL

419/615

FIGURE 415

CGGACGCGTGGGCGGACGCGTGGGCCTGGGCAAGGGCCGGGGCGCCGGGCGGAGCCACCTCTTCCCCCTCCCCCGC
TTCCCTGTGCGGCTCCGCTGGCTGGACGCGCTGGAGGAGTGGAGCAGCACCCGGCCGGCCCTGGGGGCTGACAGT
CGGCAAAGTTTGGCCCCGAAGAGGAAGTGGTCTCAAACCCCGCAGGTGGCGACACAGGCCAGACCAGGGGCGCTCG
CTGCCTGCGGGCGGGCTGTAGGCGAGGGCGCGCCCCAGTGCAGAGACCCGGGGCTTCAGGAGCCGGCCCCGGGAG
AGAAGAGTGGCGGGCGGACGGAGAAAACTCAAAGTTGGCGAAAGGCACCGCCCTACTCCCGGGCTGCCG
CCGCTCCCCGCCCCAGCCCTGGCATCCAGAGTACGGTTCGAGCCCGGGCCATGGAGCCCCCTGGGGAGGCGG
CACCAGGGAGCCTGGGCGCCCGGGGCTCCGCCGCGACCCCATCGGGTAGACCACAGAAGCTCCGGGACCCCTTCCG
GCACCTCTGGACAGCCAGGATGCTGTTGGCCACCCTCCTCCTCCTCCTTGGAGGCGCTCTGCCCCATCCAG
ACCGGATTATTTTCCAAATCATGCTTGTGAGGACCCCCAGCAGTGTCTTAGAAGTGCAGGGCACCTTACAGA
GGCCCTGGTCCGGGACAGCCGCACCTCCCCTGCCAACTGCACCTGGCTCATCCTGGGCGAGCAAGGAACAGACTG
TCACCATCAGGTTCCAGAAGCTACACCTGGCCTGTGGCTCAGAGCGCTTAACCTACGCTCCCCCTCCAGCCAC
TGATCTCCCTGTGTGAGGCACCTCCAGCCCTCTGCAGCTGCCCGGGGGCAACGTCACCATCACTTACAGCTATG
CTGGGGCCAGAGCACCATGGGCCAGGGCTTCTGCTCTCTACAGCCAAGATTGGCTGATGTGCTGCAGGAAG
AGTTTCAGTGCCTGAACACCGCTGTGTATCTGCTGTCCAGCGCTGTGATGGGGTGTATGCCTGTGCGGATGGCT
CTGATGAAGCAGGTTGCAGCTCAGACCCCTTCCCTGGCCTGACCCCAAGACCCGTCCCCTCCCTGCCCTTGAATG
TCACCTTGGAGGACTTCTATGGGGTCTTCTCCTCTCCTGGATATACACACCTAGCCTCAGTCTCCACCCCCAGT
CCTGCCATTGGCTGTGAGACCCCATGATGGCCGGCGGCTGGCCGTGCGCTTCACAGCCCTGGACTTGGGCTTTG
GAGATGCAGTGCATGTGTATGACGGCCCTGGGCCCCCTGAGAGCTCCCGACTACTGCGTAGTCTACCCACTTCA
GCAATGGCAAGGCTGTCACTGTGGAGACACTGTCTGGCCAGGCTGTTGTGTCTTACCACACAGTTGCTTGGAGCA
ATGGTCGTGGCTTCAATGCCACCTACCATGTGCGGGGCTATTGCTTGCCTTGGGACAGACCCTGTGGCTTAGGCT
CTGGCCTGGGAGCTGGCGAAGGCCCTAGGTGAGCGCTGTACAGTGAGGCACAGCGCTGTGACGGCTCATGGGACT
GTGCTGACGGCACAGATGAGGAGGACTGCCAGGCTGCCACCTGGACACTTCCCCTGTGGGGCTGTGGCACCT
CTGGTGCCACAGCCTGTACCTGCCTGTGACCGCTGCAACTACCAGACTTCTGTGCTGATGGAGCAGATGAGA
GACGCTGTGCGCATTGCCAGCCTGGCAATTTCCGATGCCGGGACGAGAAGTGCCTGTATGAGACCTGGGTGTGCG
ATGGGCGAGCCAGACTGTGCGGACGGCAGTGATGAGTGGGACTGCTCCTATGTTCTGCCCGCAAGGTCATTACAG
CTGCAGTCACTTGGACCTAGTGTGCGGCTGTCTCCTGTCATCGCCCTGGGCTGCACCTGCAAGCTCATGCCA
TTCCGACCCAGGAGTACAGCATCTTTGCCCCCTCTCCCGGATGGAGGCTGAGATTGTGCAGCAGCAGGCACCCC
CTTCTACGGGCGAGCTCATTGCCAGGGTGCCATCCCACCTGTAGAAGACTTCTTACAGAGAATCCTAATGATA
ACTCAGTGTGGGCAACCTGCGTTCTCTGTACAGATCTTACGCCAGGATATGACTCCAGGAGGTGGCCAGGTG
CCCGCGCTCGTCAGCGGGGCGCTTGATGCGACGCTGGTACGCCGTCTCCGCCGTGGGGCTTGTCCCTCGAA
CCAAACCCCCGCTCGGGCCTCTGAGGCCAGATCCCAGGTACACCTTCTGCTGCTCCCCTTGGGGCCTAGATG
GTGGCACAGGTCCAGCCCGTGAGGGCGGGGAGTGGGTGGGCAAGATGGGGAGCAGGCACCCCCACTGCCCATCA
AGGCTCCCCTCCCCTGCTAGCACGCTCCAGCCCCACTACTGTCCCTGAAGCCCCAGGGCCACTGCCCTCAC
TGCCCTAGAGCCATCACTATTGTCTGGAGTGGTGCAGGCCCTGCGAGGCCGCTGTTGCCAGCCTGGGGCCCC
CAGGACCAACCCGGAGCCCCCTGGACCCACACAGCAGTCTGGCCCTGGAAGATGAGGACGATGTGCTACTGG
TGCCACTGGCTGAGCCGGGGTGTGGGTAGCTGAGGCAGAGGATGAGCCACTGCTTACCTGAGGGGACCTGGGG
CTTACTGAGGCTTCTCCCCTGGGGGCTTACTCATAGTGGCACAACTTTTAGAGGTGGGTGAGCCTCCCCTCC
ACCCTTCTTCCCTGTCCCTGGATTTCAGGGACTTGGTGGGCCTCCCGTTGACCCATGTAGCTGCTATAAAGT
TAAGTGTCCCTCAGGCAGGGAGAGGGCTCACAGAGTCTCCTCTGTACGTGGCCATGGCCAGACACCCAGTCCCT
TCACCACCACTGCTCCCCAGCCACCACCTTTGGGTGGCTGTTTTTAAAGTAAGTTCTTAGAGGATCATA
GGTCTGGACACTCATCCTTGCCAAACCTTACCCAAAAGTGGCCTTAAGCACCGAATGCCAATTAAGTAGAGA
CCCTCCAGCCCCCAAGGGGAGGATTTGGGCAGAACCTGAGGTTTTGCCATCCCAATCCCTCCTACAGGGCCTGG
CTCACAAAAGAGTGCAACAAATGCTTCTATTCCATAGCTACGGCATTGCTCAGTAAGTTAGGTCAAAAATAAA
GGAATCATACTCTC

420/615

FIGURE 416

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49631
<subunit 1 of 1, 713 aa, 1 stop
<MW: 76193, pI: 5.42, NX(S/T): 4
MLLATLLLLLLGGALAHDPRIIFPNHACEDPPAVLLEVQGT LQRPLVRDSRTSPANCTWLILG
SKEQTVTIRFQKLHLACGSERLTLRSP LQPLISLCEAPPSPLQLPGGNVTITYSYAGARAPMG
QGFLLSYSQDWLMCLQE EFQCLNHRCSVSAVQRC DGVDACGDGSDEAGCSSDPFPGLTPRPVPS
LPCNVTLEDFYGVFSSPGYTHLASVSH PQSCHWLLDPHDGRRLAVRFTALDLGFGDAVHVYDG
PGPPESSRLRLSLTHFSNGKAVTVETLSGQAVVS YHTVAWSNGRGNATYHVRGYCLPWDRPC
GLGSLGAGEGLGERCYSEAQRCDGSWD CADGTDEEDCPGCPPGHFPCGAAGTSGATACYLPA
DRCNYQTFCADGADERRCRHCQPGNFRCRDEKCVYETWVCDGQPD CADGSDEWDCSYVLPRKV
ITAAVIGSLVCGLLLVIALGCTCKLYAIR TQEYSIFAPLSRMEAEIVQQQAPPSYGQLIAQGA
IPPVEDFPTENPNDNSVLGNLRSLLQILRQDMTPGGGPGARRRQ RGLMRRLVRRRLRRWGLLP
RTNTPARASEARSQVTPSAAPLEALDGGTGPAREGGAVGGQDGEQAPPLPIKAPLPSASTSPA
PTTVPEAPGPLPSLPLEPSLLSGVVQALRGRL LPSLGPPGPTRSPPGPHTAVLALEDEDDVLL
VPLAEPGVWVAEAEDEPLLT

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domain:

amino acids 442-462

LDL-receptor class A (LDLRA) domain proteins

amino acids 411-431, 152-171, 331-350 and 374-393

421/615

FIGURE 417

GTCTGTTCCCTTTGCTCTCTCGCGCCAGTCTCCTCCCTGTTTCTCCTCAGCCGCTGTGCGAGGAGAGCACCCGGA
GACGCGGGCTGCAGTCGCGCGGGCTTCTCCCGCCTGGGCGGCCTCGCCGCTGGGCAGGTGCTGAGCGCCCCTAG
AGCCTCCCTTGCCCGCTCCTCCTCTGCCCCGCCGAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCG
GCCCCGGAGGCGCGGTGGATGCGGCGCTGGGCAGAAAGCAGCCGCCGATTCCAGCTGCCCCGCGCGCCCCGGGCG
CCCCTGCGAGTCCCCGGTTCAGCCATGGGGACCTCTCCGAGCAGCAGCACCGCCCTCGCCTCCTGCGCCGATC
GCCGCGCGAGCCACAGCCACGATGATCGCGGGCTCCCTTCTCCTGCTTGATTCCCTTAGCACCACCACAGCTCAG
CCAGAACAGAAGGCCTCGAATCTCATTTGGCACATACCGCCATGTTGACCGTGCCACCGGCCAGGTGCTAACCTGT
GACAAGTGTCCAGCAGGAACCTATGTCTCTGAGCATTGTACCAACACAAGCCTGCGCGTCTGCAGCAGTTGCCCT
GTGGGGACCTTTACCAGGCATGAGAATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCCATGGCCAATG
ATTGAGAAATTACCTTGTGCTGCCTTGACTGACCGAGAATGCATTTGCCACCTGGCATGTTCCAGTCTAACGCT
ACCTGTGCCCCCATACGGTGTGTCTTGTGGGTGGGGTGTGCGGAAGAAAGGGACAGAGACTGAGGATGTGCGG
TGTAAGCAGTGTGCTCGGGGTACCTTCTCAGATGTGCCTTCTAGTGTGATGAAATGCAAAGCATACACAGACTGT
CTGAGTCAGAACCTGGTGGTGTGATCAAGCCGGGGACCAAGGAGACAGACAACGCTCTGTGGCACACTCCCGTCTTC
TCCAGCTCCACCTCACCTTCCCCTGGCACAGCCATCTTTCACGCCCTGAGCACATGGAAACCCATGAAGTCCCT
TCCTCCACTTATGTTCCCAAAGGCATGAATCAACAGAATCCAACCTCTTCTGCCTCTGTTAGACCAAAGGTACTG
AGTAGCATCCAGGAAGGGACAGTCCCTGACAACACAAGCTCAGCAAGGGGGAAGGAAGACGTGAACAAGACCCTC
CCAAACCTTCAGGTAGTCAACCACGCAAGGCCCCACCAACAGACACATCCTGAAGCTGCTGCCGTCCATGGAG
GCCACTGGGGGCGAGAAGTCCAGCACGCCCATCAAGGGCCCCAAGAGGGGACATCCTAGACAGAACCTACACAAG
CATTTTGACATCAATGAGCATTGTCCTGGATGATTGTGCTTTTCTGCTGCTGGTGTGTTGTGGTATTGTGGTG
TGCAATATCCGGAAGGCTCGAGGACTCTGAAAAAGGGGCCCGGCGAGGATCCAGTGCCATTGTGGAAGGCA
GGGCTGAAGAAATCCATGACTCCAACCCAGAACCAGGAGAAATGGATCTACTACTGCAATGGCCATGGTATCGAT
ATCCTGAAGCTTGTAGCAGCCCAAGTGGGAAGCCAGTGGAAAGATATCTATCAGTTTCTTTGCAATGCCAGTGAG
AGGGAGGTTGCTGCTTTCTCCAATGGGTACACAGCCGACCACGAGCGGGCCTACGCAGCTCTGCAGCACTGGACC
ATCCGGGGCCCCGAGGCCAGCCTCGCCAGCTAATTAGCGCCTGCGCCAGCACCGGAGAAACGATGTTGTGGAG
AAGATTCTGTTGGGCTGATGGAAGACACCACCGAGCTGGAACCTGACAACTAGCTCTCCCGATGAGCCCCAGCCCG
CTTAGCCCCGAGCCCCATCCCCAGCCCCAACGCGAACTTGAAGATTCCGCTCTCCTGACGGTGGAGCCTTCCCCA
CAGGACAAGAACAAGGGCTTCTTCTGATGAGTGGAGCCCTTCTCCGCTGTGACTCTACATCCAGCGGCTCC
TCCGCGCTGAGCAGGAACGGTTCTTTATTACCAAGAAAAGAAGGACACAGTGTGCGGCAGGTACGCCTGGAC
CCCTGTGACTTGCAGCTATCTTTGATGACATGCTCCACTTTCTAAATCCTGAGGAGCTGCGGGTATTGAAGAG
ATTCCCCAGGCTGAGGACAAACTAGACCGGCTATTGCAATTTATTGGAGTCAAGAGCCAGGAAGCCAGCCAGACC
CTCCTGGACTCTGTTTATAGCCATCTTCTGACCTGCTGTAGAACATAGGGATACTGCATTCTGGAAATTACTCA
ATTTAGTGGCAGGTGTTTTTTTAAATTTCTTCTGTTTCTGATTTTTGTGTTTGGGGTGTGTGTGTGTTTGT
GT
TCTCTCTCTTTTTTTTTTAAATAACTCTTCTGGGAAGTTGGTTTATAAGCCTTTGCCAGGTGTAAGTGTGTGAA
ATACCCACCACTAAAGTTTTTTTAAAGTTCCATATTTTCTCCATTTTGCTTCTTATGTATTTTCAAGATTATTCTG
TGCACTTTAAATTTACTTAACTTACCATAAATGCAGTGTGACTTTTCCACACACTGGATTGTGAGGCTCTTAAC
TTCTTAAAGTATAATGGCATCTTGTGAATCCTATAAGCAGTCTTATGTCTCTTAACATTACACCTACTTTTT
AAAAACAAATATTATTACTATTTTTATTATTGTTTGTCTTTTATAAATTTCTTAAAGATTAAGAAAATTTAAGA
CCCCATTGAGTTACTGTAATGCAATTCAACTTTGAGTTATCTTTTAAATATGTCTTGTATAGTTCAATTTATGG
CTGAAACTTGACCACACTATTGCTGATTGTATGGTTTTTCACTGGACACCGTGTAAGATGCTTATTACTTGTAC
TCTTCTTATGCTAATATGCTCTGGGCTGGAGAAATGAAATCCTCAAGCCATCAGGATTTGCTATTTAAGTGGCTT
GACAACCTGGGCCACCAAGAACTTGAACCTTCACTTTTAGGATTTGAGCTGTTCTGGAACACATTGCTGCACCTT
GGAAAGTCAAAATCAAGTGCCAGTGGCGCCCTTTCCATAGAGAATTTGCCAGCTTTGCTTTAAAGATGTCTTG
TTTTTTATATACATAATCAATAGGTCCAATCTGCTCTCAAGGCCCTGGTCTGGTGGGATTCCTTACCAATT
ACTTTAATTAATAATGCTGCAACTGTAAGAACCCTTGTCTGATATATTTGCAACTATGCTCCCATTTACAAATG
TACCTTCTAATGCTCAGTTGCCAGGTTCCAATGCAAAGGTGGCGTGGACTCCCTTTGTGTGGGTGGGGTTGTGG
GTAGTGGTGAAGGACCGATATCAGAAAAATGCCTTCAAGTGTACTAATTTATTAATAAACATTAGGTGTTTGTTA
AAAAAAA

422/615

FIGURE 418

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52594
><subunit 1 of 1, 655 aa, 1 stop
><MW: 71845, pI: 8.22, NX(S/T): 8
MGTSPPSSSTALASCSRIARRATATMIAGSLLLLGFLSTTTAQPEQKASNLIQTYRHVDRATGQ
VLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTRHENGIEKCHDCSQPCPWPMIEKLPCAAL
TDRECTCPPGMFQSNATCAPHTVCPVGWGVRRKGTETEDVRCKQCARGTFSDVPSSVMKCKAY
TDCLSQNLVVIKPGTKETDNVCGTLPSSFSSSTSPSPGTAIFPRPEHMETHEVPSSTYVPKGMN
STESNSSASVRPKVLSSIQEGTVPDNTSSARGKEDVNKTLNQLQVNVHQQGPVHRLKLLPS
MEATGGEKSSTPIKGPGRGHPRQNLHKKHFDINEHLPWMIVLFLLLVLVVIVVCSIRKSSRTLK
KGPRQDPSAIVEKAGLKKSMPTQNRKWIYYCNGHGIDILKLVAQVGSQWKDIYQFLCNAS
EREVAAFSNGYTADHERAYAALQHWITIRGPEASLAQLISALRQHRNDVVEKIRGLMEDTTQL
ETDKLALPMSPLSPSPIPSPNAKLENSALLTVEPSPQDKNKGFFVDESEPLLRCSTSSGS
SALSRNGSFITKEKKDTVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQAEDKLDRLFE
IIGVKSQEASQTLTLLDSVYSHLPDLL
```

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 350-370

423/615

FIGURE 419

ATGGCTGGTGACGGCGGGGCCGGGCAGGGGACCGGGCCGCGGCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGA
ATCACCGCCTGGCCCGACTCCACCATGAACGTCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAG
AAGGGGACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTACTGCTGGCT
GCACTGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCATCCCACAGCACCTGCCTTACA
GAGGCCTGCATTGAGTGGCTGGAAAAATCCTGGAGTCCCTGGACCGAGGGGTGAGCCCCTGTGAGGACTTTTAC
CAGTTCTCCTGTGGGGGCTGGATTTCGGAGGAACCCCTGCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGC
CTCTGGGACCAAAACCAGGCCATACTGAAGCACCTGCTTGAAAACACCACCTTCAACTCCAGCAGTGAAGCTGAG
CAGAAGACACAGCGCTTCTACCTATCTTGCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCCAGCCACTGAGA
GACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAGGACAACCTTTATGGAGGTGTTGAAG
GCAGTAGCAGGGACCTACAGGGCCACCCATTCTTCACCGTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGC
AATGTTATCCAGGTGGACCACTGCTGGGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACCTGCCAATGAG
AAAGTGCTCACTGCCTATCTGGATTACATGGAGGAACCTGGGGATGCTGCTGGGTGGGCGGCCACCTCCACGAGG
GAGCAGATGCAGCAGGTGCTGGAGTTGGAGATACAGCTGGCCAACATCACAGTGCCCCAGGACCAGCGCGCGAC
GAGGAGAAGATCTACCACAAGATGAGCATTTCGGAGCTGCAGGCTCTGGCGCCCTCCATGGACTGGCTTGAGTTC
CTGTCTTTCTTGTCTGTCACCATTTGAGTTGAGTGACTCTGAGCCTGTGGTGGTGTATGGGATGGATTATTTGCAG
CAGGTGTCAGAGCTCATCAACCGCACGGAACCAAGCATCCTGAACAATTACCTGATCTGGAACCTGGTGCAAAAG
ACAACCTCAAGCCTGGACCGACGCTTTGAGTCTGCACAAGAGAAGCTGCTGGAGACCCTCTATGGCACTAAGAAG
TCCTGTGTGCCGAGGTGGCAGACCTGCATCTCCAACACGGATGACGCCCTTGGCTTTGCTTTGGGGTCACTCTTC
GTGAAGGCCACGTTTGACCGGCAAAGCAAAGAAATTGCAGAGGGGATGATCAGCGAAATCCGGACCGCATTTGAG
GAGGCCCTGGGACAGCTGGTTTGGATGGATGAGAAGACCCGCCAGGCAGCCAAGGAGAAAGCAGATGCCATCTAT
GATATGATTGGTTTCCCAGACTTTATCCTGGAGCCCAAAGAGCTGGATGATGTTTATGACGGGTACGAAATTTCT
GAAGATTCTTTCTTCCAAAACATGTTGAATTTGTACAACTTCTCTGCCAAGGTTATGGCTGACCAGCTCCGCAAG
CCTCCCAGCCGAGACCAGTGGAGCATGACCCCCAGACAGTGAATGCCTACTACCTTCCAAC TAAGAATGAGATC
GTCTTCCCCGCTGGCATCCTGCAGGCCCTTCTATGCCCGCAACCACCCCAAGGCCCTGAACCTCGGTGGCATC
GGTGTGGTCTATGGGCCATGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACCTG
CGGCCCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACCAACAGGCCTGCATGGAGGAACAGTACAATCAA
TACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACATTACTGACAACGGGGGGCTGAAG
GCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATGGGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACC
AACCACCAGCTCTTCTCGTGGGATTTGCCAGGTGTGGTGCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGG
CTGGTGACCGACCCCAAGCCCTGCCCGCTTCCGCGTGCTGGGCACTCTCTCCAACCTCCCGTGACTTCCTGCGG
CACTTCGGCTGCCCTGTGCGCTCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACCTGGATCAGGGGA
GAAATGGCCAGCTGTACACAGACCTGGGGCAGCTCTCTGACAAAGCTGTTTGCTCTTGGGTTGGGAGGAAGCAA
ATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCCACAGGTGACATGAGTACAGACCCTCCTCAATCACCACATTG
TGCTCTGCTTTGGGGTGCCCTGCCTCCAGCAGAGCCCCACCATTCACTGTGACATCTTTCCTGTACCCCT
GCCTGGAAGAGGTCTGGGTGGGGAGGCCAGTTCCCATAGGAAGGAGTCTGCC

424/615

FIGURE 420

MNVALQELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSHS
TCLTEACIRVAGKILESIDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQAIL
KHLLENTTFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLEKIGGWNITGPWDQDNFME
VLKAVAGTYRATPFFTUVYISADSKSSNSNVIQVDQSGLEFLPSRDYYLNRTANEKVLTA YLDYM
EELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRRDEEKIYHKMSISELQALAPSMDWL
EFLSFLLSPLELSDSEPVVVYGMDYLQQVSELINRTEPSILNNYLIWNLVQKTTSSLD RRFES
AQEKLLETLYGTTKSCVPRWQTCISNTDDALGFALGSLFVKATFDRQSKEIAEGMISEIRTAF
EEALGQLVWMDEKTRQAAKEKADAIYDMIGFPDFILEPKELDDVYDGYEISEDSFFQNMLNLY
NFSAKVMADQLRKPPSRDQWSMTPQTVNAYYLPKNEIVFPAGILQAPFYARNHPKALNFGGI
GVVMGHELTHAFDDQGREYDKEGNLRPWWQNESLA AFRNHTACMEEQYNQYQVNGERLNGRQT
LGENITDNGGLKAAYNAYKAWLRKHGEEQQLPAVGLTNHQLFFVGFAQVWCSVRTPESSHEGL
VTDPHSPARFRVLGTLSNSRDFLRHFGCPVGS PMNPGQLCEVW

Type II Transmembrane domain:
amino acids 32-57

425/615

FIGURE 421

GGCGCCGCGTAGGCCCGGGAGGCCGGGCGGCGGGCTGCGAGCGCCTGCCCCATGCGCCGCC
GCCTCTCCGCACG**ATG**TTCCCCTCGCGGAGGAAAGCGGCGCAGCTGCCCTGGGAGGACGGCAG
GTCCGGGTTGCTCTCCGGCGGCCTCCCTCGGAAGTGTTCCGTCTTCCACCTGTTTCGTGGCCTG
CCTCTCGCTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGGCCCCG
GGCAGTCAGGGGACAAGGGCAGGAGACCTCGGGCCCTCCCCGTGCCTGCCCCCAGAGCCGCC
CCCTGAGCACTGGGAAGAAGACGCATCCTGGGGCCCCCACCCTGGCAGTGCTGGTGGCCTT
CCGCGAACGCTTCGAGGAGCTCCTGGTCTTCGTGCCCCACATGCGCCGCTTCTGAGCAGGAA
GAAGATCCGGCACCACATCTACGTGCTCAACCAGGTGGACCACTTCAGGTTCAACCGGGCAGC
GCTCATCAACGTGGGCTTCTGGAGAGCAGCAACAGCACGGACTACATTGCCATGCACGACGT
TGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTTCTGAGGCTGGGCCCTTCCACGT
GGCCTCCCCGGAGCTCCACCCTCTCTACCACTACAAGACCTATGTCGGCGGCATCCTGCTGCT
CTCCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTTCTGGGGCTGGGGCCGCGA
GGACGACGAGTTCTACCGGCGCATTAAGGGAGCTGGGCTCCAGCTTTTCCGCCCTCGGGAAT
CACAACCTGGGTACAAGACATTTCCGCCACCTGCATGACCCAGCCTGGCGGAAGAGGGACCAGAA
GCGCATCGCAGCTCAAAAACAGGAGCAGTTCAAGGTGGACAGGGAGGGAGGCCTGAACACTGT
GAAGTACCATGTGGCTTCCCGCACTGCCCTGTCTGTGGGCGGGGCCCCCTGCACTGTCCTCAA
CATCATGTTGGACTGTGACAAGACCGCCACACCCTGGTGCACATTCAGCT**TGA**GCTGGATGGAC
AGTGAGGAAGCCTGTACCTACAGGCCATATTGCTCAGGCTCAGGACAAGGCCTCAGGTCGTGG
GCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCAAGCTACGCAATTGCAGCCA
CCCGGCCGCCAAGGCAGGCTTGGGCTGGGCCAGGACACGTGGGGTGCCTGGGACGCTGCTTGC
CATGCACAGTGATCAGAGAGAGGCTGGGGTGTGTCCTGTCCGGGACCCCCCTGCCTTCTGC
TCACCCTACTCTGACCTCCTTCACGTGCCCAGGCCTGTGGGTAGTGGGGAGGGCTGAACAGGA
CAACCTCTCATACCCTACTCTGACCTCCTTCACGTGCCCAGGCCTGTGGGTAGTGGGGAGGG
CTGAACAGGACAACCTCTCATCACCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAA

426/615

FIGURE 422

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56531
><subunit 1 of 1, 327 aa, 1 stop
><MW: 37406, pI: 9.30, NX(S/T): 1
MFPSRRKAAQLPWEDGRSGLLSGGLPRKCSVFHLFVACLSSLGFFSLLWLQLSCSGDVARAVRG
QGQETSGPPRACPPPEPPPEHWEEDASWGPHRLAVLVPPFRERFEELLVFVPHMRRFLSRKKIRH
HIYVLNQVDHFRFNRAALINVGFLSSNSTDYIAMHDVDLLPLNEELDYGFPFAGPFHVASPE
LHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDDFYRRIKGAGLQLFRPSGITTY
KTFRHLHDPAWRKRDQKRIAAQKQEQFKVDREGGLNTVKYHVASRTALSVGGAPCTVLNIMLD
CDKTATPWCTFS

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 29-49 (type II)

N-glycosylation site.

amino acids 154-158

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 27-31

Tyrosine kinase phosphorylation site.

amino acids 226-233

N-myristoylation site.

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

427/615

FIGURE 423

CCATCCCTGAGATCTTTTTATAAAAAACCCAGTCTTTGCTGACCAGACAAAGCATACCAGATC
TCACCAGAGAGTCGCAGACACT**ATG**CTGCCTCCCATGGCCCTGCCAGTGTGTCCTGGATGCT
GCTTTCCCTGCCTCATTCTCCTGTGTCAGGTTCAAGGTGAAGAAACCCAGAAGGAAGTGCCTC
TCCACGGATCAGCTGTCCCAAAGGCTCCAAGGCCTATGGCTCCCCCTGCTATGCCTTGTTTTT
GTCACCAAAATCCTGGATGGATGCAGATCTGGCTTGCCAGAAGCGGCCCTCTGGAAACTGGT
GTCTGTGCTCAGTGGGGCTGAGGGATCCTTCGTGTCCTCCCTGGTGAGGAGCATTAGTAACAG
CTACTCATACTCTGGATTGGGCTCCATGACCCACACAGGGCTCTGAGCCTGATGGAGATGG
ATGGGAGTGGAGTAGCACTGATGTGATGAATTACTTTGCATGGGAGAAAAATCCCTCCACCAT
CTTAAACCCCTGGCCACTGTGGGAGCCTGTCAAGAAGCACAGGATTTCTGAAGTGGAAAGATTA
TAACTGTGATGCAAAGTTACCCTATGTCTGCAAGTTCAAGGACT**TAG**GGCAGGTGGGAAGTCAG
CAGCCTCAGCTTGGCGTGCAGCTCATCATGGACATGAGACCAGTGTGAAGACTCACCCTGGAA
GAGAATATTCTCCCCAACTGCCCTACCTGACTACCTTGTCATGATCCTCCTTCTTTTTCCTT
TTTCTTCACCTTCATTTTCAGGCTTTTCTCTGTCTTCCATGTCTTGAGATCTCAGAGAATAATA
ATAAAAATGTTACTTTATAAAAAAAAAAAAAAAAAAAAAA

428/615

FIGURE 424

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56965

<subunit 1 of 1, 175 aa, 1 stop

<MW: 19330, pI: 7.25, NX(S/T): 1

MLPPMALPSVSWMLLSCLILLCQVQGEETQKELPSPRISCPKGSKAYGSPCYALFLSPKSWMD

ADLACQKRPSGKLVSVLSGAEGSFVSSLVRSISNSYSYIWIGLHDPTQGSEPDGDGWEWSSTD

VMNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNCDAKLPYVCKEKD

Important features:**Signal peptide:**

amino acids 1-26

C-type lectin domain signature.

amino acids 146-171

429/615

FIGURE 425

CGGACGCGTGGGCGGCCACCTCCGGAACAAGCC**ATG**GTGGCGGCGACGGTGGCAGCGGCGTGG
CTGCTCCTGTGGGCTGCGGCCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGGCGGTC
AACATCCGGGGCAAAC TGGTGTGCTGCTGGAGAAGTACCGCGGATCGGTGTCCCTGGTGGTGAAT
GTGGCCAGCGAGTGCGGCTTACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCGAGAC
CTGGGCCCCCACCACCTTTAACGTGCTCGCCTTCCCCTGCAACCAGTTTGGCCAACAGGAGCCT
GACAGCAACAAGGAGATTGAGAGCTTTGCCCCGCCGACCTACAGTGTCTCATTTCCCATGTTT
AGCAAGATTGCAGTCACCGGTACTGGTGCCCATCCTGCCTTCAAGTACCTGGCCCAGACTTCT
GGGAAGGAGCCCACCTGGAACCTTCTGGAAGTACCTAGTAGCCCCAGATGGAAAGGTGGTAGGG
GCTTGGGACCCAAC TGTGTCAGTGGAGGAGGTCAGACCCCAGATCACAGCGCTCGTGAGGAAG
CTCATCCTACTGAAGCGAGAAGACTT**ATA**ACCACCGCTCTCCTCCTCCACCACCTCATCCCG
CCCACCTGTGTGGGGCTGACCAATGCAAAC TCAAATGGTGCTTCAAAGGGAGAGACCCACTGA
CTCTCCTTCCTTTACTCTTATGCCATTGGTCCCATCATTCTTGTGGGGGAAAAATTCTAGTAT
TTTGATTATTTGAATCTTACAGCAACAAATAGGAACTCCTGGCCAATGAGAGCTCTTGACCAG
TGAATCACCAGCCGATACGAACGTCTTGCCAACAAAAATGTGTGGCAAATAGAAGTATATCAA
GCAATAATCTCCACCCAAGGCTTCTGTAAACTGGGACCAATGATTACCTCATAGGGCTGTTG
TGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGCCAAATAGGAGGCATTC
AATGAACATTTTTTGCATATAAACCAAAAAATAACTTGTTATCAATAAAAACTTGCATCCAAC
ATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTAGTTGTTGTTATTTCTCTGTATTA
TTTTCTTCATTACAAAAGAAATGCAAGTTCATTGTAACAATCCAACAATACCTCACGATATA
AAATAAAAATGAAAGTATCCTCCTCAAAAA

430/615

FIGURE 426

MVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGKLVSLVKYRGSVSLVVNVASECGFTDQH
YRALQQLQRD LGPHHFNVLA FPCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTGAH
PAFKYLAQTS GKEPTWNFWKYL VAPDGKVVGAWDPTVSVEEVRPQITALVRKLILLKREDL

431/615

FIGURE 427

CAGTTCTGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCCATGGGGGTGGAGATTGCC
TTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCAGGTTGTTCTT
CTCCAGCCAGTTCCAACCTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGCTTT
GCCGGCCACTCATGAGAGTGTTTTTGTGTAAAGTATTTTTTAGAATACTGTTGACTTCTTCAT
GATTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCCTCAAATTT
TTGTTATACTAGATGGCTTCCATTTACCCACCACTATTTTAAGGTCCCTTTATTTTTAGGTTT
AAGGTTTCAATTTGACTTGAGAAAGTGCCCTTCTGCAGCTTCATTGATTTTGTATCTTCACTA
TTAATTGTAACGATTAAAAAAGAATAAGAGCACGCAGACCTCTAGGAGAATATTTTATCCCTG
GGTGCCCCTGACACATTTATGTAGTGATCCCAAAATGTGATTGTTAATTTAAATGTTATTCT
AATATTAGTACATTCAGTTGTGATGTAATATGAATAACCAGAATCTATTTCTTAAAGTTTTG
AGTATATTTTTCACTAGATATTTGTATAGAAAGACTGAATAGTGATG

432/615

FIGURE 428

MGVEIAFASVILTCLSLAAGVSQVLLQPVPQTQETGPKAMGDLSCGFAGHS

433/615

FIGURE 429

CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAAGGATAGAAGCTG
CACAGGGCAGCTTTACTTACTCCAGCACCTTCCTCTCCCAGGCAAATGGTGCTGACCATCTTT
GGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGGCAAT
G TTCAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGCAGGA
TCATGCTCTTCTACCACAATTTTTGACTATAAACATGGCTACATTGCATCCAGGGTGCTCTCC
CGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAATCTCCAA
TGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTGGGTCAAG
TACAACCCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCCTGCTTGGGTCACCCATTGAG
AAACTCTGCAAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAACACACATAATGTCGGT
GCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTGTGCAGACATT
CATGTTTTAGGATGATTAGCCCTCTTGTTTTATCTTTTCAAAGAAATACATCCTTGGTTTACAC
TCAAAGTCAAATTAAATTCTTCCCAATGCCCCAACTAATTTTGAGATTGAGTCAGAAAATA
TAAATGCTGTATTTATA

434/615

FIGURE 430

><ss.DNA57834
><subunit 1 of 1, 176 aa, 1 stop
><MW: 19616, pI: 7.11, NX(S/T): 0
MVLTIIFGIQSHGYEVFNIIISPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSSTTIFDYKH
GYIASRVLSRRACFILKMDHQNIPLNQLQWYIYEKQALDNMFSNKYTWVKYNPLESLIK
DVDWFLLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV

Important features:**Signal peptide:**

Amino acids 1-26

N-myristoylation sites:

Amino acids 48-54;153-159;156-162;167-173

435/615

FIGURE 431

GCGTGGGGATGTCTAGGAGCTCGAAGGTGGTGTCTGGGCCTCTCGGTGCTGCTGACGGCGGCCA
CAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTATCA
GAGACATTGAGAGGCAAATTCGGAAGGAGAGAGAGAGATGTTATTGGCAAAGGATCTCAAAAATCAT
TGACTGAGCAACTTGAAGCAGAAAGAGAGAGATGTTATTGGCAAAGGATCTCAAAAATCAT
GACTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGTTGATGGAGA
GTAGCTTAGTAGTATCTTCATCTTTTTTTTTTGGTCACTGTCCTTTTAAACTTGATCAAATAAA
GGACAGTGGGTCATATAAGTTACTGCTTTCAGGGTCCCTTATATCTGAATAAAGGAGTGTGGG
CAGACACTTTTTGGAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGGTCACTGTC
CAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGATGGATAGTA
GCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACATCGACCTCAG
AAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCGAATCC

436/615

FIGURE 432

MSRSSKVLGLSVLLTAATVAGVHVKKQQWDQQLRDGVIRDIERQIRKKENIRLLGEQIILTE
QLEAEREKMLLAKGSQKS

437/615

FIGURE 433

GAATTCGTGTCTCGGCACTCACTCCCGGCCGCCCGGACAGGGAGCTTTCGCTGGCGCGCTTGGCCGGCGACAGGA
CAGGTTTCGGGACGTCCATCTGTCCATCCGTCCGGAGAGAAATTACAGATCCGCAGCCCCGGGATGGGGCCGGCCC
CGCTGCCGCTGCTGCTGGGCTCTTCTCCCCGCGCTCTGGCGTAGAGCTATCACTGAGGCAAGGGAAGAAGCCA
AGCCTTACCCGCTATTCCCGGGACCTTTTCCAGGGAGCCTGCAAACTGACCACACACCGCTGTTATCCCTTCCCTC
ACGCCAGTGGGTACCAAGCCTGCCTTGATGTTTTTACCACCCAGCCTGGAAGACCACATACAGGAAACGTAGCCATT
CCCCAGGTGACCTCTGTGCAATCAAAGCCCCTACCGCTCTTGCCTTCAAACACACAGTTGGACACATAATACTT
TCTGAACATAAAGGTGTCAAATTTAATTGCTCAATCAATGTACCTAATATATACCAGGACACCACAATTTCTTGG
TGGAAAGATGGGAAGGAATTGCTTGGGGGACATCATCGAATTACACAGTTTATCCAGATGATGAAGTTACAGCA
ATAATCGCTTCCCTCAGCATAACCAGTGTGCAGCGTTTACAGACAATGGGTGCTATATCTGTAAGATGAAAATAAAC
AATGAAGAGATCGTGTCTGATCCCATCTACATCGAAGTACAAGGACTTCCTCACTTTACTAAGCAGCCTGAGAGC
ATGAATGTCAACAGAAACACAGCCTTCAACCTCACCTGTGAGGCTGTGGGCCCGCTGAGCCCGTCAACATTTTC
TGGGTTCAAACAGTAGCCGTGTTAACGAACAGCCTGAAAAATCCCCGCGCTGCTAACTGTTCCAGGCCTGACG
GAGATGGCGGTCTTCAGTTGTGAGGCCCCAATGACAAAGGGCTGACCGTGTCCAGGGAGTGCAGATCAACATC
AAAGCAATTCCTCCCCACCACTGAAGTCAGCATCCGTAACAGCACTGCACACAGCATTCTGATCTCCTGGGTT
CCTGTTTTTGTGATGATCTCCCGTTTCAGGAATTGACAGATTGAGGTTCAAGGTAAGCTGATCCGCTGGGTAATGCA
TCAGTCATGATTTTAAACACCTCTGCCTTACCACATCTGTACCAAAATCAAGCAGCTGCAAGCCCTGGCTAATTAC
AGCATTGGTGTCTTCTGCATGAATGAAATAGGCTGGTCTGCAGTGAGCCCTTGGATTCTAGCAAGCAGACTGAA
GGAGCCCCATCAGTAGCACCTTTAATGTCACTGTGTTTCTGAATGAATCTAGTGATAATGTGGACATCAGATGG
ATGAAGCCTCCGACTAAGCAGCAGGATGGAGAAGTGGTGGGCTACCGGATATCCACGTGTGGCAGAGTGCAGGG
ATTTCCAAAGAGCTCTTGAGGAAGTTGGCCAGAATGGCAGCCGAGCTCGGATCTCTGTTCAAGTCCACAATGCT
ACGTGCACAGTGAGGATTGACAGCCGTCAACAGAGGGGAGTTGGGCCCTTCAGTGATCCAGTGAATAATTTATC
CCTGCACACGGTTGGGTAGATTATGCCCCCTCTTCAACTCCGGCGCTGGCAACGCAGATCCTGTGCTCATCATC
TTTGCTGTCTTTTGTGATTTATTTTGTGTTGGGTTGATTTTATACATCTCCTTGGCCATCAGAAAAAGAGTCCAG
GAGACAAAGTTTGGGAATGCATTACAGAGGAGGATCTGAATTAGTGGTGAATTATATAGCAAAAGAAATCCTTC
TGTCGGCGAGCCATTGAACTTACCTTACATAGCTTGGGAGTCAGTGAGGAACACAAAATAAAGTGAAGATGTT
GTGATTGACAGGAATCTTCTAATTCTTGGAAAAATCTGGGTGAAGGAGAGTTTGGGTCTGTAATGGAAGGAAT
CTTAAGCAGGAAGATGGGACCTCTCTGAAAGTGGCAGTGAAGACCATGAAGTTGGACAACCTTTCACATCGGGAG
ATCGAGGAGTTTCTCAGTGAGGCAGCGTGCATGAAAGACTTCAGCCACCCAAATGTCAATTCGACTTCTAGGTGTG
TGATAGAAATGAGCTCTCAAGGCATCCCAAAGCCCATGGTAATTTTACCCTTCATGAAATACGGGGACCTGCAT
ACTTACTTACTTTTATCCCGATTGGAGACAGGACCAAGCATATTCTCTGCAGACACTATTGAAGTTCATGGTG
GATATTGCCCTGGGAATGGAGTATCTGAGCAACAGGAATTTTCTTCATCGAGATTTAGCTGCTCGAACTGCATG
TTGCGAGATGACATGACTGTCTGTGTGCGGACTTCGGCTCTCTAAGAAGATTTACAGTGGCGATTATTACCGC
CAAGGCCGCTTGTCTAAGATGCCTGTAAATGGATCGCCATAGAAAGTCTTGACAGCCGAGTCTACACAAGTAAA
AGTGATGTGTGGGCATTTGGCGTGACCATGTGGGAAATACGTACGCGGGGAATGACTCCCTATCCTGGGGTCCAG
AACCATGAGATGTATGACTATCTTCTCCATGGCCACAGGTTGAAGCAGCCCGAAGACTGCCTGGATGAACTGTAT
GAAATAATGTACTCTTGTGAGAAACCGATCCCTTAGACCGCCCCACCTTTTCAGTATTGAGGCTGCAGCTAGAA
AACTCTTAGAAAGTTTGCCTGACGTTCCGAACCAAGCAGACGTTATTTACGTCAATACACAGTTGCTGGAGAGC
TCTGAGGGCCTGGCCAGGGCCCCACCTTGCTCCACTGGACTTGAACATCGACCCTGACTCTATAATTGCCTCC
TGCACTCCCCGCGCTGCCATCAGTGTGGTCAACAGCAGAGTTTATGACAGCAAACCTCATGAAGGACGGTACATC
CTGAATGGGGGAGTGAGGAATGGGAAGATCTGACTTCTGCCCCCTCTGCTGCAGTCACAGCTGAAAAGAACAGT
GTTTTACCAGGGGAGAGACTTGTAGGAATGGGGTCTCCTGGTCCCATTCGAGCATGCTGCCCTTGGGAAGCTCA
TTGCCGATGAACTTTGTGTTGCTGACGACTCCTCAGAAGGCTCAGAAGTCTGATGTGAGGAGAGGTGCGGGGA
GACATTCAAAAATCAAGCCAATTCTTCTGCTGTAGGAGAATCCAATTGTACCTGATGTTTTTGGTATTTGTCTT
CCTTACCAAGTGAATCCATGGCCCCAAAGCACCAGATGAATGTTGTTAAGGAAGCTGTCAATAAAAATACATAA
TATATATTTATTTAAAGAGAAAAATATGTATATCATGAAAAAGACAAGGATATTTTAAATAAACATTACTTA
TTTCATTTCACTTATCTTGCATATCTTAAATTAAGCTTCAGCTGCTCCTTGATATTAACCTTTGTACAGAGTTG
AAGTTGTTTTTCAACTTCTTTTCTTTTTCATTACTATTAATGTAATAATATTTGTAATAATGAAATGCCATATT
TGACTTGGCTTCTGGTCTTGATGTATTTGATAAGAATGATTAATTTTCTGATATGGCTTCATAATAAATGAA
ATAGGA

438/615

FIGURE 434

MGPAPLPILLGLFLPALWRRRAITEAREEAKPYPLFPFPFPGSLQTDHTPLLSLPHASGYQPALMFSPQGRPH
GNVAIPQVTSVESKPLPPLAFKHTVGHIIILSEHKGVKFNC SINVPNIYQD TTISWWDGKELLGGHHRITQFY
PDDEVTAIIASF SITSVQRSDNGSYICKMKINNEEIVSDPIYIEVQGLPHFTKQPESMNVTNRNTAFNLTCQAVGP
PEPVNIFWVQNSSRVNEQPEKSPGVLTVPGLTEMAVFSCEAHNDKGLTVSQGVQINIKAI PPSPTTEVSIRNSTA
HSI LISWVPFGFDGYSPFRNCSIQVKEADPLNGSVMIFNTSALPHLYQIKQLQALANYSIGVSCMNEIGWSA
VSPWILASTTEGAPSVAPLNVTVFLNESSDNVDIRWMKPPTKQDGLVGYRISHVWQSAGISKELLEEVGQNGS
RARISVQVHNATCTVRIA AAVTRGGVGPFS DPVKIFIPAHGWVDYAPSSTPAPGNADPVLIIFGCFCGFI
LIGLILYISLAI RKRVTQETKFGNAFTEEDSELVNYIAKKSFCRRAIETLHSLGVSEELQNKLEDVVIDR
NLLILGKILGEGEFGS VMEGNLKQEDGTS LKVA VKTMKLDNSSHREIEEFLSEACMKDFSHPNVIRLLGVC
IEMSSQGI PKPMVILPFMK YGDLHTYLLYSRLETGPKHIPLQTLKFMDIALGMEYLSNRNFLHRDLAAR
NCMLRDDMTVCVADFGLSKKIYS GDYYRQGRIAKMPVKWIAIESLADRVYTSKSDVWAFGVTMWEIR
TRGMTPTYPGVQNHMYDYLLHGHRLKQPEDC LDELYEIMYSCWRTDPLDRPTFSVLRQLQLEKLES
LPDVRNQADVIVNTQLLESSEGLAQGP TLAPLDLNDIPD SIIASCTPRAAISVVTAEVHDSKPHEGRYI
LNGGSEEWEDLTSA PSAAVTAEKNSVLPGERLVRNGVSWSHSSML PLGSSLPDELLFADDSSEGSEVLM

Signal sequence:	Amino acids 1-18
Transmembrane domain:	Amino acids 501-520
N-glycosylation sites:	Amino acids 114-118;170-174;207-211; 215-219;234-238;294-298;316-320;329-333; 336-340;354-358;389-393;395-399;442-446; 454-458;625-629
Tyrosine kinase phosphorylation sites:	Amino acids 675-683;865-873;923-930
N-myristoylation sites:	Amino acids 41-47;110-116;171-177; 269-275;275-281;440-446;507-513;535-541; 966-972
Prokaryotic membrane lipoprotein lipid attachment site:	Amino acids 351-362
Tyrosine protein kinases specific active-site signature:	Amino acids 719-732

439/615

FIGURE 435

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTTAGCACCAGTACTGGATG
TGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTAGTGTCCGATTCTGATTCCGGCAAGGAT
CCAAGCATGGAATGCTGCCGTCGGGCAACTCCTGGCACACTGCTCCTCTTTCTGGCTTTCCTG
CTCCTGAGTTCCAGGACCGCACGCTCCGAGGAGGACCGGGACGGCCTATGGGATGCCTGGGGC
CCATGGAGTGAATGCTCACGCACCTGCGGGGAGGGGCCTCCTACTCTCTGAGGCGCTGCCTG
AGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGACTGCCCCA
CCAGAAGCAGGTGATTTCCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCACCATGGC
CAGTTTTATGAATGGCTTCCTGTGTCTAATGACCCTGACAACCCATGTTCACTCAAGTGCCAA
GCCAAAGGAACAACCCTGGTTGTTGAACTAGCACCTAAGGTCTTAGATGGTACGCGTTGCTAT
ACAGAATCTTTGGATATGTGCATCAGTGGTTTATGCCAAATTGTTGGCTGCGATCACCAGCTG
GGAAGCACCGTCAAGGAAGATAACTGTGGGGTCTGCAACGGAGATGGGTCCACCTGCCGGCTG
GTCCGAGGGCAGTATAAATCCCAGCTCTCCGCAACCAAATCGGATGATACTGTGGTTGCACTT
CCCTATGGAAGTAGACATATTCGCCTTGTCTTAAAGGTCCTGATCACTTATATCTGGAAACC
AAAACCCCTCAGGGGACTAAAGGTGAAAACAGTCTCAGCTCCACAGGAACTTTCCTTGTGGAC
AATTCTAGTGTGGACTTCCAGAAATTTCCAGACAAAGAGATACTGAGAATGGCTGGACCACTC
ACAGCAGATTTCAATTGTCAAGATTCGTAACCTCGGGCTCCGCTGACAGTACAGTCCAGTTCATC
TTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTTCTTTCTTGCTCAGCAACCTGT
GGAGGAGGTTATCAGCTGACATCGGCTGAGTGCTACGATCTGAGGAGCAACCGTGTGGTTGCT
GACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACCCAAGCTTCAGGAGTGCAAC
TTGGATCCTTGTCCAGCCAGTGACGGATACAAGCAGATCATGCCTTATGACCTCTACCATCCC
CTTCCTCGGTGGGAGGCCACCCCATGGACCGCGTGCTCCTCCTCGTGTGGGGGGGCATCCAG
AGCCGGGCAGTTTTCCTGTGTGGAGGAGGACATCCAGGGGCATGTCACTTCAGTGAAGAGTGG
AAATGCATGTACACCCCTAAGATGCCCATCGCGCAGCCCTGCAACATTTTTGACTGCCCTAAA
TGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGTGGCCAGGGCCTCAGATACCGTGTG
GTCCTCTGCATCGACCATCGAGGAATGCACACAGGAGGCTGTAGCCCCAAAACAAAGCCCCAC
ATAAAAGAGGAATGCATCGTACCCACTCCCTGCTATAAAACCCAAAGAGAACTTCCAGTCGAG
GCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTAGAAGAAGGAGCTGCTGTGTCAGAGGAG
CCCTCGTAAAGTTGTAAAAGCACAGACTGTTCTATATTTGAACTGTTTTGTTTAAAGAAAGCA
GTGTCTCACTGGTTGTAGCTTTCATGGGTCTGAACTAAGTGTAATCATCTACCAAAGCTTT
TTGGCTCTCAAATTAAAGATTGATTAGTTTCAAAAAAAAAA

440/615

FIGURE 436

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847
<subunit 1 of 1, 525 aa, 1 stop
<MW: 58416, pI: 6.62, NX(S/T): 1
MECCRRATPGTLLLFLAFLLLSSRTARSEEDRDGLWDAWGPWSECSRTC GGGASYSLRRCLSS
KSCEGRNIRYRTCSNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPVSNDPDNPSLKCQAK
GTTLVVELAPKVLDGTRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNGDGSTCRLVR
GQYKSQLSATKSDDTVVALPYGSRHIRLVLGPDHLYLETKTLQGTKGENSLSSSTGTFLVDNS
SVDFQKFPDKEILRMAGPLTADFIVKIRNSGSADSTVQFIFYQPIIHRWRETDFFPSCATCGG
GYQLTSAECYDLRSNRVVADQYCHYYPENIKPKPKLQECNLDPCPASDGYKQIMPYDLYHPLP
RWEATPWTACSSSCGGGIQSRVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNIFDCPKWL
AQEWSPTVTCGQGLRYRVVLCIDHRGMHTGGCSPKTKPHIKEECIVPTPCYKPKEKLPVEAK
LPWFKQAQEELEGA AVSEEPS

Important features:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 251-254

Thrombospondin 1

amino acids 385-399

von Willebrand factor type C domain proteins

amino acids 385-399, 445-459 and 42-56

441/615

FIGURE 437

AACTGGAAGGAAAGAAAGAAAGGTCAGCTTTGGCCCAGATGTGGTTACCCCTTGGTCTCCTGT
CTTTATGTCTTTCTCCTCTTCCTATTCTGTCATCTCCCTCACTTAAGTCTCAGGCCTGTCAGC
AGCTCCTGTGGACATTGCCATCCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATGTTA
TGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCATCTGTGCTTCTGTGATC
TCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTTGAAATCTGGCATGAGATG
GCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCCTGCCCTATTCTCCTCCCAAGTCTGT
TCTCTTATTGTCAACCTCAGCACAAACAGGCTGGCGCCAATGGCATTACAGAGAAAGCAATCTG
TGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGTAGCCACCT
CCCTGTCAGCCAGTATTAACATGTCCCCTTCCCCCTGCCCCGCCGTAGATTCAGGACATTTCGC
CCCTGTGTGCCACCAAACCAGGACTTTCCCCTTGGCTTGGCATCCCTGGCTCTCTCCTGGTAC
CCAGCAAGACGTCTGTTCCAGGGCAGTGTAGCATCTTTCAAGCTCCGTTACTATGGCGATGGC
CATGATGTTACAATCCCCTTGCCTGAATAATCAAGTGGGAAGGGGAAGCAGAGGGAAATGGG
GCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCCTGAGGAAAAACCAAAGGGAAGCAACAGG
AACTTCTGCAACTGGTTTTTATCGGAAAGATCATCCTGCCTGCAGATGCTGTTGAAGGGGCAC
AAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGTAAGGAAATAGAACAGTCTGCT
GGGAGTCAGACCTGGAATTCTGATTCCAAACTCTTTATTACTTTGGGAAGTCACTCAGCCTCC
CCGTAGCCATCTCCAGGGTGACGGAACCCAGTGTATTACCTGCTGGAACCAAGGAAACTAACA
ATGTAGGTTACTAGTGAATACCCCAATGGTTTCTCCAATTATGCCCATGCCACCAAAACAATA
AAACAAAATTCTCTAACACTGAAA

442/615

FIGURE 438

MWLPLGLLSLCLSPILSSPSLKSQACQQLLWTLPSPLVAFRANRTTYVMDVSTNQGSMEH
RNHLCFCDLYDRATSPPLKCSLL

FIGURE 439

GTTTCATCATAGTTGGCGTCTTCTAAAGGAAAAACACTAAAATGAGGAACTCAGCGGACCGGGAGCGACGCAGCTT
 GAGGGAAGCATCCCTAGCTGTTGGCGCAGAGGGGCGAGGCTGAAGCCGAGTGGCCCCGAGGTTCTTGAGGGGCTGG
 CGCAAAGGTGAAAGAGTTTCAAGAACAGCTTCTCTGGAACCCCATGACCCATGAAGTCTTGTCGACATTTATACCGT
 GTGAGGTTAGCAGCTCGAAACTAGAAGAAGTGGAGTGTGCCAGGACGCGCATATCTCTTTGTGTGACCTTGGC
 GGCCTATGGGACGTTGGCTTCAGACCTTTGTGATACACCATGCTGCGTGGGACGATGACGGCGTGGAGAGGAATG
 AGGCTGTGAGGTCACACTGGCTTGGCTCCTCTAGCCACAGCAGGCTGCTTTTGTGACTTGAACGAGGTCCCTCAG
 GTCAACCTGCAGCCTGCGTCCACCTCCAGAGCCGAGGCACTGTGATCTTGGCTGCGTGGTGGAACTCCCA
 AGGATGAATGTAACTGGCGCTGAATGAAAGGAGCTGAATGGCTCGGATGATGCTCTGGGTGCTCTCATCCAC
 CACGGGACCCTCGTCATCACTGCCCTTAACAACCACATCTGGGACGGTACCAGTGTGTGGCCCGGATGCGCTGCG
 GGGGCTGTGGCCAGGCTGCCAGCTGTGACACTAGCCAACTCCAGGACTTCAAGTTAGATGTGCAGCAGCT
 ATTGAAGTGGATGAGGGAACACAGCAGCTCATTGCCTGCCACTGCTGAGAGCCACCCCAAAGCCAGGTCCG
 TACAGCGTCAAACAAGAGTGGCTGGAGGCTCCAGAGGTAACCTGATCATGCCCTCAGGGAACCTCCAGAT
 GTGAATGCCAGCGAGGAGACGAGGCGATGTACAAGTGTGCAGCCTACAACCCAGTGAACCGGAAGTGAAGAAAC
 FCCGGCTCAGCGCAGGCTACGTGTGCGCGCTCCACCGCTGAGGCTGCCCGATCATCTACCCCCAGAGGCC
 CAAACCATCATCGTCACCAAAGGCCAGAGTCTATTCTGGAGTGTGTGGCCAGTGAATCCCCACCCCAAGGTC
 ACCTGGGCCAAGGATGGTCCAGTGTACCGGCTACAACAAGACGCGCTTCTGCTGAGCAACCTCCTCATCGAC
 ACCACGAGCGAGGAGGACTCAGGCACCTACCGCTGATGCGCCGACAATGGGTTGGGACGCCGGGGCAGCGGTC
 ATCTCTCAATAGTCTCAGGTGTTTGAACCCCTGAGGTACCATGGAGCTATCCAGCTGGTCACTCCCTGGGGC
 CAGAGTGCCAAGCTTACCTGTGAGGTGCGTGGGAACCCCCCGCCCTCCGTGCTGTGGCTGAGGAATGCTGTGCC
 CTCATCTCAGCGCAGGCGCTCCGGCTCTCCCGCAGGGCCCTGCGCGTGCTCAGATGGGGCTGAGGACGAAGGC
 GTACTACCAGTGCATGGCCGAGAAGCAGGTTGGGAGCGCCCTAGCCGTAGTCCAGCTCGGGACCTCCAGGCCAAG
 ATAACCCCAAGGCTATGGCAGGATGCTGAGCTGGCTACTGGCACACCTCCTGTATACCTCCAACTCGGCAC
 CCTGAGCAGATGCTGAGGGGGCAACCGCGCTCCCGAGACCCCAACGTAGTGGGCGCTGCTTCCCGAAGTGT
 CCAGGAGAGAAGGGGACGGGGCTCCCGCGGAGGTCCTCATCTCAGCTCGCCCGCACCTCCAGACAGAC
 TCATGTAACTGTGTGGCGGCTCGGCATGAGGGCAGTGGCCGGGCGCAATCCTCTACTATGTGTGAAACAC
 CGCAAGCAGGTACAAATTCTCTGACGATTGGACCATCTCTGGCATTCAGCCAACAGCACCGGCTGACCTC
 ACCAGACTTGACCCCGGGAGCTTGTATGAAGTGGAGATGGCAGCTTACAACCTGTGCGGGAGAGGGCCAGACAGCC
 ATGGTCACTTCCGAATGGACGCGCGGCCAAACCCGAGATCATGGCCAGCAAAAGACAGAGATCCAGAGAGAC
 GAGCTGGAGGACTCCCGAGAGCGAGCCAGCCAGACACGGCGCTCTCCCCCCAGAAGCTCCCGACAGG
 CCCACCATCTCCACGGCTCCGAGACCTCAGTGTACGTGACCTGGATTCCCGTGGGAATGTTGGGTTCCCAATC
 CAGTCTTCCGTGTGGAGTACAAGAAGCTAAAGAAAGTGGGAGACTGGATTCTGGCCACACGCGCCATCCCCCA
 TCGCGGCTGTCCGTGGAGATCAGGGGCTTAGAGAAAGGCACCTCTACAAGTTTCAGTCCGGGCTCTGAACATG
 CTGGGGGAGAGCGAGCCAGCGCCCCCTCTCGGCCCTACGTGGTGTGGGCTACAGCGGTGCGGTGTACGAGAGG
 CCGTGGCAGGTCCTTATATCACTTACCGATCGGTCATGAGACCACCATCATGCTCAAGTGGATGTACATC
 CCAGCAAGTAAACAACACCCCAATCATGGCTTTTATATCTATTATCGACCCACAGACAGTGAACATGATAGT
 GACTACAAGAAGGATATGGTGAAGGGGCAAGTACTGGCATTCATCAGCCACTGCAGCCAGACGACTCCTAC
 GACATTAAGATGCAGTGTCTTAATGAAGGAGGGGAGAGCGAGTTCAGCAACGTGATGATCTGTGAGACCAAAGCT
 CGGAAGTCTTCTGGCCAGCTTGGTGCAGTGCACACCCCAACTCTGGCCACCCACAGCGGCCCTTCTCTGAAACC
 ATAGAGCGGCCGTGGGCAGTGGGGCCTAGTGGCTCGTCCAGCAGCTGCCCTATCTGATTGTGGGGCTGTC
 CTGGGCTCCATCGTTCTCATCATCGTCACCTTCATCCCTTCTGCTTGTGGAGGGCCTGGTCTAAGCAAAACAT
 ACAACAGACAGTGGGTTTTCTCGAAGTGCCCTTCCACCTCCTGCCCCGTATCTATGGTGCCATTTGGGAGGACTC
 CCAGGCCACCGCCAGTGGACAGCCCTACCTCAGTGGCATCAGTGGACGGGCTGTGCTAATGGGATCCACATG
 AATAGGGGCTGCCCTCGGCTGCAGTGGGTACCCGGGATGAAGCCAGCAGCAGTATGCCAGGCGAGCTTCAG
 CAGCAGAGTGACACAGCAGCTGCTGAGGCAGACCATCTTGGCAATGGATATGACCCCAAAGTACCAGATC
 ACGAGGGGTCCTAAGTCTAGCCGGACGAGGGCTCTTTCTATACACTGCCCCGACGACTCCACTCACCAGCTG
 CTCGAGCCCCATCAGACTGCTGCCAACGCCAGGAGACGCTGCTGTGGGCCAGTCAAGGCTGAGGAGGCC
 CCGACAGTCTGTCTTGAAGCAGTGTGGGACCTCCATTCTACTCAGGGCCCCCATGCTGCTTGGGCTTGTG
 CCAGTTGAAGAGGTGGACAGTCTGACTCTGCCAAGTGAAGTGGAGGAGAGTGGTGTCCCCGACACCCCTAGGG
 GCTACGTAGGACAGGAACCTGGAATGCAGTCTCCCCGGGCCACTGGTGCCTGTTCTTTTGAACACCACTC
 CTACAATTTAGGCGAGAAGCTGATATCCGAAAGACTATATATGTTTTTTTTTTTTTAAAAAAAAGAGAAAAA
 AGAGACAGAAAAATTTGATTTATTTTCTATTATAGCCATATTTATATATTTATGCACTTGTAATAAATGTA
 TGTGTTTTATATTTCTGGAGAGACATAGGAGTCTACCTCCCTTGAAGTTGGAGGGGAAAAAAGAGTCCGCA
 CTTAAACAGGATCACCAGGAAGACACCGCACAGGCTGGGCGGGACAGACTCTAAGCTGGGGCTCTGCAGTG
 GCAGGCGAGGCTGCAGGAGGCCCCACAGATAAGCTGGCAAGAGGAAGGATCCAGGCACATGGTTCATCACGAGCA
 TGAGGGAACACCAAGGGGCACGATACAGCCTGGAGACACACAGATGGCTGGATCCGGTACCTTCCGGA
 CAATTTTCTAAGATGCCATGAGAACAACAGACAGATGTGTACAGCAGTATGACGATTAATAAAAGCTTCCGAA
 CATAATCCGTGGCAACATATCTCTGTAATAAACAAACACTGTAACCTCTAATAAATGTTTAGTCTTCTCTGTA

444/615

FIGURE 440

MLRGTMTAWRGMRPEVTLACLLLATAGCFADLNEVPQVTVQPASTVQKPGGTVILGCVVEPPR
MNVTWRLNGKELNGSDDALGVLITHGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTLAN
LQDFKLDVQHVEVDEGNTAVIACHLPESHKPAQVRYSVKQEWLEASRGNYLIMPSGNLQIVN
ASQEDEGMYKCAAYNPVTQEVKTSGSSDRLRVRRSTAEAAARI IYPPEAQTIIVTKGQSLILEC
VASGIPPPRVTWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVGQPGAIVILY
NVQVFEPPEVTMELSOLVIPWGQSAKLTCEVRGNPPPSVLWLRNAVPLISSQRLRLSRRALRV
LSMGPEDEGVYQCMAENEVGSAAHAVVQLRTSRPSITPRLWQDAELATGTPPVSPSKLGNPEQM
LRGQPALPRPPTSVGPASPKCPGEKGQGAPEAPIILSSPRTSKTDSYELVWRPRHEGSGRAP
ILYYVVKHRKQVTNSSDDWTISGIPANQHRLTLRLDPGSLYEVEMAAYNCAGEGQTAMVTFR
TGRRPKPEIMASKEQQIQRDDPGASPOSSSQPDHGRSLPPEAPDRPTISTASETSVYVTWIPR
GNGGFPIQSFVEYKKLKKVGDWILATSAIPPSRLSVEITGLEKGTSYKFRVRALNMLGESEP
SAPSRPYVVSIGYSGRVYERP VAGPYITFTDAVNETTIMLKWMIYPASNNNTPIHGFYIYRPT
DSDNDSYKKDMVEGDYKWSHLSHLQPETSIDIKMQCFNEGGESEFSNVMICETKARKSSGQP
GRLPPPTLAPPQPLPETIERPVGTGAMVARSSDLPYLIVGVVLGSIVLIIVTFIPFCLWRAW
SKQKHTTDLGFPRALPPSCPYTMVPLGGLPGHQASGQPYLSGISGRACANGIHMNRGCP SAA
VGYPGMKPQQHCPGELQQQSDTSSLLRQTHLGNGYDPQSHQITRGPKSSPDEGSFLYTL PDDS
THQLLQPHHDCQEQEQPAAVGQSGVRRAPDSPVLEAVWDPPFHSGPPCCLGLVPVEEVDSPD
SCQVSGGDWCPQHVPVAYVGQEPGMQLSPGPLVRVSFETPPLTI

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 16-30 (type II), 854-879

445/615

FIGURE 441

GAGAGAATAGCTACAGATTCTCCATCCTCAGTCTTTGCAAGGCGACAGCTGTGCCAGCCGGGC
TCTGGCAGGCTCCTGGCAGCATGGCAGTGAAGCTTGGGACCCTCCTGCTGGCCCTTGCCCTGG
GCCTGGCCCAGCCAGCCTCTGCCCGCCGGAAGCTGCTGGTGTTTCTGCTGGATGGTTTTTCGCT
CAGACTACATCAGTGATGAGGCGCTGGAGTCATTGCCTGGTTTCAAAGAGATTGTGAGCAGGG
GAGTAAAAGTGGATTACTTGACTCCAGACTTCCCTAGTCTCTCGTATCCCAATTATTATACCC
TAATGACTGGCCGCCATTGTGAAGTCCATCAGATGATCGGGAACCTACATGTGGGACCCACCA
CCAACAAGTCCTTTGACATTGGCGTCAACAAAGACAGCCTAATGCCTCTCTGGTGGAATGGAT
CAGAACCTCTGTGGGTCACTCTGACCAAGGCCAAAAGGAAGGTCTACATGTACTACTGGCCAG
GCTGTGAGGTTGAGATTCTGGGTGTGAGACCCACCTACTGCCTAGAATATAAAAATGTCCCAA
CGGATATCAATTTTGCCAATGCAGTCAGCGATGCTCTTGACTCCTTCAAGAGTGGCCGGGCGG
ACCTGGCAGCCATATACCATGAGCGCATTGACGTGGAAGGCCACCACTACGGGCCTGCATCTC
CGCAGAGGAAAGATGCCCTCAAGGCTGTAGACACTGTCCTGAAGTACATGACCAAGTGGATCC
AGGAGCGGGGCTGCAGGACCGCCTGAACGTCATTATTTCTCGGATCACGGAATGACCGACA
TTTTCTGGATGGACAAAGTGATTGAGCTGAATAAGTACATCAGCCTGAATGACCTGCAGCAAG
TGAAGGACCGCGGGCCTGTTGTGAGCCTTTGGCCGGCCCCCTGGGAAACACTCTGAGATATATA
ACAACTGAGCACAGTGGAACACATGACTGTCTACGAGAAAGAAGCCATCCCAAGCAGGTTCT
ATTACAAGAAAGGAAAGTTTGTCTCTCCTTTGACTTTAGTGGCTGATGAAGGCTGGTTCATAA
CTGAGAATCGAGAGATGCTTCCGTTTTGGATGAACAGCACCGGCAGGCGGGAAGGTTGGCAGC
GTGGATGGCACGGCTACGACAACGAGCTCATGGACATGCGGGGCATCTTCCTGGCCTTCGGAC
CTGATTTCAAATCCAACCTTCAGAGCTGCTCCTATCAGGTCGGTGGACGTCTACAATGTCATGT
GCAATGTGGTGGGCATCACCCCGCTGCCCCGCGCTGTCTGGCCCAGCCACTGTGCCCTGGCACTGATTC
TTCTCTTCCTGCTTGCATAACTGATCATATTGCTTGTCTCAGAAAAAACACCATCAGCAAAG
TGGGCCTCCAAAGCCAGATGATTTTCATTTTATGTGTGAATAATAGCTTCATTAACACAATCA
AGACCATGCACATTGTAAATACATTATTCTTGGATAATTCTATACATAAAAGTTCCTACTTGT
TAAA

446/615

FIGURE 442

MAVKLGTLILLALALGLAQPASARRKLLVFLLDGFERSDYISDEALES LPGFKEIVSRGVKVDYL
TPDFPSLSYPNYYTLMTGRHCEVHQMIGNYMWDPTTNKSF DIGVNKDSL MPLWWNGSEPLWVT
LTKAKRKVYMYYPGCEVEILGVRPTYCLEYKNVPTDINFANAVSDALDSFKSGRADLA AIYH
ERIDVEGHHYGPASPQRKDALKAVDTVLKYM TKWIQERGLQDRLN VII FSDHGMTDIFWMDKV
IELNKYISLNDLQQVKDRGPVVSLWPAPGKHSEIYNKLSTVEHMTVYEKEAIPSRFYKKGKF
VSPLTLVADEGWFITENREMLPFWMNSTGRREGWQRGWHGYDNELMDMRGIFLAFGPDFKSNF
RAAPIRSVDVYNVMCNVVGITPLPNNGSWSRVMCMLKGRAGTAPPVWPSHCALALILLFLLA

Important features of the protein:**Signal peptide:**

amino acids 1-22

N-glycosylation sites.

amino acids 100-104, 118-122, 341-345, 404-408

N-myristoylation sites.

amino acids 148-154, 365-371

Amidation site.

amino acids 343-347

447/615

FIGURE 443

AGTGACTGCAGCCTTCCTAGATCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAGC
ACCAGTGTGTGAGGGGAGCAGGCAGCGGTCCTAGCCAGTTCCTTGATCCTGCCAGACCACCCA
GCCCCCGGCACAGAGCTGCTCCACAGGCACCATGAGGATCATGCTGCTATTACAGCCATCCT
GGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGGTTCC
TGGCGGGGGCCGCAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTCAAAAG
CCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAAGGAATC
AACATCTCCCGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGAGGAGCGT
CCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCCCTCGGCCCTTCATCC
CAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACCTTTATAAGA
CTCTCCTACGGATGTGAATCAAGAGAACGTCCCCAGCTTTGGCATCCTCAAGTATCCCCGAG
AGCAGAAATAGGTACTCCACTTCCGGACTCCTGGACTGCATTAGGAAGACCTCTTCCCTGTCC
CAATCCCCAGGTGCGCACGCTCCTGTTACCCCTTCTCTTCCCTGTTCTTGTAACATTCTTG
CTTTGACTCCTTCTCCATCTTTTCTACCTGACCCTGGTGTGGAACTGCATAGTGAATATCCC
CAACCCCAATGGGCATTGACTGTAGAATACCCTAGAGTTCCTGTAGTGCCTACATTAATAAT
ATAATGTCTCTCTATTCTCAACAATAAAGATTTTTGCATATGAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

448/615.

FIGURE 444

MRIMLLFTAILAFSLAQSEFGAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLKA
LSQASTDPKESTSPEKRDMDHDFVGLMGKRSVQPEGKTGPFLPSVRVPRPLHPNQLGSTGKSS
LGTEEQRPL

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

449/615

FIGURE 445

TGGACTTCTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCAGTCCACCATGATCCATCTGGGTCACAT
CCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAGAGATCATCACTCCCTGCCTTTTA
CCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCCCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGA
TGCGGTGGCATCGCTGCTCATCGTGGGGGCGGTGTTCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGG
CAAAGTCTACATCAACATGCCAGGCAGGGGCTGACCCCTCCTGCAGCTTGGACCTTGACTTCTGACCTCTCATC
CTGGATGGTGTGTGGTGGCACAGGAACCCCGCCCCAACTTTTGGATTGTAATAAAACAATTGAAACACCA

450/615

FIGURE 446

MIHLGHILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCSLSLPLLAGLVAADAVASLLIVGAVFLCARPR
RSPAQDGKVYINMPGRG

Signal peptide:	Amino acids 1-18
transmembrane domain:	Amino acids 51-70
Glycosaminoglycan attachment site:	Amino acids 40-44
N-myristoylation sites:	Amino acids 34-40;37-43;52-58
Prokaryotic membrane lipoprotein lipid attachment site:	Amino acids 29-40

451/615

FIGURE 447

GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCTCCC
CGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGGGG
GCACCCCCACAGTCACGGTACCCACACTGCTACTCGGCTGAGGAAGTGCCCCCTCGGCCAGGC
CCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGTAGCCCTGGTGTG
CAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAGTGCCC
GGTGCTGCCGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCGCTCCATCTCACCCCTGGAG
ATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGTGCCTGTG
CAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTGCGGCTGCT
CCAGAGCCTGCTGGTGCTGCGCCGCCGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACC
TGGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTCGGCTGCACCTGCGTGCTGCC
CCGTTCAGTGTGACCGCCGAGGCCGTGGGGCCCCCTAGACTGGACACGTGTGCTCCCCAGAGGG
CACCCCTATTTATGTGTATTTATTGTTATTTATATGCCTCCCCAACACTACCCTTGGGGTC
TGGGCATTCCCCGTGTCTGGAGGACAGCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGT
TGGGGGTAGAAGGAGCTCAGCACCTCTTCCAGCCCTTAAAGCTGCAGAAAAGGTGTCACACGG
CTGCCTGTACCTTGGCTCCCTGTCCTGCTCCCGGCTTCCCTTACCCTATCACTGGCCTCAGGC
CCCGCAGGCTGCCTCTTCCCAACCTCCTTGAAGTACCCCTGTTTCTTAAACAATTATTTAAG
TGTACGTGTATTATTAACTGATGAACACATCCCCAAA

452/615

FIGURE 448

MTLLPGLLFLTLWHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQALP
VALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDDEDRYPQKLAF
AECLCRGCIDARTGRETAALNSVRLQLQLVLRRLRRRPCSRDGSGLPTPGAFAFHTEFIHVPVGC
TCVLPRSV

Important features:**Signal peptide:**

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 112-121

N-myristoylation sites.

amino acids 32-38, 55-61, 133-139

Leucine zipper pattern.

amino acids 3-25

Homologous region to IL-17.

amino acids 99-195

453/615

FIGURE 449

TGCAGAGCTTGTGGAGGCCATGGGGCGCGTCGTCGCGGAGCTCGTCTCCTCGCTGCTGGGGTT
GTGGCTGTTGCTGTGCAGCTGCGGATGCCCCGAGGGCGCCGAGCTGCGTGCTCCGCCAGATAA
AATCGCGATTATTGGAGCCGGAATTGGTGGCACTTCAGCAGCCTATTACCTGCGGCAGAAATT
TGGGAAAAGATGTGAAGATAGACCTGTTTGAAGAGAAGAGGTCGGGGGCCGCTGGCTACCAT
GATGGTGCAGGGGCAAGAATACGAGGCAGGAGGTTCTGTCATCCATCCTTTAAATCTGCACAT
GAAACGTTTTGTCAAAGACCTGGGTCTCTGCTGTTTCAGGCCTCTGGTGGCCTACTGGGGAT
ATATAATGGAGAGACTCTGGTATTTGAGGAGAGCAACTGGTTCATAATTAACGTGATTAAATT
AGTTTGGCGCTATGGATTTCAATCCCTCCGTATGCACATGTGGGTAGAGGACGTGTTAGACAA
GTTTCATGAGGATCTACCGCTACCAGTCTCATGACTATGCCTTCAGTAGTGTCGAAAAATTACT
TCATGCTCTAGGAGGAGATGACTTCCTTGAATGCTTAATCGAACACTTCTTGAAACCTTGCA
AAAGGCCGGCTTTTCTGAGAAGTTCCTCAATGAAATGATTGCTCCTGTTATGAGGGTCAATTA
TGGCCAAAGCACGGACATCAATGCCTTTGTGGGGGCGGTGTCACTGTCCTGTTCTGATTCTGG
CCTTTGGGCAGTAGAAGGTGGCAATAAACTTGTTTGCTCAGGGCTTCTGCAGGCATCCAAAAG
CAATCTTATATCTGGCTCAGTAATGTACATCGAGGAGAAAAACAAAGACCAAGTACACAGGAAA
TCCAACAAAGATGTATGAAGTGGTCTACCAAATTGGAAGTGAAGTCTGTTCTAGACTTCTATGA
CATCGTCTTGGTGGCCACTCCGTTGAATCGAAAAATGTCGAATATTACTTTTCTCAACTTTGA
TCCTCCAATTGAGGAATTCCATCAATATTATCAACATATAGTGACAACCTTTAGTTAAGGGGGA
ATTGAATACATCTATCTTTAGCTCTAGACCCATAGATAAAATTTGGCCTTAATACAGTTTTAAC
CACTGATAATTCAGATTTGTTCAATTAACAGTATTGGGATTTGTGCCCTCTGTGAGAGAAAAGGA
AGATCCTGAGCCATCAACAGATGGAACATATGTTTGGGAAGATCTTTTCCCAAGAACTCTTAC
TAAAGCACAAATTTTAAAGCTCTTTCTGTCCTATGATTATGCTGTGAAGAAGCCATGGCTTGC
ATATCCTCACTATAAGCCCCGGAGAAATGCCCCCTATCATTCTCCATGATCGACTTTATTA
CCTCAATGGCATAGAGTGTGCAGCAAGTGCCATGGAGATGAGTGCCATTCAGCCCACAACGC
TGCACTCCTTGCCATATCACCCTGGAACGGGCACACAGACATGATTGATCAGGATGGCTTATA
TGAGAACTTAAACTGAACTATGAAGTGACACACTCCTTTTTCCCCTCCTAGTTCCAAATGA
CTATCAGTGGCAAAAAAGAACAAATCTGAGCAGAGATGATTTTGAACCAGATATTTTGCCAT
TATCATTGTTTAATAAAAGTAATCCCTGCTGGTCATAGGAAAAAAAAAAAAA

454/615

FIGURE 450

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62880
<subunit 1 of 1, 505 aa, 1 stop
<MW: 56640, pI: 6.10, NX(S/T): 4
MGRVVAELVSSLLGLWLLLCSCGCPEGAELRAPDPKIAIIGAGIGGTSAAYYLRQKFGKDVKI
DLFEREEVGGRLATMMVQGQYEAGGSVIHPLNLHMKRFVKDLGLSAVQASGGLLGIYNGETL
VFEESNWFTIINVIKLVWRYGFQSLRMHMMWVEDVLDKFMRIYRYQSHDYAFSSVEKLLHALGGD
DFLGMLNRTLLETQLKAGFSEKFLNEMIAPVMRVNYGQSTDINAFVGAVSLSCSDSGLWAVEG
GNKLVCSGLLQASKSNLISGSVMYIEEKTCTKYTGNTKMYEVVYQIGTETRSDFYDIVLVAT
PLNRKMSNITFLNFDPPIEEFHQYYQHIVTTLVKGELNTSIFSSRPIDKFGLNTVLTDDNSDL
FINSIGIVPSVREKEDPEPSTDGTYVWKIFSQETLTKAQILKLFLSYDYAVKKPWLAYPHYKP
PEKCPSTIILHDLRYLNGIECAASAMEMSAIAAHNAALLAYHRWNGHTDMIDQDGLYEKLTTEL
```

Important features:**Signal peptide:**

amino acids 1-23

N-glycosylation sites.

amino acids 196-200, 323-327, 353-357

Tyrosine kinase phosphorylation site.

amino acids 291-298

N-myristoylation sites.amino acids 23-29, 41-47, 43-49, 45-51, 46-52, 72-78, 115-121,
119-125, 260-266, 384-390, 459-465**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 12-23, 232-243

FIGURE 451

[illegible]

456/615

FIGURE 452

MASYLYGVLEFAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLET
PSQNIFFSPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLHTPESAIHQGFQHLVHSLTVPSK
DLTLKMGSALFVKKELQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQGKVVD
IIQGLDLLTAMVLVNHIFFKAKWEKPPFHLEYTRKNFPFLVGEQVTVQVPMMHQKEQFAFGVDT
ELNCFVLQMDYKGDVAFFVLPSKGKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRESISAS
YNLETILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATTTKFIVRS
KDGPSYFTVSEFNRTFLMMITNKATDGILFLGKVENPTKS

Signal peptide:
amino acids 1-20

457/615

FIGURE 453

CTCCGGGTCCCCAGGGGCTGCGCCGGGCGGCCTGGCAAGGGGACGAGTCAGTGGACACTCCAGGAAGAGCGGC
CCCCGGGGGGGCGATGACCGTGCGCTGACCGTGACTCACTCCAGGTCCGGAGGCGGGGGCCCCGGGGCGACTCG
GGGGCGGACCGCGGGGGCGAGCTGCCGCCCGTGAGTCCGGCCGAGCCACCTGAGCCCGAGCCGCGGGACACCGTC
GCTCCTGCTCTCCGAATGCTGCGCACCCGCGATGGGCCTGAGGAGCTGGCTCGCCGCCCCATGGGGCGCGCTGCCG
CCTCGGCCACCGCTGCTGCTGCTCCTGCTGCTGCTCCTGCTGCAGCCGCCGCTCCGACCTGGGCGCTCAGC
CCCCGATCAGCCTGCCTCTGGGCTCTGAAGAGCGGCCATTCCTCAGATTGGAAGCTGAACACATCTCCAACCTAC
ACAGCCCTTCTGCTGAGCAGGGATGGCAGGACCGTGTACGTGGGTGCTCGAGAGGCCCTCTTTGCACTCAGTAGC
AACCTCAGCTTCTGCCAGGCGGGGAGTACCAGGAGCTGCTTTGGGGTGACAGCGCAGAGAAGAAACAGCAGTGC
AGCTTCAAGGGCAAGGACCCACAGCGCGACTGTCAAAACTACATCAAGATCCTCCTGCCGCTCAGCGGCAGTCAC
CTGTTACCTGTGGCACAGCAGCCTTCAGCCCCATGTGTACCTACATCAACATGGAGAATTCCACCTGGCAAGG
GACGAGAAGGGGAATGCTCCTCTGGAAGATGGCAAGGGCCGTTGTCCCTTCGACCCGAATTTCAAGTCCACTGCC
CTGGTGGTTGATGGCGAGCTCTACACTGGAACAGTCAGCAGCTTCCAAGGAATGACCCGGCCATCTCGCGGAGC
CAAAGCCTTCGCCCCACCAAGACCGAGAGCTCCCTCAACTGGCTGCAAGACCCAGCTTTTGTGGCCTCAGCCTAC
ATTCCTGAGAGCCTGGGCGAGCTTGCAAGGCGATGATGACAAGATCTACTTTTTCTTCAGCGAGACTGCCAGGAA
TTTGAGTTCTTTGAGAACACCATTTGTGTCCCGCATTGCCCGCATCTGCAAGGGCGATGAGGGTGGAGAGCGGGTG
CTACAGCAGCGCTGGACCTCCTTCTCAAGGCCAGCTGCTGTGCTCAGGCCCGACGATGGCTTCCCCTTCAAC
GTGCTGCAGGATGTCTTACGCTGAGCCCCAGCCCCAGACTGGCGTGACACCCCTTTTCTATGGGGTCTTCACT
TCCCAGTGGCACAGGGGAACCTACAGAAGGCTCTGCCGTCTGTGCTTCACAATGAAGGATGTGCAGAGAGTCTTC
AGCGCCTCTACAAGGAGGTGAACCGTGAGACACAGCAGTGGTACACCGTGACCCACCGGTGCCACACCCCGG
CCTGGAGCGTGATCACCACAGTGCCCCGGAAAGGAAGATCAACTCATCCCTGCAGCTCCCAGACCGCGTGCTG
AACTTCTCAAGGACCATTCTTGATGGACGGGCGAGTCCGAAGCCGATGCTGCTGCTGCAGCCCCAGGCTCGC
TACCAGCGGTGGCTGTACACCGCGTCCCTGGCCTGCACACACCTACGATGTCTCTTCTGGGCACTGGTGAC
GGCCGGCTCCACAAGGCAGTGAGCGTGGGCCCCGGGTGCACATCATTGAGGAGCTGCAGATCTTCTCATCGGGA
CAGCCCGTGAGAACTGTCTCCTGGACACCCACAGGGGGCTGCTGTATGCGGCCTCAGCTCGGGCGTAGTCCAG
GTGCCCATGGCCAACTGCAGCCTGTACCGGAGCTGTGGGGACTGCCTCCTCGCCCGGACCCCTACTGTGCTTGG
AGCGGCTCCAGTGCAAGCACGTGAGCCTTACAGCCTCAGCTGGCCACAGGCGGTGGATCCAGGACATCGAG
GGAGCCAGCGCCAAGGACCTTTGACGCGGTCTTGGGTGTGTGTCGCCGTCTTTGTACCAACAGGGGAGAAGCCA
TGTGAGCAAGTCCAGTTCAGCCCAACACAGTGAACACTTTGGCCTGCCCGCTCCTCTCAACCTGGCGACCCGA
CTCTGGCTACGCAACGGGGCCCCGTCAATGCTTGGCCTCCTGCCACGTGCTACCCACTGGGGACCTGCTGCTG
GTGGGCACCCAACAGCTGGGGGAGTTCCAGTGCTGGTCACTAGAGGAGGGCTTCCAGCAGCTGGTAGCCAGCTAC
TGCCAGAGGTGGTGGAGGACGGGGTGGCAGACCAACAGATGAGGGTGGCAGTGTACCCGTCAATTATCAGCACA
TCGGTGTGAGTGCACCAAGCTGGTGGCAAGGCCAGCTGGGGTGACAGACAGGTCTTACTGGAAGGAGTTCTGGTG
ATGTGCACGCTCTTTGTGCTGGCCGTGCTGCTCCAGTTTTATTCTTGCTCTACCGGCACCGGAACAGCATGAAA
GTCTTCTGAAGCAGGGGAATGTGCCAGCGTGACCCCAAGACCTGCCCTGTGGTGTGCCCCCTGAGACCCGC
CCACTCAACGGCCTAGGGCCCCCTAGCACCCCGCTCGATCACCGAGGGTACCAGTCCCTGTGAGACAGCCCCCG
GGGGCCGAGTCTTCACTGAGTCAGAGAAGAGGCCACTCAGCATCCAAGACAGCTTCGTGGAGGTATCCCCAGTG
TGCCCCCGGCCCCGGTCCGCTTGGCTCGGAGATCCGTGACTCTGTGGTGTGAGAGCTGACTTCCAGAGGACGC
TGCCCTGGGTTACAGGGGCTGTGAATGCTCGGAGAGGGTCAACTGGACCTCCCTCCGCTCTGCTCTTCGTGGAAC
ACGACCGTGGTGGCCGGCCCTTGGGAGCCTTGGAGCCAGCTGGCCTGCTGCTCTCAGTCAAGTAGCGAAGCTCC
TACCACCCAGACACCAACAGCCGTGGCCCCAGAGGTCTGGCCAAATATGGGGCCTGCCTAGGTTGGTGGAA
CAGTGCTCCTTATGTAACTGAGCCCTTTGTTTAAAAAACAATTCCAATGTGAACTAGAATGAGAGGGAAGAG
ATAGCATGGCATGCAGCACACACGGCTGCTCCAGTTCATGGCCTCCAGGGGTGCTGGGGATGCATCCAAGTGG
TTGTCTGAGACAGAGTTGGAACCCCTCACCACCTGGCCTCTTACCTTCCACATTATCCCGCTGCCACCGGCTGC
CCTGTCTCACTGCAGATTGAGGACAGCTTGGGCTGCGTGCGTCTTGCCTTGCCAGTCAGCCGAGGATGTAGTTG
TTGTGCGCGTCTGCCACACCTCAGGGACAGAGGGCTAGGTTGGCACTGCGGCCCTCACCAGGTCTGGGCTC
GGACCCAACCTCTGGACCTTTCAGCCTGTATCAGGCTGTGGCCACACGAGAGGACAGCGCGAGCTCAGGAGAGA
TTTCGTGACAATGTACGCTTTCCTCAGAATTCAGGGAAGAGACTGTGCTGCTTCTCCTCGTGTGTGCGTGA
GAACCCGTGTGCCCCCTCCACCATATCCACCCCTCGCTCCATCTTTGAACTCAAACACGAGGAATAACTGCACC
CTGGTCTCTCCCCAGTCCCCAGTTCACCTCCATCCCTCACCTTCTCCACTCTAAGGGATATCAACACTGCCC
AGCACAGGGGGCCTGAATTTATGTGGTTTTTATACATTTTTTAATAAGATGCACCTTATGTCATTTTTTAATAAA
GTCTGAAGAATTACTGTTTAAAAAATAA

458/615

FIGURE 454

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962
><subunit 1 of 1, 837 aa, 1 stop
><MW: 92750, pI: 7.04, NX(S/T): 6
MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLLLLLQPPPTWALSPRISLPLGSEERPFLRFE
AEHISNYTALLLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELLWGADAEEKQQCSFKGKD
PQRDCQNYIKILLPLSGSHLFTCGTAAFSMCTYINMENFTLARDEKGNVLLEDGKGRCPFDP
NFKSTALVVDGELYTGTVSSSQGNDPAISRSQSLRPTKTESSLNWLQDPAFVASAYIPESLGS
LQGDDDKIYFFFSETGQEFFEFFENTIVSRIARICKGDEGGERVLOQRWTSFLKAQLLCSRDD
GFPPENVLQDVFTLSPSPQDWRDTLFYGVFTSQWHRGTTEGSAVCVFTMKDVQRVFSGLYKEVN
RETQQWYTVTHPVPTPRGACITNSARERKINSSLQLPDRVLNFKDHFMDGQVRSRMLLLQ
PQARYQRVAVHRVPGLHHTYDVLFLGTGDGRHLKAVSVGPRVHIIIEELQIFSSGQPVQNLLD
THRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSPLYQPQLATRPWIQ
DIEGASAKDLCSASSVVSPSFVPTGEKPCQVQFQPNVTNLTACPLLSNLATRLWLRNGAPVN
ASASCHVLPTGDLVLVGTQQLGEFQCWSLEEGFQQLVASYCPEVVEDGVADQTDGGSVPII
STSRVSAPAGGKASWGADRSYWKEFLVMCTLFVLAVLLPVLFLLYRHRNSMKVFLKQGECAV
HPKTCPVVLPPEPTRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFTSEKRPLSIQDSFVEVSP
VCPRPRVRLGSEIRDSVV
```

Transmembrane domains:

amino acids 23-46 (type II), 718-738

459/615

FIGURE 455

TAAGATGAGGGCATCCCTCACGTTACACCCCCTGGTGGCATCTGCCAGCCCTGTTCTGGGGAC
AAGGCGGGCTTTTCGTGGGAGCCATGCTCAGCCTGCCAGGAAGCCAAGCCCTACAGTGCAGAGG
AAACAGAATTTCAACGGGAAGCTGGTTTGCTTCATACCATTGGGATCTGCTGGTAAAGCTGTT
ATTTGGGTTTAGGGACTGATCCCTTGACGTTTACTTCTGGATCACCATGAATGGCCAAGATGG
TGGCAGAACACGCTGTGGACCCTGAGTTAGAGACAATGCAAATGTTGGATTGGGTGTAATTCT
TTTTGAATCCCAGATCCAGTCTGTACTTGAATATGAGCAGAAGATCTACAAGAATGCTGACAG
GGAACCGTGTTAAGACCCAGCACCCCTATTCCCAGGAGCTTCTGGCCTGACCATCTGCAGCCA
AAGCACTAACAGGGACAGATATGGGAATGTCCACCTTTGATCCGCATCCTGCACAATAGTGGT
CCCACCATGGCTGCCACTTTTTTATACTATTTGGAGAAAAGACCTTGTATAAATTCGAGGCCC
GAGTGACTAACGTCTCTGTACACGGAAATGGGTACTTGGTGGCATAGAGAAACACAATTAGC
CACTTTTTTCAGCTACACTTCTCACTCAGCTGCACCCCTACACTTCTCACTCAGGTGCACCCCT
TCTGCTGTCTTTTCCCCAACGTACTGGGTCCCAGCGTGGTGGGTATTTGCCACACTGGGTGC
CAGCTCAGCAGCCCCCACCTCTCTTTATTTCTCTCCAAAGCTGGTCTTTCTGACTATCATTGT
GGTAGGGGGAGGACAGATGCTAAAGGTGGAAGCTGACCTGGAGAAAGAGACACACGGGGTGAC
TGTGGCAAAGGACAGCTGGAAAAGAACTCTATCACTTCTTCATTGGCAACCACAAGGCACCC
GAGGCCATGGCACTCCCAGAGGCTGTGCGCAGAGCCAAGCCTCTCAACCTCTTCTGGCCCTGC
GTCCTGCAGCGAAGTCTCTGCTGTAAGACAGTAGACTCCTTCGATGAGGTGCTCAAAAATGCT
ACCCGGGGTGGTGGTGTCTGGCTTGACGTCTGGCCAGTTCAGAGAAAGTTGCAGAGATCAGGG
GCCAAGGATGTCATAGCCCCAGGTTGTCTCAGGGTCCCAATCCTAGGGCAGGGTGTGCATGG
AAGCAAGAACTATGGAAACCTAGCTCCAGTCTGCAGGCTCTGAGCCCCTAGTTTCTCACTCCA
GCGGGGCTCCCTCACTGCACAGAACCCACCCCTTCTGTGTGGGCACTGCTGACCACACAGATG
ACCCAGACCCAAAGAGCCTGGCAGAAGCTCTGTGGTTGGAGCTGGGCTCCGTCTCCAGGTCTG
GTTGAGGGGGATCAGGAAGGCTCTTTTCCACCTGTGGCTTCACTGGCCCTTTGAGATTTCTTA
TCTCACCGTTACTTCAGTTACCCTTGCAGGGGGCCAGGGAGTCAAGAATATACCGTGTTCCTC
CAGGGTTTAAGCCGGCCATGCCTTCCCGAGAGCATAACCAACTTGACAGGGGTGCCAGTTAC
CCCACAACTGAAGGAAGGAGATCCTTCCCCCGTCCCCAGGAGTGCTCTCAACCAGCCTCAGA
AAGCTTGAGAAGATGGACCCTTTGCCCACCAGGGTTAATTCCTGGTGGGGCAGCTCGGCTGTG
ATCAGGGCAACCAAACCTATAGGAAGCCTTCCAGTGTGAGCTGGAATTAGACTGAACATGTGC
TTGGGCTGCTCTCCCTAGACGCAGTTGCGGGGCACTCCAGGGAATGAACCAGCTCAAGTGT
GTCCCTAACAGCAGCCTGGAGCTACCCCAATCCCTCACAGCCTGACCCTCTCATTCATCA
GATCTCGTGCCG

460/615

FIGURE 456

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA69555
><subunit 1 of 1, 148 aa, 1 stop
><MW: 16214, pI: 10.22, NX(S/T): 0

MGTWWHRETQLATFSATLLTQLHPTLLTQVHPLLLSFPQRTGSRAWVVFATLGASSAAPH
LSLFSPKLVFLTIIVVGGGQMLKVEADLEKETHGVTVAKDSWKRNSITSSLATTRHPRPW
HSQRLCAEPSLSTSSGPASCSEVSAVRQ

Important features of the protein:**Signal peptide:**

Amino acids 1-28

Transmembrane domain:

Amino acids 64-78

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 103-107

N-myristoylation sites:

Amino acids 53-59;94-100

461/615

FIGURE 457

CCCCGCGCGCCCTGGCACTCAATCCCCGCCATGTGGGGGCTCCTGCTCGCCCTGGCCGCCTTC
GCGCCGGCCGTCGGCCCGGCTCTGGGGGCGCCAGGAACTCGGTGCTGGGCCTCGCGCAGCCC
GGGACCACCAAGGTCCCAGGCTCGACCCCGGCCCTGCATAGCAGCCCGGCACAGCCCGCGCG
GAGACAGCTAACGGGACCTCAGAACAGCATGTCCGGATTGAGTCATCAAGAAGAAAAAGGTC
ATTATGAAGAAGCGGAAGAAGCTAACTCTAACTCGCCCCACCCCACTGGTGACTGCCGGGCCC
CTTGTGACCCCACTCCAGCAGGGACCCCTCGACCCCGCTGAGAAACAAGAAACAGGCTGTCTT
CCTTTGGGTCTGGAGTCCCTGCGAGTTTCAGATAGCCGGCTTGAGGCATCCAGCAGCCAGTCC
TTTGGTCTTGGAACACACCGAGGACGGCTCAACATTTCAGGCCTGGAGGACGGCGATCTA
TATGATGGAGCCTGGTGTGCTGAGGAGCAGGACGCCGATCCATGGTTTCAGGTGGACGCTGGG
CACCCACCCGCTTCTCGGGTGTTATCACACAGGGCAGGAACCTCTGTCTGGAGGTATGACTGG
GTCACATCATAAAGGTCCAGTTCAGCAATGACAGTCGGACCTGGTGGGGAAGTAGGAACCAC
AGCAGTGGGATGGACGCAGTATTTCTGCCAATTTCAGACCCAGAACTCCAGTGCTGAACCTC
CTGCCGGAGCCCCAGGTGGCCCGCTTCATTGCGCTGCTGCCCCAGACCTGGCTCCAGGGAGGC
GCGCCTTGCCCTCCGGGCAGAGATCCTGGCCTGCCAGTCTCAGACCCCAATGACCTATTCCTT
GAGGCCCCCTGCGTCGGGATCCTCTGACCTCTAGACTTTCAGCATCACAATTACAAGGCCATG
AGGAAGCTGATGAAGCAGGTACAAGAGCAATGCCCCAACATCACCCGCATCTACAGCATTGGG
AAGAGCTACCAGGGCCTGAAGCTGTATGTGATGGAAATGTCGGACAAGCCTGGGGAGCATGAG
CTGGGGGAGCCTGAGGTGCGCTACGTGGCTGGCATGCATGGGAACGAGGCCCTGGGGCGGGAG
TTGCTTCTGCTCCTGATGCAAGTTCTGTGCCATGAGTTCTGCGAGGGAACCCACGGGTGACC
CGGCTGCTCTCTGAGATGCGCATTACCTGCTGCCCTCCATGAACCCTGATGGCTATGAGATC
GCCTACCACCGGGGTTTCAGAGCTGGTGGGCTGGGCCGAGGGCCGCTGGAACAACCAGAGCATC
GATCTTAACCATAATTTTGCTGACCTCAACACACCACTGTGGGAAGCACAGGACGATGGGAAG
GTGCCCCACATCGTCCCCAACCATCACCTGCCATTGCCCACTTACTACACCCCTGCCCAATGCC
ACCGTGGCTCCTGAAACGCGGGCAGTAATCAAGTGGATGAAGCGGATCCCCTTTGTGCTAAGT
GCCAACCTCCACGGGGGTGAGCTCGTGGTGTCTACCCATTCGACATGACTCGCACCCCGTGG
GCTGCCCCGCGAGCTCACGCCCACACCAGATGATGCTGTGTTTCGCTGGCTCAGCACTGTCTAT
GCTGGCAGTAATCTGGCCATGCAGGACACCAGCCGCCGACCCTGCCACAGCCAGGACTTCTCC
GTGCACGGCAACATCATCAACGGGGCTGACTGGCACACGGTCCCCGGGAGCATGAATGACTTC
AGCTACCTACACACCAACTGCTTTGAGGTCACTGTGGAGCTGTCCTGTGACAAGTTCCCTCAC
GAGAATGAATTGCCCCAGGAGTGGGAGAACAACAAGACGCCCTCCTCACCTACCTGGAGCAG
GTGCGCATGGGCATTGCAGGAGTGGTGAGGGACAAGGACACGGAGCTTGGGATTGCTGACGCT
GTCAATTGCCGTGGATGGGATTAACCATGACGTGACCACGGCGTGGGGCGGGGATTATTGGCGT
CTGCTGACCCCGAGGGGACTACATGGTGACTGCCAGTGCCGAGGGCTACCATTTCAGTGACACGG
AACTGTGGGTCACCTTTGAAGAGGGCCCCCTTCCCCTGCAATTTTCGTGCTCACCAAGACTCCC
AAACAGAGGCTGCGCGAGCTGCTGGCAGCTGGGGCCAAGGTGCCCCCGGACCTTCGAGGGCGC
CTGGAGCGGCTAAGGGGACAGAAGGATTGAATACCTGCGGTTTAAGAGCCCTAGGGCAGGCTGG
ACCTGTCAAGACGGGAAGGGGAAGAGTAGAGAGGGAGGGACAAAGTGAGGAAAAGGTGCTCAT
TAAAGCTACCGGGCACCTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

462/615

FIGURE 458

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71162
><subunit 1 of 1, 734 aa, 1 stop
><MW: 81677, pI: 6.60; NX(S/T): 6
MWGLLLALAAFAVGPALGAPRNSVLGLAQPGETTKVPGSTPALHSSPAQPPAETANGTS
EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL
ESLRVSDSRLEASSSQSFGLGPHRGRLNIHSGLEDGDLYDGAWCAEEQDADPWFQVDAGH
PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL
NLLPEPQVARFIRLLPQTLWQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH
NYKAMRKLKQVQECPNITRIYSIGKSYQGLKLYMEMSDKPGHEHELGEPEVRYVAGMH
GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAYHRGSELVG
WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYTTLPNATVAPETR
AVIKWMKRIPFVLSANLHGGEVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGSN
LAMQDTSRRPCHSQDFSVHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE
NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTELGIADAVIAVDGINHDVTTAWGGDY
WRLTPGDYMTASAEGYHSVTRNCRVTFEEGFPFCNFVLTKTPKQRLRELLAAGAKVPP
DLRRRLERLRGQKD
```

463/615

FIGURE 459

TAAACAGCTACAATATTCCAGGGCCAGTCACTTGCCATTTCTCATAACAGCGTCAGAGAGAA
AGAACTGACTGAAACGTTTGAGATGAAGAAAGTTCTCCTCCTGATCACAGCCATCTTGGCAGT
GGCTGTTGGTTTCCAGTCTCTCAAGACCAGGAACGAGAAAAAAGAAGTATCAGTGACAGCGA
TGAATTAGCTTCAGGGTTTTTTGTGTTCCCTTACCCATATCCATTTGCCCCACTTCCACCAAT
TCCATTTCCAAGATTTCCATGGTTTAGACGTAATTTTCCTATTCCAATACCTGAATCTGCCCC
TACAACTCCCCTTCCTAGCGAAAAGTAAACAAGAAGGATAAGTCACGATAAACCTGGTCACCT
GAAATTGAAATTGAGCCACTTCCTTGAAGAATCAAAATTCCTGTAAATAAAAGAAAAACAAAT
GTAATTGAAATAGCACACAGCATTCTCTAGTCAATATCTTTAGTGATCTTCTTTAATAAACAT
GAAAGCAAAGATTTTGGTTTCTTAATTTCCACA

464/615

FIGURE 460

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71290
><subunit 1 of 1, 85 aa, 1 stop
><MW: 9700, pI: 9.55, NX(S/T): 0
MKKVLILLITAILAVAVGFVVSQDQEREKRSISDSDELASGFFVFPYPYFPRPLPPIPFPRFPW
FRRNFPIPIPIESAPTTPLPSEK

Important features of the protein:**Signal peptide:**

amino acids 1-17

Homologous region to B3-hordein:

amino acids 47-85

Important features of the protein:**Signal peptide:**

Amino acids 1-20

N-glycosylation sites:

Amino acids 57-61;210-214;220-224;318-322;428-432;472-476

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 80-84

N-myristoylation sites:Amino acids 3-9;20-29;39-48;152-161;161-170;262-271;358-364;
538-544;560-566;637-643**Zinc carboxypeptidases, zinc-binding region 2 signature:**

Amino acids 498-509

Zinc carboxypeptidases:

Amino acids 391-411

465/615

FIGURE 461

AGCAGGAGCAGGAGAGGGACAATGGGAAGCTGCCCCGTCCAGGTTTCATGTTCTTCTTATTTCTC
CTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCCTGGT
GCTGCCCAGGAACCCACGTGGCTCACAGATGTCCAGCTGCCATGGAATTCATTGCTGCCACT
GAGGTGGCTGTCATAGGCTTCTTCCAGGATTTAGAAATACCAGCAGTGCCCATACTCCATAGC
ATGGTGCAAAAATTCCCAGGCGTGTCAATTTGGGATCAGCACTGATTCTGAGGTTCTGACACAC
TACAACATCACTGGGAACACCATCTGCCTCTTTTCGCCTGGTAGACAATGAACAACCTGAATTTA
GAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTTCATTGAGATCAACAGC
CTCCACATGGTGACAGAGTACAACCCTGTGACTGTGATTGGGTTATTCAACAGCGTAATTCAG
ATTCATCTCCTCCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATGCACAGATAC
CAGAAGGCAGCCAAGCTCTTCCAGGGGAAGATTCTCTTTATTCTGGTGGACAGTGGTATGAAA
GAAAATGGGAAGGTGATATCATTTTTTCAAACCTAAAGGAGTCTCAACTGCCAGCTTTGGCAATT
TACCAGACTCTAGATGACGAGTGGGATACACTGCCCACAGCAGAAGTTTCCGTAGAGCATGTG
CAAACTTTTGTGATGGATTCCCTAAGTGGAAAATTGTTGAAAGAAAATCGTGAATCAGAAGGA
AAGACTCCAAAGGTGGAACCTCTGA~~CT~~CTTCTCCTTGGAACCTACATATGGCCAAGTATCTACTTTA
TGCAAAGTAAAAAGGCACAACCTCAAATCTCAGAGACACTAAACAACAGGATCACTAGGCCCTGC
CAACCACACACACACGCACGTGCACACACGCACGCACGCGTGCACACACACACGCGCACACAC
ACACACACACAGAGCTTCATTTCTGTCTTAAATCTCGTTTTCTCTTCTTCTTCTTTTAAA
TTTCATATCCTCACTCCCTATCCAATTTCTTCTTATCGTGCATTCATACTCTGTAAGCCCAT
CTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATGCCTCTATGAAAGAGAGGCA
TTCCTAGAGAAAGATTGTTCCAATTTGTCATTTAATATCAAGTTTGTATACTGCACATGACTT
ACACACAACATAGTTCCTGCTCTTTTAAGGTTACCTAAGGGTTGAACTCTACCTTCTTTCAT
AAGCACATGTCCGTCTCTGACTCAGGATCAAAAACCAAAGGATGGTTTTAAACACCTTTGTGA
AATTGTCTTTTGGCCAGAAGTTAAAGGCTGTCTCCAAGTCCCTGAACTCAGCAGAAATAGACC
ATGTGAAAACCTCCATGCTTGGTTAGCATCTCCAACCTCCCTATGTAAATCAACAACCTGCATAA
TAAATAAAAGCAATCATGTTATA

466/615

FIGURE 462

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401

><subunit 1 of 1, 273 aa, 1 stop

><MW: 30480, pI: 4.60, NX(S/T): 1

MEAAPSRFMFLFLLTCELAEEVAAEVEKSSDGPAAQEPTWLTDVPAAMEFIAATEVAVIGF
FQDLEIPAVPILHSMVQKFPGVSGISTDSEVLTHYNITGNTICLFRDVDNEQLNLEDEDIES
IDATKLSRFIEINSLHMTYNPVTVIGLFNSVIQIHLLIMNKASPEYEENMHRYQKAAKLF
QGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDDEWDTLPTAEVSVEHVQNFCDF
LSGKLLKENRESEGKTPKVEL

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 143-162

467/615

FIGURE 463

CTCGCTTCTTCCTTCTGGATGGGGGCCCAGGGGGCCCAGGAGAGTATAAAGGCGATGTGGAGG
GTGCCCCGGCACAACCAGACGCCCAGTCACAGGCGAGAGCCCTGGG**ATG**CACCGGCCAGAGGCC
ATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTATGGC
CCTGGAGGAGGCAAGTATTTTCAGCACCACTGAAGACTACGACCATGAAATCACAGGGCTGCGG
GTGTCTGTAGGTCTTCTCCTGGTGAAAAGTGTCCAGGTGAAACTTGGAGACTCCTGGGACGTG
AAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCACCCTGCAGCCAGGCGAATACATCACA
AAAGTCTTTGTCGCCTTCCAAGCTTTCCTCCGGGGTATGGTCATGTACACCAGCAAGGACCGC
TATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCAGCCAAGAGGGGCGAG
GTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTGGCTTTGAATGG
AATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTCAGCAAACCTCA
CCCGTGGGTGCT**TAG**GGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGTGTGGTGGTGGC
TGATGGTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAATAAATAAAGCTTCT
GCAGAAAA

468/615

FIGURE 464

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19600, pI: 5.89, NX(S/T): 1
MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSQVQKL
GDSWDVKLGALGGNTQEVTLQPGYITKVFAFQAFLRGMVMTSKDRYFYFGKLDGQISSAY
PSQEGQVLVGIYGQYQLLGKISIGFEWNYPLEEPTTEPPVNLTYSANSPVGR
```

Signal peptide:
amino acids 1-22

469/615

FIGURE 465

CGGACGCGTGGGTCCGGCGGCCTGAGGCTGCACCGGGCACGGGTCCGCCGCAATCCAGCCTGGGCGGAGCCGGAG
TTGCGAGCCGCTGCCTAGAGGCCGAGGAGCTCACAGCTATGGGCTGGAGGCCCCGAGAGCTCGGGGGACCCCGT
TGCTGCTGCTGCTACTACTGCTGCTGCTGCTGGCCAGTGCCAGGCGCCGGGTGCTTCAAGGACATATCCCTGGGC
AGCCAGTCACCCCGCACTGGGTCTGGATGGACAACCCTGGCGCACCGTCAGCCTGGAGGAGCCGGTCTCGAAGC
CAGACATGGGGCTGGTGGCCCTGGAGGCTGAAGGCCAGGAGCTCCTGCTTGAGCTGGAGAAGAACCACAGGCTGC
TGGCCCCAGGATACATAGAAACCCACTACGGCCCAGATGGGCAGCCAGTGCTGCTGGCCCCCAACCACACGGATC
ATTGCCACTACCAAGGGCGAGTAAGGGGCTTCCCCGACTCCTGGGTAGTCTCTGCACCTGCTCTGGGATGAGTG
GCCTGATCACCTCAGCAGGAATGCCAGCTATTATCTGCGTCCCTGGCCACCCCGGGGCTCCAAGGACTTCTCAA
CCCACGAGATCTTTTCGATGGAGCAGCTGCTCACCTGGAAGGAACCTGTGGCCACAGGGATCCTGGGAACAAAG
CGGGCATGACCAGCCTTCTGGTGGTCCCCAGAGCAGGGGCGAGCGAGAAGCGCGCAGGACCCGGAAGTACCTGG
AACTGTACATTGTGGCAGACCACACCTGTTCTTGACTCGGCACCGAACTTGAACCACACCAACAGCGTCTCC
TGAAGTCGCCAATACTACGTGGACCAGCTTCTCAGGACTCTGGACATTCAGGTGGCGCTGACCGGCTGGAGGTGT
GGACCGAGCGGGACCGCAGCCGCTCACGCAGGACGCCAACGCCACGCTCTGGGCTTCTGTCAGTGGCGCCGGG
GGTGTGGGCGCAGCGCCCCACGACTCCGCGCAGCTGCTCACGGGCCGCGCTTCCAGGGCGCCACAGTGGGCC
TGGCGCCCGCTCGAGGGCATGTGCCGCGCCGAGAGCTCGGGAGGCGTGAGCACGGACCACTCGGAGCTCCCCATCG
GCGCGCAGCCACCATGGCCCATGAGATCGGCCACAGCCTCGGCTCAGCCACGACCCCGACGGCTGCTGCGTGG
AGGCTGCGGCGGAGTCCGGAGGCTGCGTCATGGCTGCGGCCACCGGGCACCCGTTTCCGCGCGTGTTCAGCGCCT
GCAGCCGCGCCAGCTGCGCGCCTTCTTCCGCAAGGGGGGCGGCGCTTGCCTCTCCAATGCCCGGACCCCGGAC
TCCCGGTGCCCGCGCGCTCTGCGGGAACGGCTTCTGGAAGCGGGCGAGGAGTGTGACTGCGGCCCTGGCCAGG
AGTGCCGCGACCTCTGCTGCTTTGCTCACAACCTGCTGCTGCGCCCGGGGGCCAGTGCGCCACGGGGACTGCT
GCGTGCGCTGCTGCTGAAGCCGGCTGGAGCGCTGTGCCGCCAGGCCATGGGTGACTGTGACCTCCCTGAGTTTT
GCACGGGCACCTCCTCCCACTGTCCCCCAGACGTTTACCTACTGGACGGCTCACCTGTGCCAGGGGCGAGTGGCT
ACTGCTGGGATGGCGCATGTCCCACGCTGGAGCAGCAGTGCCAGCAGCTCTGGGGGCTGGCTCCCACCCAGCTC
CCGAGGCCTGTTTCCAGGTGGTGAATCTGCGGGAGATGCTCATGGAACCTGCGGCCAGGACAGCGAGGGCCACT
TCTGCGCCTGTGCAGGGAGGGATGCCCTGTGTGGGAAGTGCAGTGCCAGGGTGGAAAGCCAGCCTGCTCGCAC
CGCATATGGTGCCAGTGGACTCTACCGTTCACCTAGATGGCCAGGAAGTGAATGTGCGGGAGCCTTGGCACTCC
CCAGTGCCCAGCTGGACCTGCTTGGCCTGGGCTGGGTAGAGCCAGGCACCCAGTGTTGACCTAGAATGGTGTGCC
AGAGCAGGCGCTGCAGGAAGAATGCCTTCCAGGAGCTTCAGCGCTGCCTGACTGCCTGCCACAGCCACGGGGTTT
GCAATAGCAACCATAACTGCCACTGTGCTCCAGGCTGGGCTCCACCCTTCTGTGACAAGCCAGGCTTTGGTGGCA
GCATGGACAGTGGCCTGTGCAGGCTGAAAACCATGACACCTTCTGCTGGCCATGCTCCTCAGCGTCTGCTGC
CTCTGCTCCCAGGGGCGGCGCTGGCCTGGTGTGTGCTACCGACTCCAGGAGCCCATCTGCAGCGATGCAGCTGGG
GCTGCAGAAGGGACCTTGGTGCAGTGGCCCCAAAGATGGCCCCACACAGGGACCAACCCCTGGGCGCGCTTCAACC
CCATGGAGTTGGGCCCCACAGCCACTGGACAGCCCTGGCCCTGGACCTGAGAACTCTCATGAGCCACAGAGCC
ACCCTGAGAAGCCTCTGCCAGCAGTCTGCCTGACCCCCAAGCAGATCAAGTCCAGATGCCAAGATCCTGCCTCT
GGTGAGAGGTAGCTCCTAAATGAACAGATTTAAAGACAGGTGGCCACTGACAGCCACTCCAGGAACCTGAACTG
CAGGGGCGAGCCAGTGAATCACCGGACCTCCAGCACCTGCAGGCAGCTTGGAGTTTCTTCCCCGAGTGGAGCT
TCGACCCACCCACTCCAGGAACCCAGAGCCACATTAGAAGTTCTTGAGGGCTGGAGAACTGCTTGGGCACACT
CTCCAGCTCAATAAACCATCAGTCCCAGAAAGCAAGGTACACAGCCCTGACCTCCCTCACCAGTGGAGGCTGG
GTAGTGCTGGCCATCCCAAAAGGGCTCTGTCTGGGAGTCTGGTGTGTCTCTACATGCAATTTCCACGGACCCA
GCTCTGTGGAGGCGATGACTGCTGGCCAGAAGCTAGTGGTCTGGGGCCCTATGGTTGCACTGAGTCCACACTCC
CCTGCAGCCTGGCTGGCCTCTGCAACAAACATAATTTTGGGGACCTTCTTCTGTTTCTTCCCACCTGTCTT
CTCCCTAGGTGGTTCTGAGCCCCACCCCAATCCAGTGCTACACCTGAGGTCTGGAGCTCAGAATCTGAC
AGCCTCTCCCCATTTCTGTGTGTGTCCGGGGGACAGAGGGAACCATTTAAGAAAAGATACCAAGTAGAAGTCAA
AAGAAAGACATGTGGCTATAGGCGTGGTGGCTCATGCCTATAATCCAGCACTTTGGGAAGCCGGGTAGGAGG
ATCACCAGAGGCCAGCAGGTCCACACCAGCCTGGGCAACACAGCAAGACACCGCATCTACAGAAAAATTTTAAAA
TTAGCTGGGCGTGGTGGTGTGTACCTGTAGGCCTAGCTGCTCAGGAGGCTGAAGCAGGAGGATCACTTGAGCCTG
AGTTCAACACTGCAGTGAAGTATGGTGGCACCCTGCACTCCAGCCTGGGTGACAGAGCAAGACCCCTGTCTCTAA
AATAAATTTTAAAGGACTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGAAAA

470/615

FIGURE 466

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76788
><subunit 1 of 1, 813 aa, 1 stop
><MW: 87739, pI: 6.94, NX(S/T): 5

MGWRPRRARGTPLLLLLLLLLLWPVPGAGVLQGHIPGPVTPHWVLDGQPWRTVSLEEPVSKPDMGLVALEAEGQ
ELLLLELEKNHRLRLAPGYIETHYGPDGQPVVLPNHTDHCHYQGRVRFPPDSWVVLCTCSGMSGLITLSRNASYLL
RPWPPRGSKDFSTHEIFRMEQLLTWKGTGCHRDPGNKAGMTSLPGGPQSRGRREARRTRKYLELYIVADHTLFLT
RHRNLNHTKQRLLEVANYVDQLRLTDIQVALTGLEVWTERDRSRVTQDANATLWAFLOWRRGLWAQRPHDSAQL
LTGRAFGATVGLAPVEGMCRASSGGVSTDHSELPIGAAATMAHEIGHSLGLSHDPDGCCVEAAAESGGCVMAA
ATGHPFPRVFSACSRRLRAFFRKGGGACLSNAPDPGLPVPPALCGNGFVEAGEECDGPGQECRDLCCFAHNCS
LRPGAQCAHGDCCVRCLLKPAGALCRQAMGDCDLPEFCTGTSSHCPPDVYLLDGSPCARGSGYCWDGACPTLEQQ
CQQLWGPSPGSHPAPEACFQVNSAGDAHGNCQDSEGFLPCAGRDALCGKLQCQGGKPSLLAPHMVPVDSTVHLD
GQEVTCRGALALPSAQLDLLGLGLVEPGTQCGPRMVCQSRRCRKNAFQELQRCITACHSHGVCNSNHNCHCAPGW
APFFCDKPGFGGSMDSGPVQAENHDTFLLAMLLSVLLPLLPAGLAWCCYRLPGAHLQRCSWGCCRDPACSGPKD
GPHRDHPLGGVHPMELGPTATGQPWFLDPENSHEPSSHPEKPLPAVSPDPQADQVQMPRSLW

Important features of the protein:**Signal peptide:**

Amino acids 1-27

Transmembrane domain:

Amino acids 702-720

N-glycosylation sites:

Amino acids 109-113;145-149;231-235;276-280;448-452

Tyrosine kinase phosphorylation site:

Amino acids 236-244

N-myristoylation sites:

Amino acids 29-35;185-191;195-201;308-314;318-324;326-332;338-344;370-376;
400-406;402-408;454-460;504-510;510-516;517-523;580-586;
601-607;661-667;687-693;717-723;719-725

Amidation site:

Amino acids 200-204

Neutral zinc metalloproteinases, zinc-binding region signature:

Amino acids 342-352

FIGURE 467

[illegible]

472/615

FIGURE 468

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77623

><subunit 1 of 1, 97 aa, 1 stop

><MW: 10160, pI: 6.56, NX(S/T): 0

MQLGTGLLLAAVLSLQLAAAEAIWCHQCTGFGGCSHGSRCLRDSTHCVTATRVLSNTEDLPL

VTKMCHIGCPDIPSLGLGPYYSIACCQTSLCNHD

Important features of the protein:**Signal peptide:**

amino acids 1-20

N-myristoylation sites.

amino acids 6-11 and 33-38

Prokaryotic membrane lipoprotein lipid attachment sites.

amino acids 24-34 and 78-88

473/615

FIGURE 469

CATGGAGCCTCTTGCAGCTTACCCGCTAAAATGTTCCGGGCCCAGAGCAAAGGTATTTGCAGT
TTTGCTGTCTATAGTTCTATGCACAGTAACGCTATTTCTTCTACAACATAAAATTCCTCAAACC
TAAAATCAACAGCTTTTATGCCTTTGAAGTGAAGGATGCAAAAGGAAGAACTGTTTCTCTGGA
AAAGTATAAAGGCAAAGTTTCACTAGTTGTAAACGTGGCCAGTGACTGCCAACTCACAGACAG
AAATTACTTAGGGCTGAAGGAAGTGCACAAAGAGTTTGGACCATCCCACTTCAGCGTGTGGC
TTTTCCCTGCAATCAGTTTGGAGAATCGGAGCCCCGCCAAGCAAGGAAGTAGAATCTTTTGC
AAGAAAAAACTACGGAGTAACTTTCCCATCTTCCACAAGATTAAGATTCTAGGATCTGAAGG
AGAACCTGCATTTAGATTTCTTGTTGATTCTTCAAAGAAGGAACCAAGGTGGAATTTTGGAA
GTATCTTGTCAACCCTGAGGGTCAAGTTGTGAAGTTCTGGAGGCCAGAGGAGCCCATTTGAAGT
CATCAGGCCTGACATAGCAGCTCTGGTTAGACAAGTGATCATAAAAAAGAAAGAGGATCTATG
AGAATGCCATTGCGTTTCTAATAGAACAGAGAAATGTCTCCATGAGGGTTTGGTCTCATTTTA
AACATTTTTTTTTTGGAGACAGTGTCTCACTCTGTCACCCAGGCTGGAGTGCAGTAGTGCCTT
CTCAGCTCATTGCAACCTCTGCCTTTTTTAAACATGCTATTAAATGTGGCAATGAAGGATTTT
TTTTAATGTTATCTTGCTATTAGTGGTAATGAATGTTCCCAGGATGAGGATGTTACCCAAAG
CAAAAATCAAGAGTAGCCAAAGAATCAACATGAAATATATTAATACTACTTCCTCTGACCATACT
AAAGAATTCAGAATACACAGTGACCAATGTGCCTCAATATCTTATTGTTCAACTTGACATTTT
CTAGGACTGTACTTGATGAAAATGCCAACACACTAGACCACTCTTTGGATTCAAGAGCACTGT
GTATGACTGAAATTTCTGGAATAACTGTAAATGGTTATGTTAATGGAATAAACACAAATGTT
GAAAAATGTAAATATATATACATAGATTCAAATCCTTATATATGTATGCTTGTTTTGTGTAC
AGGATTTTGTTTTTTCTTTTTAAGTACAGGTTCCTAGTGTTTTACTATAACTGTCACATATGTA
TGTAAGTACATATATAAATAGTCATTTATAAATGACCGTATTATAACATTTGAAAAAGTCTT
CATCAAAAAAAAAAAAAA

474/615

FIGURE 470

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA80136
><subunit 1 of 1, 209 aa, 1 stop
><MW: 23909, pI: 9.68, NX(S/T): 0
MEPLAAYPLKCSGPRAKVFAVLLSIVLCTVTLFLLQLKFLKPKINSFYAFEVKDAKGRTVSLE
KYKGKVSILVNVASDCQLTDRNYLGLKELHKEFGPSHFSVLAFPCNQFGESEPRPSKEVESFA
RKNYGVTFPIFHKIKILGSEGEPAFRFLVDSSKKEPRWNFWKYLVNPEGQVVKFWRPEEPIEV
IRPDIAALVRQVVIKKKEDL

Important features of the protein:**Signal peptide:**

amino acids 1-31

Glutathione peroxidases signature 2.

amino acids 104-112

Glutathione peroxidases.

amino acids 57-82

475/615

FIGURE 471

GCCCTAACCTTCCCAGGGCTCAGCTCTTTGGAGCTGCCATTCTCCGGCTGCGAGAAAGGACGCGCGCCCTGCG
TCGGGCGAAGAAAAGAAGCAAACTTGTGCGGAGGGTTTCGTCAATCAACCTCCTTCCCAGCAACCTAAACCTCCT
GCCGGGGCCATCCCTAGACAGAGGAAAGTTCTGCGAGAGCCGACCAGCCCTAGTGGATCTGGGGCAGGCAGCGGC
GCTGGCTGTGGAATTAGATCTGTTTTGAACCCAGTGGAGCGCATCGCTGGGGCTCGGAAGTCAACGTCGCGGGC
ACCGGGTTGGCGCTGCCGAGTGAACCGACAGTTTGGCAGCCTCGGCTGCAAGTGGCCTCTCCTCCCCGCGGTT
GTTGTTCACTGTCGGGTGAGGGCTGCGAGTGTGGCAAGTTGCAAAGAGAGCCTCAGAGGTCCGAAGAGCGCTGCG
CTCCTACTCGCGTTGCTTCTTCTCTCGGTTCCCTACTGTGAAATCGCAGCGACATTTACAAAGGCCTCCG
GGTCTACCGAGACCGATCCGAGCGTTTGGCCCGGTCGTGCCTATTGCATCGGGAGCCCCGAGCACCGGCGAA
GGACTGGCGGGTGGGGTAGGGAGGTGGCGGCGGGCAGTGGCGAGGTTCCCGAAGGCCGACCTGGCCGCTGCAGG
AGTTATGTTACTTTGCCACTTCTTCACGGACAGTTTCAGTTTCGCGGATGGGAAACCCGAGACCAATCCTTGA
TTGGCAGTATGGAGTTACTCAGGCCTTCCCTCACACAGAGGAGGAGGTGGAAGTTGATTCACACGCGTACAGCCA
CAGGTGGAAAAGAACTTGGACTTCTCAAGGCGGTAGACACGAACCGAGCAAGCGTCGGCCAGAGCTCTCCTGA
GCCCAGAAGCTTCACAGACCTGCTGCTGGATGATGGGCAGGACAATAACACTCAGATCGAGGAGGATACAGACCA
CAATTACTATATATCTGAATATATGTCATCTGATTTCTGCCAGCCGGGATTTATGGGTGAACATAGACCAAAT
GGAAAAAGATAAAGTGAAGATTCATGGAATATTGTCCAATACTCATCGGCAAGCTGCAAGAGTGAATCTGTCTT
CGATTTTCCATTTTATGGCCACTTCTACGTGAAATCACTGTGGCAACCGGGGGTTTCATATACACTGGAGAAGT
CGTACATCGAATGCTAACAGCCACACAGTACATAGCACCTTTAATGGCAAATTTGATCCCAGTGTATCCAGAAA
TTCAACTGTCAGATATTTTGATAATGGCACAGCACTTGTGGTCCAGTGGGACCATGTACATCTCCAGGATAATTA
TAACCTGGGAAGCTTCACATTCCAGGCAACCTGCTCATGGATGGACGAATCATCTTTGGATACAAAGAAATTC
TGTCTTGGTCACACAGATAAGTTCAACCAATCATCCAGTGAAAGTCGGACTGTCCGATGCATTTGTGCTGTCCA
CAGGATCCAACAAATTTCCAATGTTGGAAGAAGAACAATTTATGAATACCACCGAGTAGAGCTACAAATGTCAA
AATTACCAACATTTTCGGCTGTGGAGATGACCCCATTTACCCACATGCCTCCAGTTTAACAGATGTGGCCCTGTGT
ATCTTCTCAGATTGGCTTCACTGCAGTTGGTGTAGTAACTTCAAAGATGTTCCAGTGGATTTGATCGTCATCG
GCAGGACTGGTGGACAGTGGATGCCCTGAAGAGTCAAAGAGAAGATGTGTGAGAATACAGAACCAGTGGAAAC
TTCTTCTCGAACCACCACAACCGTAGGAGCGACAACCACCCAGTTTCAGGGTCTTAACCTACCACCAGAAGAGCAGT
GACTTCTCAGTTTCCCACCAGCCTCCCTACAGAAGATGATACCAAGATAGCACTACATCTAAAAGATAATGGAGC
TTCTACAGATGACAGTGCAGCTGAGAAGAAAGGGGAACCTCCACGCTGGCCTCATCTTGGAAATCCTCATCCT
GGTCTCATTTAGCCACAGCCATTCTTGTGACAGTCTATATGTATCACCACCCAAACATCAGCAGCCAGCATCTT
CTTTATTGAGAGACGCCCCAAGCAGATGGCCTGCGATGAAGTTTGAAGAGGCTCTGGACATCTGCTATGCTGA
AGTTGAACCAAGTTGGAGAGAAAGAAGGCTTTATTGTATCAGAGCAGTGTAAATTTCTAGGACAGAAACACACC
AGTACTGGTTTACAGGTGTTAAGACTAAATTTTGCCTATACCTTTAAGACAAACAAACACACACACAAAC
AAGCTCTAAGCTGCTGTAGCCTGAAGAAGACAAGATTTCTGGACAAGCTCAGCCAGGAAACAAAGGGTAAACAA
AAAATAAACTTATACAAGATACCATTTACACTGACATAGAATTCCTAGTGAATGTCTCTATAGTTCACT
CGGAACATCTCCCGTGGACTTATCTGAAGTATGACAAGATTATAATGCTTTTGGCTTAGGTGCAGGGTTGCAAAG
GGATCAGAAAAAAAATCATAATAAGCTTTAGTTTCATGAGG

476/615

FIGURE 472

MARFPKADLAAAGVMLLCHFFTDQFQFADGKPGDQILDWQYGVQTQAFPHTEEEVEVD SHAYSH
RWKRNLDFLKAVDTNRASVGQDSPEPRSFTDLLDDGQDNNTQIEEDTDHNYISRIYGPSDS
ASRDLWVNIDQMEKDKVKIHGILSNTHRQAARVNLSFDFFPYGHFLREITVATGGFIYTGEVV
HRMLTATQYIAPLMANFDPSVSRNSTVRYFDNGTALVVQWDHVHLQDNYNLGSFTFQATLLMD
GRIIFGYKEIPVLVTQISSTNHPVKVGLSDAFVVVHRIQQIPNVRRTIYEHYHVELQMSKIT
NISAVEMTPLPTCLQFNRCGPCVSSQIGFNCWSCSKLQRCSSGFDRHRQDWVDSGCPEESKEK
MCENTEPVETSSRTTTTGVGATTTQFRVLTTRRAVTSQFPTSLPTEDDTKIALHLKDNGASTD
DSAAEKKGGTLHAGLIIGILILVLIVATAILVTVMYHHPTSAAASIFFIERRPSRWPAMKFRR
GSGHPAYAEVEPVGEKEGFIVSEQC

Important features of the protein:**Transmembrane domain:**

amino acids 454-478

N-glycosylation sites.

amino acids 103-107, 160-164, 213-217, 221-225, 316-320, 345-349

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 297-301, 492-496, 503-507

N-myristoylation sites.amino acids 42-48, 100-106, 147-153, 279-285, 397-403, 450-456,
455-461

477/615

FIGURE 473

CGCGGAGCCCTGCGCTGGGAGGTGCACGGTGTGCACGCTGGACTGGACCCCATGCAACCCCG
CGCCCTGCGCCTTAACCAGGACTGCTCCGCGCGCCCTGAGCCTCGGGCTCCGGCCCGGACCT
GCAGCCTCCCAGGTGGCTGGGAAGAACTCTCCAACAATAAATACATTTGATAAGAAAGATGGC
TTTAAAGTGTACTAGAACAAAGAGAAAACGTTTTTCACTCTTTTAGTATTACTAGGCTATTT
GTCATGTAAAGTGAAGTGTGAATCAGGAGACTGTAGACAGCAAGAATTCAGGGATCGGTCTGG
AAACTGTGTTCCCTGCAACCAAGTGTGGGCCAGGCATGGAGTTGTCTAAGGAATGTGGCTTCGGC
TATGGGGAGGATGCACAGTGTGTGACGTGCCGGCTGCACAGGTTCAAGGAGGACTGGGGCTTC
CAGAAATGCAAGCCCTGTCTGGACTGCGCAGTGGTGAACCGCTTTCAGAAGGCAAATTTGTTCA
GCCACCAAGTATGCCATCTGCGGGGACTGCTTGCCAGGATTTTATAGGAAGACGAACTTGTG
GGCTTTCAGACATGGAGTGTGTGCCTTGTGGAGACCCCTCCTCCTTACGAACCGCACTGT
GCCAGCAAGGTCAACCTCGTGAAGATCGCGTCCACGGCCTCCAGCCCACGGGACACGGCGCTG
GCTGCCGTTATCTGCAGCGCTCTGGCCACCGTCTGCTGGCCCTGCTCATCCTCTGTGTCATC
TATTGTAAGAGACAGTTTATGGAGAAGAAACCCAGCTGGTCTCTGCGGTCGCAGGACATTCAG
TACAACGGCTCTGAGCTGTGCTGTTTGTACAGACCTCAGCTCCACGAATATGCCCACAGAGCC
TGCTGCCAGTGCCGCCGTGACTCAGTGCAGACCTGCGGGCCGGTGCCTGCTCCCATCCATG
TGCTGTGAGGAGGCTGCAGCCCCAACCCGGCAGCTCTTGGTTGTGGGGTGCATTCTGCAGCC
AGTCTTCAGGCAAGAAACGCAGGCCCAGCCGGGAGATGGTGCCGACTTCTTTCGGATCCCTC
ACGCAGTCCATCTGTGGCGAGTTTTCAGATGCCTGGCCTCTGATGCAGAATCCCATGGGTGGT
GACAACATCTCTTTTTGTGACTCTTATCCTGAACCTCACTGGAGAAGACATTCATTCTCTCAAT
CCAGAACTTGAAAGCTCAACGTCTTTGGATTCAAATAGCAGTCAAGATTTGGTTGGTGGGGCT
GTTCCAGTCCAGTCTCATTCTGAAAACTTTACAGCAGCTACTGATTTATCTAGATATAACAAC
ACACTGGTAGAATCAGCATCAACTCAGGATGCACTAACTATGAGAAGCCAGCTAGATCAGGAG
AGTGGCGCTGTCATCCACCCAGCCACTCAGACGTCCCTCCAGGAAGCTTAAAGAACCTGCTTC
TTTCTGCAGTAGAAGCGTGTGCTGGAACCCAAAGAGTACTCCTTTGTTAGGCTTATGGACTGA
GCAGTCTGGACCTTGTCATGGCTTCTGGGGCAAAAATAAATCTGAACCAAACCTGACGGCATTG
AAGCCTTTCAGCCAGTTGCTTCTGAGCCAGACCAGCTGTAAGCTGAAACCTCAATGAATAACA
AGAAAAGACTCCAGGCCGACTCATGATACTCTGCATCTTTCCTACATGAGAAGCTTCTCTGCCAC
AAAAGTGACTTCAAAGACTGATGGGTGAGCTGGCAGCCTATGAGATTGTGGACATATAACAA
GAAACAGAAATGCCCTCATGCTTATTTTCATGGTGATTGTGGTTTTACAAGACTGAAGACCCA
GAGTATACTTTTTCTTCCAGAAATAATTTATACCGCCTATGAAATATCAGATAAATTACCT
TAGCTTTTATGTAGAATGGGTTCAAAAGTGAAGTGTCTTATTTGAGAAGGACACTTTTTCATC
ATCTAAACTGATTGCGCATAGGTGGTTAGAATGGCCCTCATATTGCCTGCCTAAATCTTGGGT
TATTAGATGAAGTTTACTGAATCAGAGGAATCAGACAGAGGAGGATAGCTCTTTCAGAAATCC
ACACTTCTGACCTCAGCCTCGGTCTCATGAACACCCGCTGATCTCAGGAGAACACCTGGGCTA
GGGAATGTGGTGCAGAAAGGGCAGCCCATTTGCCAGAAATTAACACATATTGTAGAGACTTGTA
TGCAAAGGTTGGCATATTTATATGAAAATTAGTTGCTATAGAAACATTTGTTGCATCTGTCCC
TCTGCCTGAGCTTAGAAGGTTATAGAAAAAGGGTATTTATAAACATAAATGACCTTTTACTTG
CATTGTATCTTATACTAAAGGCTTTAGAAATTACAACATATCAGGTTCCCTACTACTGAAGT
AGCCTTCCGTGAGAACACACCACATGTTAGGACTAGAAGAAAATGCACAATTTGTAGGGGTTT
GGATGAAGCAGCTGTAACCTGCTTAGTGTAGTTTGAACAGGACATTGTCGTGCTCCTTCCAAT
TGTGTAAGATTAGTTAGCACATCATCTCCTACTTTAGCCATCCGGTGTGGATTTAAGAGGAC
GGTGCTTCTTTCTATTAAAGTGCTCCATCCCCCTACCATCTACACATTAGCATTGTCTCTAGAG
CTAAGACAGAAATTAACCCCGTTCAAGTCAAAAGCAGGGAATGGTTCAATTTACTCTTAATCTT
TATGCCCTGGAGAAGACCTACTTGAACAGGGCATATTTTTTAGACTTCTGAACATCAGTATGT
TCGAGGGTACTATGATATTTTGGTTTGGAAATGGCCCTGCCCAAGTCACTGTCTTTTAACTTTT
AAACTGAATATTAAATGTATCTGTCTTTCCT

478/615

FIGURE 474

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84210
><subunit 1 of 1, 417 aa, 1 stop
><MW: 45305, pI: 5.12, NX(S/T): 6
MALKVLLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQOQEFRDRSGNCVPCNQCGPGMELSK
ECGFGYGEDAQCVTCLHRFKEDWGFQKCKPCLDCAVVNRFOKANCSATSDAICGDCLPG
FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT
VLLALLILCVIYCKRQFMKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD
SVQTCGPVRLLPSCCEEACSPNPATLGC GVHSAASLQARNAGPAGEMVPTFFGSLTQSI
CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV
PVQSHSENFATAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQEA
```

Important features of the protein:**Signal peptide:**

Amino acids 1-25

Transmembrane domain:

Amino acids 169-192

N-glycosylation sites:

Amino acids 105-109;214-218;319-323;350-354;368-372;379-383

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 200-204;238-242

Tyrosine kinase phosphorylation site:

Amino acids 207-214

N-myristoylation sites:

Amino acids 55-61;215-221;270-276

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 259-270

TNFR/NGFR family cysteine-rich region proteins:

Amino acids 89-96

479/615

FIGURE 475

AGCCAGGCAGCACATCACAGCGGGAGGAGCTGTCCCAGGTGGCCCAGCTCAGCAATGGCAATG
GGGGTCCCCAGAGTCATTCTGCTCTGCCTCTTTGGGGCTGCGCTCTGCCTGACAGGGTCCCAA
GCCCTGCAGTGCTACAGCTTTGAGCACACCTACTTTGGCCCCTTTGACCTCAGGGCCATGAAG
CTGCCCAGCATCTCCTGTCCTCATGAGTGCTTTGAGGCTATCCTGTCTCTGGACACCGGGTAT
CGCGCGCCGGTGACCCTGGTGCGGAAGGGCTGCTGGACCGGGCCTCCTGCGGGCCAGACGCAA
TCGAACCCGGACGCGCTGCCGCCAGACTACTCGGTGGTGCGCGGCTGCACAACTGACAAATGC
AACGCCCACCTCATGACTCATGACGCCCTCCCCAACCTGAGCCAAGCACCCGACCCGCCGACG
CTCAGCGGGCGCCGAGTGCTACGCCTGTATCGGGGTCCACCAGGATGACTGCGCTATCGGCAGG
TCCCGACGAGTCCAGTGTCACCAGGACCAGACCGCCTGCTTCCAGGGCAGTGGCAGAATGACA
GTTGGCAATTTCTCAGTCCCTGTGTACATCAGAACCTGCCACCGGCCCTCCTGCACCACCGAG
GGCACCACCAGCCCCTGGACAGCCATCGACCTCCAGGGCTCCTGCTGTGAGGGGTACCTCTGC
AACAGGAAATCCATGACCCAGCCCTTCACCAGTGCTTCAGCCACCACCCCTCCCCGAGCACTA
CAGGTCTTGGCCCTGCTCCTCCCAGTCCTCCTGCTGGTGCGGCTCTCAGCATAGACCGCCCCT
CCAGGATGCTGGGGACAGGGCTCACACACCTCATTCTTGCTGCTTCAGCCCCCTATCA[^]CATAGC
TCACTGGAAAATGATGTTAAAGTAAGAATTGCAAAA

480/615

FIGURE 476

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA86576
><subunit 1 of 1, 251 aa, 1 stop
><MW: 26935, pI: 7.42, NX(S/T): 2
MAMGVPRVILLCLFGAALCLTGSQALQCYSFEHTYFGPFDLRAMKLPSISCPHECFEAILSLD
TGYRAPVTILVRKGCWTGPPAGQTQSNPDALPPDYSVVRGCTTDKCNAHLMTHDALPNLSQAPD
PPTLSGAECYACIGVHQDDCAIGRSRRVQCHQDQTACFQSGRMTVGNFSPVYIRTCHRPSC
TTEGTTSPWTAIDLQSCCEGYLCNRKSMTQPFTSASATTPPRALQVLALLLPVLLLVGLSA

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 233-251

N-glycosylation sites.

amino acids 120-124, 174-178

N-myristoylation sites.

amino acids 15-21, 84-90

481/615

FIGURE 477

CCCACGCGTCCGGGACAGATGAACTTAAAAGAGAAGCTTTAGCTGCCAAAGATTGGGAAAGGGAAAGGACAAAA
AGACCCCTGGGCTACACGGCGTAGGTGCAGGGTTTCTACTGCTGTTCTTTTATGCTGGGAGCTGTGGCTGTAAAC
CAACTAGGAAATAACGTATGCAGCAGCTATGGCTGTGAGAGAGTTGTGCTTCCCAAGACAAAGGCAAGTCTGT
TCTTTTTCTTTTTTGGGGAGTGTCTTGGCAGGTCTGGGTTTGGACGTTATTTCGGTGACTGAGGAAACAGAGAA
AGGATCCTTTGTGGTCAATCTGGCAAAGGATCTGGGACTAGCAGAGGGGGAGCTGGCTGCAAGGGGAACCAAGGT
GGTTCCGATGATAACAAACAATACTGCTCCTGGATTACATACCGGAATTTGCTCACAAATGAGAACTGGA
CCGAGAGAAGCTGTGTGGCCCTAAAGAGCCCTGTATGCTGTATTTCCAAATTTTAAATGGATGATCCCTTTT
TTACCGGGCTGAGCTGAGAGTCAGGGATATAAATGATCAGCGCCAGTATTTTCCAGGACAAAGAAACAGTCTTAA
AATATCAGAAAATACAGCTGAAGGGACAGCATTTAGACTAGAAAGAGCACAGGATCCAGATGGAGGACTTAACGG
TATCCAAAACCTACACGATCAGCCCCAACTCTTTTCCATATTAACATTAGTGGCGGTGATGAAGGCATGATATA
TCCAGAGCTAGTGTGGACAAAGCACTGGATCGGGAGGAGCAGGGAGAGCTCAGCTTAACCTCACAGCGCTGGA
TGGTGGGTCTCCATCCAGGTCTGGGACCTCTACTGTACGCATCGTTGTCTTGGACGTCAATGACAATGCCACACA
GTTTGGCCAGGCTCTGTATGAGACCCAGGCTCCAGAAAACAGCCCCATTGGGTTCTTATTGTTAAGGTATGGGC
AGAAGATGTAGACTCTGGAGTCAACGCGGAAGTATCCTATTCTTTTTTGTGCTCAGAAAATATTGGAACGAC
CTTTCAAATCAATCCTTTTTCTGGGGAAATCTTTCTCAGAGAAATGCTTGATTATGAGTTAGTAAATTTTACAA
AATAAATATACAGGCAATGGACGGTGGAGGCCCTTTCTGCAAGATGTAGGGTTTTAGTGGAAAGTATTGGACACCAA
TGACAATCCCCCTGAACCTGATCGTATCATCATTTTCCAACCTCTGTGCTGAGAATCTCTGAGACGCGCTGGC
TGTTTTTAAGATTAATGACAGAGACTCTGGAGAAAATGGAAGATGGTTTTGCTACATTCAAGAGAATCTGCCATT
CCTACTAAAACCTTCTGTGGAGAATTTTACATCCTAATTACAGAAGGCGCGCTGGACAGAGAGATCAGAGCCGA
GTACAACATCACTATCACCCTCACTGACTTGGGGACACCCAGGCTGAAAACCGAGCACAACATAACGGTCTGGT
CTCCGACGTCAATGACAACGCCCCCGCCTTACCCCAAACCTCCTACACCCTGTTCTGTCGCGGAGAACACAGCCC
CGCCTGCACATCGGCAGCGTCAAGCGCCACAGACAGAGACTCGGGACCAACGCCCAGGTCACTACTCGCTGCT
GCCGCCCCAAGACCCGCACCTGCCCTCGCCTCCCTGGTCTCCATCAACGCGGACACAGGCCACCTGTTCCGCCCT
CAGGTGCTGACTACGAGGCCCTGCAGGCTTTCAGTTCGCGTGGGCGCCACAGACCGCGGCTCCCCCGCGCT
GAGCAGAGAGGCGCTGGTGCAGCTGCTGGTGTGACGCCAACGACAACCTCGCCCTTCGTGCTGTACCCGCTGCA
GAACGGCTCCGCGCCCTGCACCGAGCTGGTGGCCCGGGCGGCCGAGCCGGGCTACCTGGTGACCAAGGTGGTGGC
GGTGGACGGCGACTCGGGCCAGAACGCCCTGGCTGTCTACAGCTGCTCAAGGCCACGGAGCCCCGGGCTGTTCCG
TGTGTGGGCGCACAATGGGAGGTGCGCACCGCCAGGCTGCTGAGCGAGCGGACGCGAGCCAAGCACAGGCTCGT
GGTGTCTGTCAAGGACAATGGCGAGCCTCCTCGCTCGGCCACCGCCACGCTGCACTTGTCTCTGTTGGACGGCTT
CTCCAGCCCTACCTGCCTCTCCCGAGGCGGCCCCGGGCCAGGCCAGGCCGAGGCCGACTTGCTCACCCTCTA
CCTGGTGGTGGCGTTGGCCTCGGTGTCTTCGCTCTTCTCCTCTCGGTGCTCCTGTTCTGTCGGGTGCGGCTGTG
CAGGAGGAGCAGGGCGGCCCTCGGTGGGTGCTGCTCGGTGCCCCAGGGTCTTTTCCAGGGCATCTGGTGGACGT
GAGGGGCGCTGAGACCTGTCCAGAGCTACCAGTATGAGGTGTGTCTGACGGGAGGCCCGGGACCATGAGTT
CAAGTTCTTGAACACAGTTATTTCCGATATTACAGGCACAGGGCCCTGGGAGGAAGGGTGAAGAAAATTTCCACCTT
CCGAAATAGCTTTGGATTTAATATTCAGTAAAGTCTGTTTTAGTTTTCATATACTTTTGGTGTGTTACATAGCCA
TGTTTCTATTAGTTTACTTTTAAATCTCAAATTTAAGTTATTTATGCAACTTCAAGCATTATTTTCAAGTAGTATA
CCCCTGTGGTTTTACAATGTTTCATCATTTTTTGCATTAATAACAACCTGGGTTTTAATTTAATGAGTATTTTTT
CTAAATGATAGTGTAAAGTTTTAATTCTTTCCAACCTGCCAAGGAATTAATTACTATTATATCTCATACAGAA
ATCTGAGGTTTTGATTCATTTTCAAGCTTGCATCTCATGATTCTAATCACTTCTGTCTATAGTGTACTTGTCTTA
TTAAGAAGGCATATCTACATTTCCAACTCATTCTAACATTCTATATATTCTGTTTGAACCATGTCATTTA
TTTCTACATCATGTATTTAAAAAGAAATATTTCTCTACTACTATGCTCATGACAAAATGAACAAAGCATATTGT
GAGCAATACTGAACATCAATAATACCCTTAGTTTATATACTTATTATTTTATCTTTAAGCATGCTACTTTTACTT
GGCCAATATTTCTTATGTTAACTTTTGTGATGTATAAAACAGACTATGCCTTATAATTGAATAAAATATATA
TCTGCCTGAAAATGAATAAAATAAAACATTTTGAATGTGAAAAAAAAAAAAAAAAAAAAA

482/615

FIGURE 478

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA87976
><subunit 1 of 1, 800 aa, 1 stop
><MW: 87621, pI: 4.77, NX(S/T): 7
MAVRELCFPRQRQVLFLFLFWGVSLAGSGFGGRYSVTEETEKGSFVVNLAKDLGLAEGELAARG
TRVVSDDNKQYLLLDSTHTGNLLTNEKLDREKLCGPKEPCMLYFQILMDDPFQIYRAELRVRDI
NDHAPVFQDKETVLKISENTAEGTAFRLERAQDPDGLNGIQNYTISPNSFFHINISGGDEGM
IYPELVLDKALDREEQGELSLLTALDGGSPSRSGTSTVRIVVLDVNDNAPQFAQALYETQAP
ENSPIGFLIVKVWAEDVDSGVNAEVSYSFFDASENIRTTTFQINPFSGEIFLRELLDYELVNSY
KINIQAMDGGGLSARCRVLVEVLDTNDNPPELIVSSFSNSVAENSPETPLAVFKINDRDSGEN
GKMVCYIQENLPFLKPSVENFYILITEGALDREIRAEYNITITVTDLGTPLRKTEHNITVLV
SDVNDNAPAFQTSTYTLFVRENNSPALHIGSVSATDRDSGTNAQVTYSLLPQDPEHLPLASLV
SINADNGHLFALRSLDYELQAFEFVRVGATDRGSPALSREALVRVLVLDANDNSPFVLYPLQN
GSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKATEPGLFGVWAHNGEVRTARLL
SERDAAKHRLVVLVKDNGEPPRSATATLHLLLVDGFSQPYLPLPEAAPAQAEADLLTVYLV
VALASVSSLFLLSVLLFVAVRLCRRSRAASVGRCSVPEGPFPGLVDVRGAETLSQSYQYEVC
LTGGPGTSEFKFLKPVISDIQAQGPGRKGEENSTERNSEFGFNIQ

Important features of the protein:**Signal peptide:**

amino acids 1-26

Transmembrane domain:

amino acids 687-711

N-glycosylation sites.

amino acids 169-173, 181-185, 418-422, 436-440, 567-571, 788-792

Glycosaminoglycan attachment site.

amino acids 28-32

Tyrosine kinase phosphorylation sites.

amino acids 394-402, 578-585

N-myristoylation sites.amino acids 22-28, 27-33, 53-59, 82-88, 162-168, 184-190,
217-223, 324-330, 325-331, 471-477, 568-574, 759-765**Amidation site.**

amino acids 781-785

Aminoacyl-transfer RNA synthetases class-II signature 1.

amino acids 117-138

Cadherins extracellular repeated domain signature.

amino acids 121-132, 230-241, 335-346, 439-450, 549-560

483/615

FIGURE 479

CTCGGCTGGATTTAAGGTTGCCGCTAGCCGCCTGGGAATTTAAGGGACCCACACTACCTTCCC
GAAGTTGAAGGCAAGCGGTGATTGTTTGTAGACGGCGCTTTGTCT**AT**GGGACCTGTGCGGTTGG
GAATATTGCTTTTTCCTTTTTTTTGGCCGTGCACGAGGCTTGGGCTGGGATGTTGAAGGAGGAGG
ACGATGACACAGAACGCTTGCCGAGCAAATGCGAAGTGTGTAAGCTGCTGAGCACAGAGCTAC
AGGCGGAACAGAGTCGCACCGGTGATCTCGAGAGGTGCTGGAGCTGGGGCAGGTGCTGGATA
CAGGCAAGAGGAAGAGACACGTGCCTTACAGCGTTTCAGAGACAAGGCTGGAAGAGGCCTTAG
AGAATTTATGTGAGCGGATCCTGGACTATAGTGTTCACGCTGAGCGCAAGGGCTCACTGAGAT
ATGCCAAGGGTCAGAGTCAGACCATGGCAACACTGAAAGGCCTAGTGCAGAAGGGGGTGAAGG
TGGATCTGGGGATCCCTCTGGAGCTTTGGGATGAGCCCAGCGTGGAGGTCACATACCTCAAGA
AGCAGTGTGAGACCATGTTGGAGGAGTTTGAAGACATTGTGGGAGACTGGTACTTCCACCATC
AGGAGCAGCCCCCTACAAAATTTTCTCTGTGAAGGTCATGTGCTCCAGCTGCTGAAACTGCAT
GTCTACAGGAAACTTGGACTGGAAAGGAGATCACAGATGGGGAAGAGAAAACAGAAGGGGAGG
AAGAGCAGGAGGAGGAGGAGGAAGAGGAGGAAGAGGAAGGGGGAGACAAGATGACCAAGACAG
GAAGCCACCCCAAACCTTGACCGAGAAGATCTTT**TGA**CCCTTGCCCTTTGAGCCCCCAGGAGGGGA
AGGGATCATGGAGAGCCCTCTAAAGCCTGCACTCTCCCTGCTCCACAGCTTTCAGGGTGTGTT
TATGAGTGAATCCACCCAAGCTTGTAGCTGTTCTCTCCCATCTAACCTCAGGCAAGATCCTGG
TGAAACAGCATGACATGGCTTCTGGGGTGGAGGGTGGGGGTGGAGGTCTGCTCCTAGAGATG
AACTCTATCCAGCCCCTTAATTGGCAGGTGTATGTGCTGACAGTACTGAAAGCTTTCTCTTTT
AACTGATCCACCCCCACCCAAAAGTCAGCAGTGGCACTGGAGCTGTGGGCTTTGGGGAAGTC
ACTTAGCTCCTTAAGGTCTGTTTTTAGACCTTCCAAGGAAGAGGCCAGAACGGACATTCTCT
GCGATCTATATACATTGCCTGTATCCAGGAGGCTACACACCAGCAAACCGTGAAGGAGAATGG
GACACTGGGTGATGGCCTGGAGTTGCTGATAATTTAGGTGGGATAGATACTTGGTCTACTTAA
GCTCAATGTAACCCAGAGCCCACCATATAGTTTTATAGGTGCTCAACTTTCTATATCGCTATT
AACTTTTTTCTTTTTTTCTA

484/615

FIGURE 480

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92256
><subunit 1 of 1, 248 aa, 1 stop
><MW: 28310, pI: 4.63, NX(S/T): 0
MGPVRLGILLFLFLAVHEAWAGMLKEEDDDTERLPSKCEVCKLLSTELQAELSRTGRSREVLE
LGQVLDTGKRKRHPYPSVSETRLEEALNLCERILDYSVHAERKGSRLRYAKGQSQTMATLKGL
VQKGVKVDLGIPLELWDEPSVEVTYLKKQCETMLEEFEDIVGDWYFHHQEQPLQNFLCEGHVL
PAAETACLQETWTGKEITDGEEKTEGEEEEEEEEEEEEEGGDKMTKTGSHPKLDREDL

Important features of the protein:

Signal peptide:

amino acids 1-21

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 106-110

N-myristoylation site.

amino acids 115-121

Amidation site.

amino acids 70-74

485/615

FIGURE 481

GGCGTGTGCAAGGCGGGGTCCGGCCCGCGCAGGTCGGGTAAGCGCGTCTAGGGCGCTGCGCGG
CGCAGCGAAAA**ATG**GCGGCTTCCAGGTGGGCGCGCAAGGCCGTGGTCTGCTTTGTGCCTCTGA
CCTGCTGCTGCTGCTGCTACTGCTACCACCGCCTGGGTCTGCGCGGCCGAAGGCTCGCCCGG
GACGCCCCGACGAGTCTACCCACCTCCCCGGAAGAAGAAGGATATTGCGGATTACAATGA
TGCAGACATGGCGCGTCTTCTGGAGCAATGGGAGAAAGATGATGACATTGAAGAAGGAGATCT
TCCAGAGCACAAGAGACCTTCAGCACCTGTCGACTTCTCAAAGATAGACCCAAGCAAGCCTGA
AAGCATATTGAAAATGACGAAAAAAGGAAGACTCTCATGATGTTTGTCACTGTATCAGGAAG
CCCTACTGAGAAGGAGACAGAGGAAATTACGAGCCTCTGGCAGGGCAGCCTTTTCAATGCCAA
CTATGACGTCCAGAGGTTCAATTGTGGGATCAGACCGTGCTATCTTCATGCTTCGCGATGGGAG
CTACGCTGGGAGATCAAGGACTTTTTGGTCTGGTCAAGACAGGTGTGCTGATGTAACCTCTGGA
GGGCCAGGTGTACCCCGGCAAAGGAGGAGGAAGCAAAGAGAAAAATAAACAAAGCAAGACAA
GGGCAAAAAAAGAAGGAAGGAGATCTGAAATCTCGGTCTTCCAAGGAAGAAAATCGAGCTGG
GAATAAAAGAGAAGACCTG**TGAT**GGGGCAGCAGTGACGCGCTGTGGGGGGACAGGTGGACGTG
GAGAGCTCTTTGCCAGCTCCTGGGGTGGGAGTGGTCTCAGGCAACTGCACACCGGATGACAT
TCTAGTGTCTTCTAGAAAGGGTCTGCCACATGACCAGTTTGTGGTCAAAGAATTACTGCTTAA
TAGGCTTCAAGTAAGAAGACAGATGTTTTCTAATTAATACTGGACACTGACAAATTCATGTTT
ACTATAAAATCTCCTTACATGGAAATGTGACTGTGTGCTTTTTCCATTTACACTTGGTGAG
TCATCAACTCTACTGAGATTCCACTCCCCTCCAAGCACCTGCTGTGATTGGGTGGCCTGCTCT
GATCAGATAGCAAATTCTGATCAGAGAAGACTTTAAACTCTTGACTTAATTGAGTAAACTCT
TCATGCCATATACATCATTTTCATTATGTTAAAGGTAAAATATGCTTTGTGAACCTCAGATGTC
TGTAGCCAGGAAGCCAGGGTGTGTAAATCCAAATCTATGCAGGAAATGCGGAGAATAGAAAA
TATGTCACTTGAAATCCTAAGTAGTTTTGAATTTCTTTGACTTGAATCTTACTCATCAGTAAG
AGAACTCTTGGTGTCTGTCAGGTTTTATGTGGTCTGTAAAGTTAGGGGTTCTGTTTTGTTTTCC
TTATTTAGGAAAGAGTACTGCTGGTGTGCGAGGGGTATATGTTCCATTTAATGTGACAGTTTT
AAAGGATTTAAGTAGGGAATCAGAGTCCTTTGCAGAGTGTGACAGACGACTCAATAACCTCAT
TTGTTTTCTAAACATTTTTCTTTGATAAAGTGCCTAAATCTGTGCTTTTCGTATAGAGTAACATG
ATGTGCTACTGTTGATGTCTGATTTTGCCGTTTCATGTTAGAGCCTACTGTGAATAAGAGTTAG
AACATTTATATACAGATGTCATTTCTAAGAACTAAAATTTCTTTGGGAAAAACCCTCAAAAAA
AAAAAAAAAAAAAAAAAAAAA

486/615

FIGURE 482

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92289
><subunit 1 of 1, 234 aa, 1 stop
><MW: 26077, pI: 8.13, NX(S/T): 1
MAASRWARKAVVLLCASDLLLLLLLLPPPGSCAAEGSPGTPDESTPPPRKKKKDIRDYND
ADMARLLEQWEKDDDDIEEGDLPEHKRPSAPVDFSKIDPSKPESILKMTKKGKTLMMFVTV
SGSPTEKETEEITSLWQGSLEFNANYDVQRFIVGSDRAIFMLRDGSYAWWEIKDFLVGQDRC
ADVTLEGQVYPGKGGGSKEKNKTKQDKGKKKKEGDLKSRSSKEENRAGNKREDL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-32

N-glycosylation site:

Amino acids 201-205

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 85-89

Tyrosine kinase phosphorylation site:

Amino acids 50-59

N-myristoylation sites:

Amino acids 30-36;138-144;153-159;176-182

Amidation site:

Amino acids 207-211

FIGURE 483

[illegible]

488/615

FIGURE 484

MALPPGPAALRHTLLLLPALLSSGWGELEPQIDGQTTAERALRENERHAFTCRVAGGPQTPL
AWYLDGQLQEASTSRLLSVGGEAFSGGTSTFTVTAHRAQHELNCSLQDPRSGRSANASVILNV
QFKPEIAQVGAKYQEAQGPGLLVVLFALVRANPPANVTWIDQDGPVTVNTSDFLVLD AQNYPW
LTNHTVQLQLRSLAHNLSVVATNDVGVTSASLPAPGPSRHPSLISSDSNNLKLNNVRLPRENM
SLPSNLQLNDLTPDSRAVKPADRQMAQNNSRPELLDPEPGGLLTSQGFIRLPVLGYIYRVSSV
SSDEIWL

N-glycosylation sites:

amino acids 106-110, 119-123, 162-166, 175-179, 192-196, 205-209,
251-255, 280-284

Glycosaminoglycan attachment site:

amino acids 23-27

Casein kinase II phosphorylation sites:

amino acids 36-40, 108-112, 164-168, 282-286, 316-320

N-myristoylation sites:

amino acids 34-40, 89-95, 215-221, 292-298, 293-299

489/615

FIGURE 485

AGAGTTCCTTTTTCTAGGTCGATTAGGTTATACATTGTTGAAGTATAGTTTCGAGTTAGAATT
GGTCATTTTATTTTCAGTGTTTCACAGAAATCGAAGAAGACAGAAATGGCGCTTCTGTGGTGG
ATATCTACAGTAGCAATACTGTTGTTTACTTCGACGATTTTGGGAACATACGTTGAAGCTGGT
GCCGCTAAGTCTAACGAAGAAGAGATTGTGAACAAAAGCGAATTTGGAAGATTTCCACGAGGG
TCGAGAAAGGATGCATCGGGGTGCCACAAGCCGGGCTACCCTGTACCCCTCATTCTCGCTGC
CCTCCACCTCCCCATGTGCAGCGTCCTCGTCCTATTCTGCATGCTTAGTCTAACACCATCAGG
CTCGTTTATCTTTTCTGTCAATTGATCTCACCAGGAGCAAATCACTAGTGCGTGCTTCTGATTC
ACGTAACGTAGTATGTAAATAAATGTCAGTGATATTATGAATTGGTAAAACATTTCTGTTATC
TAAATAAAACAGTGAAGTTTGTGTTGACTAAAAAAA

490/615

FIGURE 486

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96855
><subunit 1 of 1, 84 aa, 1 stop
><MW: 9274, pI: 9.70, NX(S/T): 1
MALLWWISTVAILLFTSTILGTYVEAGAAKSNEEEIVNKSEFGRFPRGSRKDASGCHKPG
YPVPPHSRCPPPPHVQRPRPILHA
```

Signal peptide:

Amino acids 1-21

N-glycosylation site:

Amino acids 38-42

N-myristoylation site:

Amino acids 27-33

491/615

FIGURE 487

CGGGGACGGAAGCGGCCCTGGGCCCCGAGGGGCTGGAGCCGGGCCGGGGCGATGTGGAGCGCG
GGCCGCGGCGGGGCTGCCTGGCCGGTGCTGTTGGGGCTGCTGCTGGCGCTGTTAGTGCCGGGC
GGTGGTGCCGCCAAGACCGGTGCGGAGCTCGTGACCTGCGGGTCGGTGCTGAAGCTGCTCAAT
ACGCACCACCGCGTGCGGCTGCACTCGCACGACATCAAATACGGATCCGGCAGCGGCCAGCAA
TCGGTGACCGGCGTAGAGGCGTCGGACGACGCCAATAGCTACTGGCGGATCCGCGGCGGCTCG
GAGGGCGGGTGCCCGCGCGGGTCCCCGGTGCGCTGCGGGCAGGCGGTGAGGCTCACGCATGTG
CTTACGGGCAAGAACCTGCACACGCACCACTTCCCGTCGCCGCTGTCCAACAACCAGGAGGTG
AGTGCCTTTGGGGAAGACGGCGAGGGCGACGACCTGGACCTATGGACAGTGCGCTGCTCTGGA
CAGCACTGGGAGCGTGAGGCTGCTGTGCGCTTCCAGCATGTGGGCACCTCTGTGTTCTGTCA
GTCACGGGTGAGCAGTATGGAAGCCCCATCCGTGGGCAGCATGAGGTCCACGGCATGCCCAGT
GCCAACACGCACAATACGTGGAAGGCCATGGAAGGCATCTTCATCAAGCCTAGTGTGGAGCCC
TCTGCAGGTACAGATGAACTCTGAGTGTGTGGATGGATGGGTGGATGGAGGGTGGCAGGTGGG
GCGTCTGCAGGGCCACTCTTGGCAGAGACTTTGGGTTTGTAGGGTCTCTCAAGTGCCTTTGTG
ATTAAAGAATGTTGGTCTATGAAA

492/615

FIGURE 488

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96857
><subunit 1 of 1, 221 aa, 1 stop
><MW: 23598, pI: 6.96, NX(S/T): 0
MWSAGRGGAAWPVLLGLLALLVPGGGAAGTGAELVTCGSVLKLLNTHHRVRLHSHDIKYGSG
SGQQSVTGVEASDDANSYWRIRGGSEGGCPRGSPVRCCQAVRLTHVLTGKNLTHHFPSPLSN
NQEVSAFGEDGEGDDLWLTVRCSGQHWEREAAVRFQHVGTSVFLSVTGEQYGSPIRGQHEVH
GMPSANTHNTWKAMEGIFIKPSVEPSAGHDEL

Important features of the protein:**Signal peptide:**

amino acids 1-28

Glycosaminoglycan attachment site.

amino acids 62-66

N-myristoylation sites.amino acids 16-22, 25-31, 27-33, 61-67, 71-77, 86-92, 87-93,
91-97, 190-196**Endoplasmic reticulum targeting sequence.**

amino acids 218-223

493/615

FIGURE 489

CAGCAGCCGAGACAGCAGCTGAGACGGCAGCGGAGCTTCTCAGGGCCGAGCCAGTTCTTGGAGGAGACTCTGC
ACAGGGCATGGATCACTGTGGTGCCCTTTTCTGTGCCTGTGCCTTCTGACTTTGCAGAATGCAACAACAGAGAC
ATGGGAAGAACTCCTGAGCTACATGGAGAATATGCAGGTGTCCAGGGGCCGAGCTCAGTTTTTCTCTCGTCA
ACTCCACCAGCTGGAGCAGATGCTACTGAACACCAGCTTCCCAGGCTACAACCTGACCTTGCAGACACCCACCAT
CCAGTCTCTGGCCTTCAAGCTGAGCTGTGACTTCTCTGGCCTCTCGCTGACCAGTGCCACTCTGAAGCGGGTGCC
CCAGGCAGGAGGTGAGCATGCCCCGGGGTCAAGCAGCCATGCAGTTCCCCGCCGAGCTGACCCGGGACGCTGCAA
GACCCGCCCCAGGGAGCTGCGGCTCATCTGTATCTACTTCTCCAACACCCACTTTTTCAAGGATGAAAACAATC
ATCTCTGCTGAATAACTACGTCTCTGGGGGCCAGCTGAGTCATGGGCACGTGAACAACCTCAGGGATCCTGTGAA
CATCAGCTTCTGGCACAAACAAAGCCTGGAAGGCTACACCTGACCTGTGTCTTCTGGAAGGAGGGAGCCAGGAA
ACAGCCCTGGGGGGGCTGGAGCCCTGAGGGCTGTGTCAGAGCAGCCCTCCCACTCTCAGGTGCTCTGCCGCTG
CAACCACCTCACCTACTTTGCTGTTCTCATGCAACTCTCCCCAGCCCTGGTCCCTGCAGAGTTGCTGGCACCTCT
TACGTACATCTCCCTCGTGGGCTGCAGCATCTCCATCGTGGCCTCGCTGATCACAGTCTGCTGCACTTCCATTT
CAGGAAGCAGAGTGACTCCTTAACACGTATCCACATGAACCTGCATGCCTCCGTGCTGCTCCTGAACATCGCCTT
CCTGCTGAGCCCCGCTTCGCAATGTCTCCTGTGCCCGGTGAGCATGCACGCTCTGCGCGCTGCCCTGCACTA
CGCGCTGCTCAGCTGCCCTCACCTGGATGGCCATCGAGGGCTTCAACCTCTACCTCCTCGGGCGTGTCTACAA
CATCTACATCCGCAGATATGTGTCAAGCTTGGTGTGCTAGGCTGGGGGGCCCCAGCCCTCCTGGTGTGCTTTT
CCTCTCTGTCAAGAGCTCGGTATACGGACCCTGCACAATCCCCGTCTTCGACAGCTGGGAGAATGGCACAGGCTT
CCAGAACATGTCCATATGCTGGGTGCGGAGCCCCGTGGTGCACAGTGTCTGGTATGGGCTACGGCGGCTCAC
GTCCCTCTTCAACCTGGTGGTGTGCTGGCTGGGCGCTGTGGACCCTGCGCAGGCTGCGGGAGCGGGCGGATGCACC
AAGTGTGAGGGCCTGCCATGACACTGTCACTGTGCTGGGCTCACCGTGTGCTGGGAACACCTGGGCCTTGGC
CTTCTTTTCTTTTGGCGTCTTCTGCTGCCCCAGCTGTTCTCTTACCATCTTAACTCGCTGTACGGTTTCTT
CCTTTTCTGTGGTTCTGCTCCCAGCGGTGCCGCTCAGAAGCAGAGGCCAAGGCACAGATAGAGGCTTTCAGCTC
CTCCAAACAACACAGTAGTCCGGGCTCCTGGCCTGGAATCCTCAGCCTCTCTGGCCGCCAGTAGCCTGAGGCT
ACGGCTCCTGCTAGAGAGGGGTGGCAGGCTGCTGCTGGACCCAGAGGCCACTGTGACCGCCAAGGGGCTTTTC
CACTTCCACGGCCTCTCCAGGCACTGAGGGGAAGGCATTGTCTACCTCTCCCTGACATTTTGCTCCGGGGCAGA
TCCAACCTTACCTGGGGCAGCAAACCTTTGTCTGGTACCTGGGGCCAGCTCGCCAGGGATGTGGGCAGAGCACA
GCCTGGGCATCAGGAAGCCAAGTTTCAAGGACTGTCTTTGAGTCTGTCTGTATGACCTTGGGCTGCCACTTCTC
ACAGACCCTAGGTATCCACAGCTGTGACATGGGGGAAGCAGCTTTGTTTCAGCCTAACCCAGGAGCTTAGTAAA
AATTGCATAAGACCAGGGGAAGAGTGTGAGCGTGGGGTGGGAATTCGCGCGCTCCACCTGCTTGCTAGGGGC
AGGATCTCATTACGGCTGCCCTGGAAGCACCTGCTTGGCCCTGCCACCTTCTCCAGGGGAGGGCCAGATGGCAT
CCTGGCTTGGGGCGGTGGACCTACCCAGGCTCTGAGACTTTACTGGCCTATGCCTGAGGCCTCTTTTCTTTA
ACTCCCTAAATTATGATGACTCCAAGTCCAAGCCCACCCTTCCCAAGATTGGGAGGTTCCGCGCTTCCAGAGG
CTCCTCCTGCGGTGCTCCCAAGACTTCCATAGACCATCTGGACCAGTAGCCCATCCCGCAGTTTTCTTGGGGGCA
GAGGAAAACGCTTCTTCTCCTCCAGCTGAATCAGCTGGATCCAGTGTCTGGCTGTTTGGTGATTGGGCAAGA
TTGAATTTGCCAGGTAGGCGTGAGAGTGTGGGTTTTAAATTCCAAGCTCAGGCCATAGTTTTCAGAGAATCACCC
TTACCCAGACCTTCATGAGACAGTGCTCATGAAGCCAGTGCGTTTCCAGAACGAACACTAGGCGGCACCGTTG
GTCCCACTCAGAGGCCCTTGGCGCCAAGACTGCATCTAGAATCGCTCAAACACCTGTTTGCAAGCCCCATGCAC
CAGCTGGAGGGGGCGTAACTGCAGGACTGCGCTACTGAGTGACCCATTTCTCCAGGAGGAAAGGCAAGACAG
CTTACACGGCCATTTGTCTCTTTTCCCAATGCGGCGGTGCATTTCTGCTCTTGGGGGCTGCACCCAGACATAGC
TGGCACCAGAGCAGGGTGTCTCAGGTGGTGGGTGCTCAGGGCCCTGCCCCAGGCCACTGGGCGGTTTTGATGACCT
CAAAGGTCACAGGCAGAAAATAGGAGCAGGATTTCCCTGGGAAAAGTTATCTGGGACATCTTCTGCTCTTCT
GTACATTTCTAGATGCAAATAACTCCTTACCAGGCAGTGAGTGGCGTAGGCTCTGGAGCCAGGCTGCCTGGGCT
CCAATGCCAGCTCTGCCACTTGCTAGCTGTGAGACTGTGGACAAACCACTCAGCCTCTGTGTGCTCAGTTTTCC
TATTTGTAAAATAGAGACCATAGTGGTACCTATTTTGAAGACTAAGTAAAAGAATTCAAATAAGAGACTTGGCA
CAGAGTAAGTGCTCAGTAAAAA

494/615

FIGURE 490

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96860
><subunit 1 of 1, 528 aa, 1 stop
><MW: 59000, pI: 8.73, NX(S/T): 9
MDHCGALFLCLCLLTQLQATTETWEELLSYEMNQVSRGRSSVFSSRQLHQLEQMLLNTS
FPGYNLTQLQPTIQSLAFKLSCDFSGLSLTSATLKRVPQAGGQHARGQHAMQFPAELTRD
ACKTRPRELRLICIYFSNTHFFKDENNSSLNNYVLGAQLSHGHVNNLRDPVNISFWHNQ
SLEGYTLTCVFWKEGARKQPWGGWSPEGCRTEQPSHSQVLCRCNHLTYFAVLMQLSPALV
PAELLAPLTYISLVGCSISIVASLITVLLHFHFRKQSDSLTRIHMLHASVLLLNI AFLL
SPAFAMSPVPGSACTALAAALHYALLSCLTWM AIEGFNLYLLGRVYNIYIRRYVFKLG V
LGWGAPALLVLLSLSVKSSVYGPC TIPVFD SWENGTGFQNM SICWVRSPV VHSVLVMGYG
GLTSLFNLVVLAWALWTLRRLRERADAPSVRACHDTVTVLGLTVLLGTTWALAFFSFGVF
LLPQLFLFTILNSLYGFFLFLWFCSQRCSRSEAEAKAQIEAFSSSQTTQ
```

Important features of the protein:**Signal peptide:**

Amino acids 1-21

Transmembrane domains:

Amino acids 244-264;290-309;316-344;358-376;411-431;468-491

N-glycosylation sites:Amino acids 18-22;58-62;65-69;146-150;147-151;173-177;
179-183;394-398;400-404**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 274-278

N-myristoylation sites:86 GLSLTS
101 GGQHAR
157 GAQLSH
255 GCSISI
311 GSACTA
420 GGLTSL
467 GTTWAL**Prokaryotic membrane lipoprotein lipid attachment sites:**

Amino acids 246-257;318-329

Eukaryotic thiol (cysteine) proteases histidine active site:

Amino acids 410-421

G-protein coupled receptors family 2 proteins:

Amino acids 273-302;314-343

495/615

FIGURE 491

CTTGGCTGCCCCGACAACAAGCTCGCCACCTGCGCTGGGCGCATCCACCATCCAAGGCCAGCT
GAGGGGCACCAGACAGAGGATGAGGAGAGAGAGTCGCACACGGGCTGCCCTGAGAGACATTTCC
CATGGACATCCTCATGCTGCTTCTGCTTTTGTGTGTAATATATGGGAGATTTTCCCAAGATGA
ATACTCCCTCAATCAAGCTATCCGGAAAGAATTTACAAGAAATGCCAGAACTGCTTGGGTGG
CCTGAGAAACATCGCTGACTGGTGGGACTGGAGTCTGACCACACTTCTGGATGGCCTGTACCC
GGGAGGCACCCCGTCAGCCCGTGTGCCGGGGGCTCAGCCTGGAGCTCTTGGAGGAAAATGCTA
CCTAATAGGCAGTTCCGTAATTAGGCAGCTAAAAGTTTTTCCTAGGCATTTATGCAAGCCTCC
CAGGCCATTTTCAGCACTCATCGAAGACTCTATTCTACATGTAGTCCCGAAGTTGGAGGCC
TGAGAACCCCTACCTGATAGACCCAGAGAACCAAAACGTGACCCTGAATGGTCCTGGGGGCTG
TGGGACAAGGGAGGACTGTGTGCTCAGCCTGGGCAGAACAAAGGACTGAAGCCACACAGCCCT
GTCCCGACTCAGGGCCAGCATGTGGATTGACCGCAGCACCAGGGCTGTGTCTGTGCACTTCAC
TCTCTATAACCCCTCCAACCCAACTCTTCACCAGCGTGTCCCTGAGAGTGGAGATCCTCCCTAC
GGGGAGTCTCGTCCCTCATCCCTGGTGGAGTCATTAGCATCTTCCGCAGCGACTCAGCCCT
GCAGTACCACCTCATGCTTCCCAGCTGGTCTTCCTGGCACTCAGCCTGATCCACCTCTGTGT
TCAACTCTACCGTATGATGGACAAGGGCGTCCTCAGCTACTGGCGAAAGCCAAGGAAGTGGCT
GGAGGTAGCCTCTCTTGTGTCATTTTCTTTTGA AAAAATAACAATAAACTGTTTATATCTTGAA
AAAATAATTTAAATAAGAAATTGATTATGCACTAGCTACTGCCAACATTATTGCAGTTTTCTC
CCTCTGTAGTGTTAATCTCAAACAGCATTTGAGATCAGGTATCATTTAGTGTGTTACAGTT
ACCGTCATGTACCACACGAATTTAGCCAAGGTGGTGGTCCCATAAGATCATATGGTGCTAAG
AAATTTCTGTACCTAATGACATCTTGATTCTGACCTTGTATGTAGGCCTAGGCTAAATATGT
CTGTTTGTATCTTAGCTTTTAATAAAGAAGTTTAAAAATAAAAAA

496/615

FIGURE 492

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96861
><subunit 1 of 1, 300 aa, 1 stop
><MW: 33649, pI: 9.26, NX(S/T): 1
MRRESRTRAALRDISMDILMLLLLLLCVIYGRFSQDEYSLNQAIRKEFTRNARNCLGGLRN
IADWWDWSLTLLDGLYPGGTPSARVPGAQPGALGGKCYLIGSSVIRQLKVFPRHLCKPP
RPFSAIEDSIPTCSPEVGGPENPYLIDPENQNVTLNGPGGCGTREDCVLSLGRTRTEAH
TALSRLRASMWIDRSTRAVSVHFTLYNPPTQLFTSVSLRVEILPTGSLVPSSLVESFSIF
RSDSALQYHMLPQLVFLALSLIHLVCVQLYRMMDKGVLSYWRKPRNWLEVASLVSFSFEK

Important features of the protein:**Signal peptide:**

Amino acids 1-30

Transmembrane domain:

Amino acids 250-267

N-glycosylation site:

Amino acids 153-157

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 2-6

N-myristoylation sites:

Amino acids 56-62;75-81;79-85;80-86;88-94;92-98;160-166

497/615

FIGURE 493

TCTCAGGGCTTCATACAGGAAATCTATTGCTGTGTCAAGTTCAGAGAAAAGCTTCTGTTTCGT
CCAAGTTACTAACCAGGCTAAACCACATAGACGTGAAGGAAGGGGCTAGAAGGAAGGGAGTGC
CCCACCTGTTGATGGGGTAAGAGGATCCTGTACTGAGAAGTTGACCAGAGAGGGTCTCACCATG
CGCACAGTTCTTCTGTACCTGTGTGGAGGAAAAGTACTGAGTGAAGGGCAGAAAAAGAGAAA
ACAGAAATGCTCTGCCCTTGGGAGAACTGCTAACCTAGGGCTACTGTTGATTTTGACTATCTTC
TTAGTGGCCGAAGCGGAGGGTGCTGCTCAACCAAACAACTCATTAATGCTGCAAACCTAGCAAG
GAGAATCATGCTTTAGCTTCAAGCAGTTTATGTATGGATGAAAAACAGATTACACAGAACTAC
TCGAAAGTACTCGCAGAAGTTAACACTTCATGGCCTGTAAAGATGGCTACAAATGCTGTGCTT
TGTTGCCCTCCTATCGCATTAAGAAATTTGATCATAATAACATGGGAAATAATCCTGAGAGGC
CAGCCTTCCTGCACAAAAGCCTACAGGAAAGAAACAAATGAGACCAAGGAAACCAACTGTACT
GATGAGAGAATAACCTGGGTCTCCAGACCTGATCAGAATTCGGACCTTCAGATTCGTCCAGTG
GCCATCACTCATGACGGGTATTACAGATGCATAATGGTAACACCTGATGGGAATTTCCATCGT
GGATATCACCTCCAAGTGTTAGTTACACCTGAACCTGACCTGTTTCAAAACAGGAATAGAAT
GCAGTATGCAAGGCAGTTGCAGGGAAGCCAGCTGCGCAGATCTCCTGGATCCCAGAGGGCGAT
TGTGCCACTAAGCAAGAATACTGGAGCAATGGCACAGTGAAGTGTAAAGAGTACATGCCACTGG
GAGGTCCACAATGTGTCTACCGTGACCTGCCACGTCTCCCATTTGACTGGCAACAAGAGTCTG
TACATAGAGCTACTTCTGTTCCAGGTGCCAAAAAATCAGCAAAATTATATATTTCCATATATC
ATCCTTACTATTATTATTTTGACCATCGTGGGATTCATTTGGTTGTTGAAAGTCAATGGCTGC
AGAAAATATAAATTGAATAAAACAGAATCTACTCCAGTTGTTGAGGAGGATGAAATGCAGCCC
TATGCCAGCTACACAGAGAAGAACAATCCTCTCTATGATACTACAACAAGGTGAAGGCATCT
CAGGCATTACAAAGTGAAGTTGACACAGACCTCCATACTTTATAAGTGTTGGACTCTAGTAC
CAAGAAACAACAACAAACGAGATACATTATAATTACTGTCTGATTTTCTTACAGTTCTAGAAT
GAAGACTTATATTGAAATTAGGTTTTCCAAGGTTCTTAGAAGACATTTTAATGGATTCTCATT
CATACCCTTGTATAATTGGAATTTTTGATTCTTAGCTGCTACCAGCTAGTTCTCTGAAGAACT
GATGTTATTACAAAGAAAATACATGCCCATGACCAATATTCAAATTGTGCAGGACAGTAAAT
AATGAAAACCAAATTTCTCAAGAAATAACTGAAGAAGGAGCAAGTGTGAACAGTTTCTTGTG
TATCCTTTTCAGAAATATTTTAATGTACATATGACATGTGTATATGCCTATGGTATATGTGTCAA
TTTATGTGTCCCCTTACATATACATGCACATATCTTTGTCAAGGCACCAGTGGGAACAATACA
CTGCATTACTGTTCTATACATATGAAAACCTAATAATATAAGTCTTAGAGATCATTTTATATC
ATGACAAGTAGAGCTACCTCATTCTTTTTAATGGTTATATAAAATTCATTGTATAGTTATAT
CATTATTTAATTAAAAACAACCCTAATGATGGATATTTAGATTCTTTTAAGTTTGTGTTATTT
CTTTTAAGTTTGTGTTGTGGTATAAACAATACCACATAGAATGTTTCTTGTTCATATATCTCT
TTGTTTTTGAGTATATCTGTAGGATAACTTTCTTGAGTGGAATTGTCAGGTCAAAGGGTTTGT
GCATTTTACTATTGATATATATGTTAAATTGTGTCAAATATATATGTCAAATCCCTCCAACA
TTGTTTAAATGTGCCTTTCCCTAAATTTCTATTTTAATAACTGTACTATTCTGCTTCTACAG
TTGCCACTTTCTCTTTTAAATCAACCAGATTAAATATGATGTGAGATTATAATAAGAATTATA
CTATTTAATAAAAAATGGATTTATA

498/615

FIGURE 494

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96866
><subunit 1 of 1, 348 aa, 1 stop
><MW: 39069, pI: 8.13; NX(S/T): 10
MLCPWRTANLGLLLILTIFLVAEAEAGAAQPNNSMLQTSKENHALASSSLCMDEKQITQN
YSKVLAEVNTSWPVKMATNAVLCCPPIALRNLIITWEIILRGQPSTKAYRKETNETKE
TNCTDERITWVSRPDQNSDLQIRPVAITHDGYRCIMVTPDGNFHRGYHLQVLVTPELTL
FQNRNRTAVCKAVAGKPAAQISWIPEGDCATKQEYWSNGTVTVKSTCHWEVHNVSTVTCH
VSHLTGNKSLYIELLPVPGAKKSALYIPYIILTIILTIIVGFIWLLKVNGCRKYKLNKT
ESTPVVEEDEMOPYASYTEKNNPLYDTTNKVKASQALQSEVDTDLHTL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-24

Transmembrane domains:

Amino acids 78-98;267-286

N-glycosylation sites:Amino acids 31-35;60-64;69-73;116-120;122-126;185-189;
218-222;233-237;247-251;298-302**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 112-116

N-myristoylation sites:

Amino acids 103-109;259-265

499/615

FIGURE 495

CCAGGTGCACAGCGCATCGCCCGAGGCTGTCACCGCCCTGCCCCGCCACCCAGCTGTCCTG
GACCCAGGGGCAGGGAGAGGCTGGACGCCAGGTGCGCGGACACAGAAGCGTCTAAGCACAGCT
TCCTCCTTGCCGCTCCGGAAGTGGGCAGCCAGCCAGGAACCAGTACCACCTGCACCAATGGG
GCTGTCCCGGAAGGAGCAGGTCTTCTTGCCCTGCTGGGGGCTCGGGGGTCTCAGGCCTCAC
GGCACTCATTTCTCTCTGGTGGAGGCCACCAGCGTGCTCCTGCCACAGACATCAAGTTTGG
GATCGTGTTTGATGCGGGCTCCTCCACACGTCCCTCTTCCTGTATCAGTGGCCGGCGAACAA
GGAGAATGGCACGGGTGTGGTCAGCCAGGCCCTGGCCTGCCAGGTGGAAGGGCTGGAATCTC
CTCCTACACTTTCTAATGCTGCACAGGCTGGTGAGAGCCTGCAGGGCTGCTTGGAGGAGGCGCT
GGTGCTGATCCCAGAGGCCCAGCATCGGAAAACACCCACGTTCTGGGGGCCACGGCTGGCAT
GAGGTTGCTCAGCCGGAAGAACAGCTCTCAGGCCAGGGACATCTTTGCAGCAGTCAACCAGGT
CCTGGGCCGGTCTCCCGTGGACTTTTGGGGTGCCGAGCTCCTGGCCGGGCAGGCCGAAGGTGC
CTTTGGTTGGATCACTGTCAACTACGGCTTGGGGACGCTGGTCAAGTACTCCTTCACTGGAGA
ATGGATCCAGCCTCCGGAGGAGATGCTGGTGGGTGCCCTGGACATGGGAGGGGCTCCACCCA
GATCACGTTTCGTGCCTGGGGGCCCCATCTTGGACAAGAGCACCCAGGCCGATTTTGCCTCTA
CGGCTCCGACTACAGCGTCTACACTCACAGCTACCTGTGCTTTGGACGGGACCAGATGCTGAG
CAGGCTCCTCGTGGGGCTGGTGCAGAGCCGCCCGCTGCCCTGCTCCGTCACCCGTGCTACCT
CAGCGGCTACCAGACCACACTGGCCCTGGGCCCGCTGTATGAGTACCCTGTGTCCACGCCAC
GCCCCCGCTGAGCCTCCCCAGAACCTCACAGTTGAAGGGACAGGCAACCCTGGAGCCTGCGT
CTCAGCCATCCGGGAACTTTTCAACTTCTCCAGCTGCCAGGGCCAGGAGGACTGCGCCTTTGA
CGGGGTCTACCAGCCCCCGCTGCGGGGCCAGTTCTATGTGGAGGCCAGCTACCCTGGGCAGGA
CCGCTGGCTGCGGGACTACTGTGCCTCAGGCCTGTACATCCTCACCTCCTGCACGAGGGCTAC
GGGTTACGCGAGGAGACCTGGCCAGCCTCGAGTTCCGAAAGCAGGCGGGCGGTGTGGACATT
GGCTGGACACTGGGCTACATGCTGAACCTGACCGGGATGATCCCGGCCGATGCGCCGGCTCAG
TGGCGGGCAGAGAGCTACGGCGTCTGGGTGGCCAAAGTGGTGTTTCATGGTGCTGGCCCTGGTG
GCGGTGGTGGGGGCTGCCTTGGTCCAGCTCTTCTGGTTGCAGGACTAGTGGGAAGGCGGAGGT
GGGCCCCACAGAGCCACAGGCAGCTGCGTCCCGGATGCTGGAGGCTTCCTGAGCCCTGAGC
GCCGTGGGGCCTTGCTCTGTGGCTCTGCCACGGTCAGGTGACAGCCACCTCCAGGGCACCGT
CAGGGTGGTGCTGGCCACAGAGGCTGCATGACCTCCCCCTCCCGGCGTCCCTCCCCAACCTCC
TTCCGCAACTGGGCTTCCAGGGCCGTAGGTGCCTTTCTGCACACAGGCCGCCAGGACTCGTGG
TGTCTCCAGGCTGTGTGACTGCAGGGCCACATGCTGCCTGCAAACAGGGCAAGACCACGGAGG
CACAGGGGTCCTGCTCCTGATGGGGCCTCAGGAGGGGCGGAGAGGGGTGGAAGGGAGGGAGCT
GCCCCACCTGGACCCCCGCTCTCCCTGCTGTTGTCTGAGCAGATGGATGGAGTCCAGGCCTGG
GGGCTTCTGCTGGGCCAGCCCGGCCTCCACACCCACTTGGAGGGTGAGACTGCAGTGGGGGT
TGTTTTTATTAAAAGCATCATGGACACAGCAAAAAAAAAAAAAAAAAA

500/615

FIGURE 496

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96870
><subunit 1 of 1, 458 aa, 1 stop
><MW: 49377, pI: 4.98, NX(S/T): 5
MGLSRKEQVFLALLGASGVSGLTALILLVEATSVLLPTDIKFGIVFDAGSSHTSLFLYQ
WPANKENGTVVVSQALACQVEGPGISSYTSNAAQAGESLQGCLEEALVLIPEAQRKTPT
FLGATAGMRLLSRKNSSQARDIFAAVTQVLGRSPVDFWGAELLAGQAEGAFGWITVNYGL
GTLVKYSFTGEWIQPPPEMLVGALDMGGASTQITFVPGGPILDKSTQADFRLYGSDYSVY
THSYLCFGRDQMLSRLLVGLVQSRPAALLRHPCYLSGYQTTLALGPLYESPCVHATPPLS
LPQNLTVEGTGNPGACVSAIRELFNFSSCQGEDCAFDGVYQPPLRGQFYVEASYPGQDR
WLRDYCASGLYILTLLHEGYGFSEETWPSLEFRKQAGGVDIGWTLGYMLNLTGMIPADAP
AQWRAESYGVVWAKVVFVVLALVAVVGAALVQLFWLQD
```

Important features of the protein:**Signal peptide:**

Amino acids 1-21

Transmembrane domain:

Amino acids 428-449

N-glycosylation sites:

Amino acids 67-71;135-139;304-308;325-329;410-414

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 133-137

N-myristoylation sites:Amino acids 50-56;123-127;165-171;207-213;234-240;
259-265;311-317;314-320;331-337;398-404;
413-419;429-435**GDA1/CD39 family of nucleoside phosphatases proteins:**

Amino acids 43-59;202-215

501/615

FIGURE 497

GCCTTATAAAGTAGCCTCTGCATCTGCCTGCCTCGGGCAGAGGAGGGCTACCCTGGGGCTGAG
AGTTACCTGTCTCAGGAACACCTGAGCCACAGATCCTGTGGGCAGCGCCAGGGCAGCCA
TGGCTTGGGCAAGTAGGCTGGGCCTGCTGCTGGCACTGCTGCTGCCCCTGGTTCGGTGCCTCCA
CGCCAGGCACCGTGGTCCGACTCAACAAGGCAGCATTGAGCTACGTGTCTGAAATTGGGAAAG
CCCCTCTCCAGCGGGGCCCTGCAGGTCACTGTCCCTCATTTCTGGACTGGAGTGGAGAGGCGC
TTCAGCCCACCAGGATCCGGATTCTGAATGTCCATGTGCCCCGCCTCCACCTGAAATTCATTG
CTGGTTTTCGGAGTGCGCCTGCTGGCAGCAGCTAATTTTACTTTCAAGGTCTTTTCGCGCCCCAG
AGCCCCTGGAGCTGACGCTGCCTGTGGAAGTGTGGCTGACACCCGCTGACCCAGAGCTCCA
TCAGGACCCCTGTGGTCAAGCATCTCTGCCTGCTCTTTATTCTCGGGCCACGCCAACGAGTTTG
ATGGCAGTAACAGCACCTCCCACGCGCTGCTGGTCTGGTGCAGAAGCACATTAAAGCTGTCT
TGAGTAACAAGCTGTGCCCTGAGCATCTCCAACCTGGTGCAGGGTGTCAATGTCCACCTGGGCA
CCTTAATTGGCCTCAACCCCGTGGGTCTGAGTCCCAGATCCGCTATTCCATGGTCACTGTGC
CCACTGTCAACAGTGAATACATTTCCCTGGAAGTCAATGCTGTTCTCTTCTGCTGGGCAACC
CCATCATCTGCCCACGGATGCCACCCCTTTTGTGTTGCCAAGGCATGTGGGTACCGAGGGCT
CCATGGCCACCGTGGGCCTCTCCAGCAGCTGTTTGACTCTGCGCTCCTGCTGCTGCAGAAGG
CCGGTGGCCTCAACCTGGACATCACAGGGCAGCTGAGGTCCGATGACAACCTGCTGAACACCT
CTGCTCTGGGCCGGCTCATCCCGAGGTGGCCCGCCAGTTTCCCGAGCCCATGCCTGTGGTGC
TCAAGGTGCGGCTGGGTGCCACACCTGTGGCCATGCTCCACACAAACAACGCCACCCCTGCGGC
TGCAGCCCTTCGTGGAGGTCTGGCCACAGCCTCCAACCTCGGCTTTCCAGTCCCTCTTCTCCC
TGGATGTGGTAGTGAAGTGTGAGACTCCAGCTCTCTGTGTCCAAGGTGAAGCTTCAGGGGACCA
CGTCTGTGCTGGGGGATGTCCAGCTCACGGTGGCCTCCTCCAACGTGGGCTTCATTGATACAGAT
CAGGTGCGCACACTGATGGGCACCGTTTTTGTAGAAGCCCCTGCTGGACCATCTCAATGCTCTC
TTGGCCATGGGAATTGCCCTCCCTGGTGTGGTCAACCTCCACTATGTTGCCCTGAGATCTTT
GTCTATGAGGGCTACGTGGTGTATATCCAGTGGACTCTTCTACCAGAGCTTGAGGCAAGACCACT
GGGAGGCCTGAGAGTGGGCCAGCTCGCTGCTCAGGCGAATTTCTCATTTCAAGCCACTGGGGA
AACTGAGGCAAAACCATACTTAGTCATCACCACAAGCTGGACTGCTTAGCTGGGCTGTTTTA
TCTTCCCTGAGTGCCTGGGTCTCCCTCCCTCACTTCTGCCCTTTCCCTTCCTCCTCTTCT
CCTCCCTCTTCCCTCATCTCCCCCTCCTTCTGCCCCACCCAGGGGGGAGCAGACTGCT
CCTCCAGGCTGTATAGACCTGCCCTCTTGCAATTAACAACCTTCTCTTGAGCTGC

502/615

FIGURE 498

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96872
><subunit 1 of 1, 458 aa, 1 stop
><MW: 49158, pI: 8.72, NX(S/T): 4
MAWASRLGLLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQRALQVTVPHFLDWS
GEALQPTRIRILNVHVPRLHLKFIAGFGVRLLAANFTFKVFRAPEPLELTLPVELLADT
RVTQSSIRTPVVSISACSLFSGHANEFDSNSTSHALLVLVQKHIKAVLSNKLCLSISNL
VQGVNVHLGTLIGLNPVGPESQIRYSMVSVPVTSDYISLEVNAVLFLLGNPIILPTDAT
PFVLPRHVGTEGSMATVGLSQQLFDSALLLQKAGALNLDITGQLRSDDNLLNTSALGRL
IPEVARQFPEPMPVVLKVRLGATPVAMLHTNNTLRLQPFVEVLATASNSAFQSLFSLDV
VVLRLQLSVSKVKLQGTTSVLGDVQLTVASSNVGFIDTDQVRTLMGTVFEEKPLLDHLNA
LLAMGIALPGVVNLHYVAPEIFVYEGYVVISSGLFYQS
```

Important features of the protein:**Signal peptide:**

Amino acids 1-20

Transmembrane domain:

Amino acids 217-236

N-glycosylation sites:

Amino acids 96-100;151-155;293-297;332-336

N-myristoylation sites:

Amino acids 8-14;149-155;189-195;249-255;252-258;283-289

LBP / BPI / CETP family proteins:

Amino acids 22-50; 251-287

503/615

FIGURE 499

TTGAAAATCTACTCTATCAGCTGCTGTGGTTGCCACCATTCTCAGGACCCTCGCCATGAAAGC
CCTTATGCTGCTCACCCCTGTCTGTTCTGCTCTGCTGGGTCTCAGCTGACATTCGCTGTCACTC
CTGCTACAAGGTCCTGTGCTGGGCTGTGTGGACCGGCAGTCCTGCCGCCTGGAGCCAGGACA
GCAATGCCTGACAACACATGCATACCTTGGTAAGATGTGGGTTTTCTCCAATCTGCGCTGTGG
CACACCAGAAGAGCCCTGTCAGGAGGCCTTCAACCA[^]ACCAACCGCAAGCTGGGTCTGACATA
TAACACCACCTGCTGCAACAAGGACAAGTCAACAGCGCAGGACCCCGCCCACTCCAGCCCT
GGGCCTTGCTCTCCTTACCTCCTTGGCTGGCCTTGGCCTCTGGCTGCTGCACTTGAGACTCATT
CCATTGGCTGCCCTCCTCCCACCTGCCTTGGCCTGAGCCTCTCTCCCTGTGTCTCTGTATCC
CCTGGCTTTACAGAATCGTCTCTCCCTAGCTCCCATTTCCTTAATTAAACACTGTTCCGAGTG
GTCTCCTCATCCATCCTTCCCACCTCACACCCTTCACTCTCCTTTTTCTGGGTCCCTTCCCAC
TTCCTTCCAGGACCTCCATTGGCTCCTAGAGGGCTCCCCACTTTGCTTCCTATACTCTGCTG
TCCCCTACTTGAGGAGGGATTGGGATCTGGGCCTGAAATGGGGCTTCTGTGTTGTCCCCAGTG
AAGGCTCCCACAAGGACCTGATGACCTCACTGTACAGAGCTGACTCCCCAAACCCAGGCTCCC
ATATGTACCCCATCCCCATACTCACCTCTTCCATTTTGAGTAATAAATGTCTGAGTCTGGA
AAAAAAAAAAAAAAAAAAAA

504/615

FIGURE 500

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96878
><subunit 1 of 1, 125 aa, 1 stop
><MW: 13821, pI: 8.60, NX(S/T): 2
MKALMLLTLSVLLCWVSADIRCHSCYKVPVLGCVDRQSCRLEPGQQCLTTHAYLGKMWVFSNL
RCGTPEEPCQEAFNQTNRKLGTYNTTCCNKDNCNSAGPRPTPALGLVFLTSLAGLGLWLLH

Important features of the protein:**Signal peptide:**

amino acids 1-18

N-glycosylation sites.

amino acids 77-81, 88-92

N-myristoylation site.

amino acids 84-90

Ly-6 / u-PAR domain protein signature.

amino acids 85-98

505/615

FIGURE 501

GGAGCCTCCTAATGCAGTCTTCTGCACAGTCCTGGGGACTGACTGACTGAATCACACCTCTGG
GGCTGGGGGCTGCTGACATGTGTGCCTTTCCTTGGCTGCTTCTTCTCCTGCTGCTCCAGGAGG
GCAGCCAAAGGAGACTCTGGAGATGGTGTGGATCCGAGGAAGTGGTTGCGGTCTTCAGGAGT
CCATCAGCCTCCCCCTGGAAATACCACCAGATGAAGAGGTTGAGAACATCATCTGGTCCTCTCAC
AAAAGTCTTGCCACTGTGGTGCCAGGGAAAGAGGGACATCCAGCTACCATCATGGTGACCAAT
CCACACTACCAGGGCCAAGTGAGCTTCCTGGACCCCAGCTATTCCCTGCATATCAGCAATCTG
AGCTGGGAGGATTACAGGGCTTTACCAAGCTCAAGTCAACCTGAGAACATCCCAGATCTCTACC
ATGCAGCAGTACAATCTATGTGTCTACCATCCTAACTATGCTTCTGAGAAGCCTTCAACAGCC
TTCTGCCTCCTGGCCAAGGGATTGCTCATCTTCTTGCTCTTGGTAATTCTGGCCATGGGACTC
TGGGTCATCCGAGTCCAGAAAAGACACAAAATGCCAAGGATGAAGAAACTCATGAGAAACAGA
ATGAAATTGAGGAAGGAGGCAAAGCCTGGCTCCAGCCCTGCCTGACTGCTCCTTGGAACCCC
AGTCCTGAGCTTGGTTTCTTCCCAGCACCCAGAGAATCCTTCCTCAGCTCTCTTCTTTCCAGG
GGAAGGAGGTGCTCAGGGGTGGGTATCCAGAGAGCCATACTTCTGAGGGAAGACTGGCTGGCA
ATAAAGTCAAATTAAGTGACCACA

506/615

FIGURE 502

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96879
><subunit 1 of 1, 198 aa, 1 stop
><MW: 22584, pI: 9.40, NX(S/T): 1
MCAFPWLLLLLLLLQEGSQRRLLWRWCGSEEVVAVLQESISLPLEIPPDEEVENIIWSSHKS
LATVVPKGKEGHPATIMVTNPHYQGQVSFLDPSYSLHISNLSWEDSGLYQAQVNLRTSQIS
TMQQYNLCVYHPNYASEKPSTAFCLLAKGLLI FLLL VILAMGLWVIRVQKRHKMPRMKKL
MRNRMKLRKEAKPGSSPA
```

Important features of the protein:**Signal peptide:**

Amino acids 1-18

Transmembrane domain:

Amino acids 144-165

N-glycosylation site:

Amino acids 99-103

N-myristoylation site:

Amino acids 106-112

507/615

FIGURE 503

ACGGGCCCGCAGCGGCAGTGACGTAGGGTTGGCGCACGGATCCGTTGCGGCTGCAGCTCTGCAG
TCGGGCCCGTTCCTTCGCCGCCAGGGGTAGCGGTGTAGCTGCGCAGCGTCGCGCGCGCTAC
CGCAGCCAGGTTTCGGCCCCGTAGGCGTCTGGCAGCCCCGGCGCCATCTTCATCGAGCGCCATGGC
CGCAGCCTGCGGGCCGGGAGCGGCCGGGTACTGCTTGCTCCTCGGCTTGCATTTGTTTCTGCT
GACCGCGGGCCCTGCCCTGGGCTGGAACGACCCCTGACAGAATGTTGCTGCGGGATGTAAAAGC
TCTTACCCTCCACTATGACCGCTATACCACCTCCCGCAGGCTGGATCCCATCCCACAGTTGAA
ATGTGTTGGAGGCACAGCTGGTTGTGATTCTTATACCCCAAAGTCATACAGTGTGAGAACA
AGGCTGGGATGGGTATGATGTACAGTGGGAATGTAAGACGGACTTAGATATTGCATACAAATT
TGGAAAAGTGTGGTGAGCTGTGAAGGCTATGAGTCCTCTGAAGACCAGTATGTACTAAGAGG
TTCTTGTGGCTTGGAGTATAATTTAGATTATACAGAACTTGGCCTGCAGAACTGAAGGAGTC
TGGAAAGCAGCACGGCTTTGCCTCTTTCTCTGATTATTATTATAAGTGGTCCTCGGCGGATTC
CTGTAACATGAGTGGATTGATTACCATCGTGGTACTCCTTGGGATCGCCTTTGTAGTCTATAA
GCTGTTTCTGAGTGACGGGCAGTATTCTCCTCCACCGTACTCTGAGTATCCTCCATTTTCCCA
CCGTTACCAGAGATTACCAACTCAGCAGGACCTCCTCCCCAGGCTTTAAGTCTGAGTTCAC
AGGACCACAGAATACTGGCCATGGTGCAACTTCTGGTTTTGGCAGTGCTTTTACAGGACAACA
AGGATATGAAAATTCAGGACCAGGGTTCTGGACAGGCTTGGGAACTGGTGGAACTAGGATA
TTTGTGTTGGCAGCAATAGAGCGGCAACACCCTTCTCAGACTCGTGGTACTACCCGTCCTATCC
TCCCTCCTACCCTGGCACGTGGAATAGGGCTTACTACCCCTTCATGGAGGCTCGGGCAGCTA
TTCGGTATGTTCAAATCAGACACGAAAACCAGAACTGCATCAGGATATGGTGGTACCAGGAG
ACGATAAAGTAGAAAGTTGGAGTCAAACACTGGATGCAGAAATTTTGGATTTTTCATCACTTT
CTCTTTAGAAAAAAAGTACTACCTGTAAACAATTGGGAAAAGGGGATATTCAAAGTCTGTG
GTGTTATGTCCAGTGTAGCTTTTTGTATTCTATTATTTGAGGCTAAAAGTTGATGTGTGACAA
AATACTTATGTGTTGTATGTCAGTGTAACATGCAGATGTATATTGCAGTTTTTGAAAGTGATC
ATTACTGTGGAATGCTAAAAATACATTAATTTCTAAAACCTGTGATGCCCTAAGAAGCATTA
GAATGAAGGTGTTGTACTAATAGAACTAAGTACAGAAAATTTAGTTTTAGGTGGTGTAGC
TGATGAGTTATTACCTCATAGAGACTATAATATTCTATTGTTGTTATTATTTGATGTTTG
CTGTTCTTCAAACATTTAAATCAAGCTTTGGACTAATTATGCTAATTTGTGAGTTCTGATCAC
TTTTGAGCTCTGAAGCTTTGAATCATTAGTGGTGGAGATGGCCTTCTGGTAACTGAATATTA
CCTTCTGTAGGAAAAGGTGGAAAATAAGCATCTAGAAGGTTGTTGTGAATGACTCTGTGCTGG
CAAAAATGCTTGAAACCTCTATATTTCTTTCGTTTCATAAGAGGTAAAGGTCAAATTTTCAAC
AAAAGTCTTTTAATAACAAAAGCATGCAGTTCTCTGTGAAATCTCAAATATTGTTGTAATAGT
CTGTTTCAATCTTAAAAAGAATCA

508/615

FIGURE 504

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96889
><subunit 1 of 1, 339 aa, 1 stop
><MW: 36975, pI: 7.85, NX(S/T): 1
MAAACGPGAAGYCLLLGLHLFLLTAGPALGWNDPDRMLLRDVKALTLHYDRYTTSRRLDPIQ
LKCVGGTAGCDSYTPKVIQCQNKGDGYDVQWECKTDLDIAYKFGKTVVSCEGYESSEDQYVL
RGSCGLEYNLDYTELGLQKLKESGKQHGFASFSDYIYKWSSADSCNMSGITIVVLLGIAFVV
YKLFLSDGQYSPPPYSEYPPFSHRYQRFTNSAGPPPPGFKSEFTGPQNTGHGATSGFGSAFTG
QQGYENSGPGFWTGLGTGGILGYLFGSNRAATPFSDSWYYPSYPPSYPGTWNRAYSPLHGGSG
SYSVCSNSDTKTRTASGYGGTTRRR

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 171-190

N-glycosylation site.

amino acids 172-176

Glycosaminoglycan attachment sites.

amino acids 244-248, 259-263, 331-335

Tyrosine kinase phosphorylation site.

amino acids 98-106

N-myristoylation sites.amino acids 68-74, 69-75, 131-137, 241-247, 247-253, 266-272,
270-276, 278-284, 312-318

509/615

FIGURE 505

GCAAAAGGAAGGGAGGGAAGCACTCCATCATCTCACTGGGAAGAACGGGCACGGGCATACCTGC
AGCTACTGGGGTTCCACTGGGCTTGAGGGTCGATTTTTTCACCTTTTGAAGGACAAGATGCATT
GGAAGATGTTGCTGCTTCTGCTGTTGTATTACAATGCTGAGGCTTCTATGTGCCACAGGTGGA
GCAGGGCTGTGCTCTTCCCTGCCGCCACCGGCCAAAGAGGTCCTCATCACTGCCATTGAACC
CAGTCCTGCAGACCTCCCTGGAGGAGGTGGAGCTGCTCTACGAGTTCCTGCTGGCCGAACCTTG
AGATCAGCCCTGACCTGCAGATCTCCATCAAGGACGAGGAGCTGGCCTCCTTGCGGAAGGCCT
CAGACTTCCGCACCGTCTGCAACAACGTCATCCCCAAGAGCATCCCAGACATCCGCCGGCTCA
GCGCCAGCCTCTCCAGCCACCCTGGCATCCTCAAGAAAGAAGACTTTGAAAGGACAGTGCTGA
CCCTGGCCTACACAGCCTACCGCACAGCCCTGTCCCACGGCCATCAGAAGGACATCTGGGCGC
AGTCCCTCGTTAGCCTCTTCCAGGCCCTGAGGCACGACTTGATGCGCTCCTCACAGCCGGGAG
TACCTCCCTGAGAGACTGGCCACACCAGGACCTCAGAGCAGGGACCAGCACAGTAATCCAGA
AAGTCTTCATTCTCTACTCCATTTACAGAGACCAGCAACAAAACACTTACCGCTGACACAGAG
CAGCAGAGATCAAACAGTAACCCCGATGCTCTTTTCTCCTTGATGTTTCTGGAAGACACATC
TGATTCATGCCATCATGTGACCTGGGCTGGAAGAAAGGGCTGGAATGGTCATTCAAGACGCCT
CCATGGGCAGAATGGTTTGCCTATGGCAGGCAGAATTCTGATATGCTTCAACCCAGAGCAGTG
GCCACACACTCAAGAGTGAGAACAGGCGTGAGCCACCGTGCCTGGCCCAGGATCTAAAACTT
TCTAAGTTTCTCCTCCATCGTTGGCATCCTCACAGCTATCTCCAATGTCACTCAAGAGACATCAA
CAGACATTTAACTGCTGCAGACTTCATTGCTCTGTACCTCACCTTGAATCTAACAAATCAA
GTATTTCTGCAGGTCCAATGGTCTAAATCAAATGCTTGTTAAATGACTTTTTTACAACACCCCTT
ACTTTCTAATCCATTTCAATCTTATTTTTTTTATTGTGGTAAAAACACATCACGTAAATG
TACCATCTTAACCATTTTAAAGCATATGGTACAGCAGTGTTAACTCCATGCATGTTGTGAAAC
AGACCCCGGAACCTTTCTCATCTTGTAATCTGAAGTCTATACCCACCGAACAACCTCCTCTT
TTCCCCTTCCCCCTGCCTGCCCCAGCTCTTGGCACCATTATTCTGCTTTCTGTTTTTGTGAGAGT
CTGACTACTTAAGATACCTCATACAAGCGGGATCTGGCTTACATTTCTTGAGCATTGTATTCT
GGAAAAGTGTTTCCTTCTGAAAAATGGGTAGAGTTCTGAAGGAGAACTACTGGTCTTATT
GTACACTTGCTGTACCTATTTTTATTTAAACAATATTCATCTATGGTATAATAAAGATGTCAT
GGTTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

510/615

FIGURE 506

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96893
><subunit 1 of 1, 173 aa, 1 stop
><MW: 19733, pI: 8.78, NX(S/T): 0
MHWKMLLLLLLYNAEASMCHRWSRAVLFPAAHRPKRSSSLPLNPVLQTSLEEVELLYEF
LLAELEISPDQLQISIKDEELASLRKASDFRTVCNNVIPKSIPDIRRLSASLSSHPGILKK
EDFERTVLTLAYTAYRTALSHGHQKDIWAQSLVSLFQALRHDLMRSSQPGVPP
```

Important features of the protein:**Signal peptide:**

Amino acids 1-17

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 36-40;84-88;105-109

511/615

FIGURE 507

GGCGGCGGGCTGCGCGGAGCGGCGTCCCCTGCAGCCGCGGACCGAGGCAGCGGCGGCACCTGC
CGGCCGAGCAATGCCAAGTGAGTACACCTATGTGAACTGAGAAGTGATTGCTCGAGGCCTTC
CCTGCAATGGTACACCCGAGCTCAAAGCAAGATGAGAAGGCCAGCTTGTTATTAAAAGACAT
CCTCAAATGTACATTGCTTGTGTTTGGAGTGTGGATCCTTTATATCCTCAAGTTAAATTATAC
TACTGAAGAATGTGACATGAAAAAATGCATTATGTGGACCCTGACCATGTAAAGAGAGCTCA
GAAATATGCTCAGCAAGTCTTGCAAGGAATGTCGTCCCAAGTTTGCCAAGACATCAATGGC
GCTGTTATTTGAGCACAGGTATAGCGTGGACTTACTCCCTTTTGTGCAGAAGGCCCCCAAAGA
CAGTGAAGCTGAGTCCAAGTACGATCCTCCTTTTGGGTTCGGAAGTTCTCCAGTAAAGTCCA
GACCTCTTGGAACCTTGCCAGAGCACGACCTCCCTGAACACTTGAAAGCCAAGACCTGTGCG
GCGCTGTGTGGTTATTGGAAGCGGAGGAATACTGCACGGATTAGAAGTGGGCCACACCCTGAA
CCAGTTCGATGTTGTGATAAGGTTAAACAGTGCACCAGTTGAGGGATATTCAGAACATGTTGG
AAATAAACTACTATAAGGATGACTTATCCAGAGGGCGCACCAGTGTCTGACCTTGAATATTAT
TCCAATGACTTATTTGTTGCTGTTTTATTTAAGAGTGTGATTTCAACTGGCTTCAAGCAATG
GTAAAAAAGGAAACCCTGCCATTCTGGGTACGACTCTTCTTTTGAAGCAGGTGGCAGAAAAA
ATCCCACTGCAGCCAAAACATTTAGGATTTTGAATCCAGTTATCATCAAAGAGACTGCCTTT
GACATCCTTCAGTACTCAGAGCCTCAGTCAAGTTCTGGGGCCGAGATAAGAACGTCCCCACA
ATCGGTGTCATTGCCGTTGTCTTAGCCACACATCTGTGCGATGAAGTCAGTTTGGCGGGTTTT
GGATATGACCTCAATCAACCCAGAACACCTTTGCACTACTTCGACAGTCAATGCATGGCTGCT
ATGAACTTTCAGACCATGCATAATGTGACAACGGAAACCAAGTTCCTCTTAAAGCTGGTCAA
GAGGGAGTGGTGAAAGATCTCAGTGGAGGCATTGATCGTGAATTTTGAACACAGAAAACCTCA
GTTGAAAATGCAACTCTAACTCTGAGAGCTGTTTTTGACAGCCTTCTTGATGTATTTCTCCAT
CCTGCAGATACTTTGAAGTGCAGCTCATGTTTTTAACCTTTTAATTTAAAAACACAAAAAAAT
TTTAGCTCTTCCCACTTTTTTTTTTCTATTTATTTGAGGTCAGTGTTTGTGTTTGCACACCAT
TTTGTAATGAACTTAAGAATTGAATTGGAAGACTTCTCAAAGAGAATTGTATGTAACGAT
GTTGTATTGATTTTTTAAGAAAGTAATTTAATTTGTAACCTTCTGCTCGTTTACACTGCACAT
TGAATACAGGTAACATAATTGGAAGGAGAGGGGAGGTCACTCTTTTGATGGTGGCCCTGAACCT
CATTCTGGTTCCTGCTGCGCTGCTTGGTGTGACCCACGGAGGATCCACTCCAGGATGACGT
GCTCCGTAGCTCTGCTGCTGATACTGGGTCTGCGATGCAGCGGCGTGAGGCCTGGGCTGGTTG
GAGAAGGTCACAACCCTTCTCTGTTGGTCTGCCTTCTGCTGAAAGACTCGAGAACCAACCAGG
GAAGCTGTCTGGAGGTCCCTGGTGGGAGAGGGACATAGAATCTGTGACCTCTGACAACTGTG
AAGCCACCCTGGGCTACAGAAACCACAGTCTTCCAGCAATTATTACAATTCTTGAATTCCTT
GGGGATTTTTTACTGCCCTTTCAAAGCACTTAAGTGTTAGATCTAACGTGTTCCAGTGTCTGT
CTGAGGTGACTTAAAAATCAGAACAAAACCTTCTATTATCCAGAGTCATGGGAGAGTACCCC
TTTCCAGGAATAATGTTTTGGGAAACACTGAAATGAAATCTTCCAGTATTATAAATTGTGTA
TTTAA

512/615

FIGURE 508

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96897
><subunit 1 of 1, 362 aa, 1 stop
><MW: 41736, pI: 8.80, NX(S/T): 3
MRRPSLLLKDILKCTLLVFGVWILYILKLNYTTEECMDKMKMHYVDPDHVKRAQKYAQQVL
QKECRPKFAKTSMA LLFEHRYSDLLPFVQKAPKDSEAESKYDPPFGFRKFSSKVQTLLE
LLPEHDLPEHLKAKTCRRCVVIGSGGILHGLELGH TLNQFDVVIRLNSAPVEGYSEHVGN
KTTIRMTYPEGAPLSDLEYYSNDLFVAVLFKSVDFNWLQAMVKKETLPFWVRLFFWKQVA
EKIPLQPKHFRILNPVVIKETAFDILQYSEPQSRFWGRDKNVPTIGVIAVVLATHLCDEV
SLAGFGYDLNQPRTP LHYFDSQCMAAMNFQTMHNVTTETKFL LKL VKEGVVKDLSSGGIDR
EF
```

Important features of the protein:**Transmembrane domains:**

Amino acids 11-27;281-297

N-glycosylation sites:

Amino acids 30-34;180-184;334-338

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 2-6;109-113;223-227

N-myristoylation sites:

Amino acids 146-152;150-156;179-185;191-197

513/615

FIGURE 509

GGGCGGACGCAGTGCAGTAAGAGCAGATGGGCGGACCCAAATTTCTTCGGCTTCACGATTTTG
CCGAGGTCTAGCCCTGCATCCAGCCTTGAAACAGGGTGGGGAGGAGGCAGAAAGGGGAGGGAC
TGCACTCCCTCTGAGCGTGCTAGCTCCGACTGCCTGACGGATCACCCCTCCGCTCCAACATGG
CTAGTTCTCTCAACGCCGTGACTCAAGCCTGTTGTGCCAGGCAGGGCGCACTCAGCAGCGCAGC
CCCACAGGTGGCGAAGGCTCCGCGAGAGGGTTCGCCGAGGCTAGACAGTGGAGTGCCGCACA
GCGCGCCTTCCAGCCTCGCAGCCGCCACCCTAGCGGTTCCGACCCGGCGCCAGCAGGCCTGCT
TGGTCGATCTTCGAGCCAAAGATGCGGCGAGGCTGGAAGATGGCTCTGTCTGGGGGGCTGCGG
TGCTGCCGCCGGGTACTGTCCTGGGTGCCAGTGCTCGTTATTGTCCTCGTCGTGCTCTGGTCC
TACTATGCCTACGTCTTTGAACTCTGCCTGGTTATTTACCTCATACTCTACCATGCCATCTTT
GTGTTCTTTTACCTGGACCTACTGGAAGTCTATCTTTTACACTCCCACAGCAGCCAAACCAGAAG
TTCCACTTGTCCTACACAGACAAGGAGCGCTATGAAAATGAAGAAAGACCTGAGGTCCAGAAG
CAGATGCTTGTTGATATGGCCAAAAGCTACCGGTTTACACAAGAAGTGGAAAGTGGAGGTCAG
TTCATCCAAAGGCAGCTAGAGAGGCAGCTCAGCAAGTATCTCAGAAAGGCTAAGTCATATATG
TTCTCAAACTAGCCCTTTTTTTTCTCCCCTCTTCTGAAAACCACTATGGAGATTTTTTCTCCA
CATTTTATTTCTAAAAAATTTTAAACACATATCAAAGCTGGAAGAATTGTATAGTAAACAAAC
TGTATACCCCAAAGTGGATTCTTCTGCTAACATTTTTCTGTGTTGCTATATCACATATCTATC
CACATATGCATACCTCTATTTATCTTTGTCAGCCATCTTATGTTTCTGATGCATTTCAAAG
TAAATAGCTGACATCAGTAAGACATCTACCTAAATATTTTATTCTGTTTGTAAAATTTACA
TACAAAACATGCATAATCTTAAGGGTACCATTCCATGTATTTGAAAAGTGACACATCTGT
GTAATAAACCCCAATAAAATTGCCATCACCTCAG

514/615

FIGURE 510

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA98564
><subunit 1 of 1, 143 aa, 1 stop
><MW: 17255, pI: 9.99, NX(S/T): 0
MRRGWKMALSGGLRCCRRVLSWVPVLVIVLVVLWSYYAYVFELCLVIYLILYHAIFVFFT
WTYWKSIFTLPQQPNQKFHLSYTDKERYENEERPEVQKQMLVDMAKKLPVYTRTGSGGQF
IQQLERQLSKYLRKAKSYMFSN
```

Important features of the protein:**Transmembrane domain:**

Amino acids 24-45

N-myristoylation sites:

Amino acids 11-17;12-18

515/615

FIGURE 511

CAGCCGGGGCG**ATG**CGGGGCTCTGGCTGGGGCTCGTGTGGCAGAAGCTGCTGCTGTGGGGCG
CGGCGAGTGCCCTTTCCCTGGCCGGCGCCAGTCTGGTCCTGAGCCTGCTGCAGAGGGTGGCGA
GCTACGCGCGGAAATGGCAGCAGATGCGGGCCCATCCCCACGGTGGCCCCGCGCCTACCCACTGGTG
GGCCACGCGCTGCTGATGAAGCCGGACGGGCGAGGTAAGGGCCGGCGCTCCTCCTGGAGCGCA
ACGGGGTCCGAGCCCCGTCCCACCTCCGATCAGCCAGGAACCCGCTGCTTGTGGCGCTGG
CCGAGGAGAGAGGAGCCTGTCAACCCTGTGGAGAATGCACTCCAGTTCTAGTCGTTGCCCCCT
TGGCACCCGCCGACACTGCTAGTGCCCATCCCAAAGTGAGCATTTTCTTTGTGTGTAGCACA
GGATGCGGTATTTCCAAACCCCTGCCCTCGGTCTTTTCCACCTCACCGCTGCTCAGCTCTCA
AAGCCCTGCCGTTTTCTCCTGCCTTGGCTTGGGAAGCCT**TAG**GAACAGAAGCTCCCTGGGAGC
ACAGAGCGGTTTTAAACTGGCCAACACCTTAACGCCAGAGCCGCCCTCCTCTCGCTGCCACT
TTGGAAAATAAGAGACTAGAGATTCAGTGGACGCTTCCTCCCGGCATCACAAGACTTGACTGC
TGCTTCAGTTCCCGCTTGACCTTCATACTTTAGCCCTTTAAAGGATGTTACATAATAACAATT
AAGAGACGGCAGGGCCTTCAGGCAGACTTCTTTGGAGGGTGTCAAACGCCTTGTTTATTAAAG
AGTGAATTTTTTAATTAATAATCATGTTTTAAACAGAGATGGACATTTTATTGATGGAAAAAA
ATCACGTTAAGTTAGAAAGCTCTCAAAGTACCTGGTATTTACAACCTCCCTGTCAGGGAGGGC
GAACTCGATCTCAGAGTTTATTTTCATCAGGGATTACGTTGAGGTACCCAGAAATGAGAAGA
TTTGCCCAAATGGCATATTTTAAATTTGGCCAGACCAGAACCCAGTTTCCTCTGGGATTAT
TTGTTAGTAATCGTTTTACAGGCTGAGCATTAACCTCAAGCTTGAAGGACTTTTCTC
ATTTTCACTTGTTTTCTCTAATAAAAAATAATGCTGTAATTTCAACTTCACAAGATGAGGCCTC
ATGGAAGAGTGTTTACCAAATATTAATAATACTTTGACAGAAAAAATCAAGCGAACTCTT
GCCAACCAAATATCATCATGACTGATGTAACAAGTAATCCAACACAGATATGAAAATCACTGG
TAAAAATCATCTCAGTTAATTCTAAAAGCAGAGCTAACCACCCCTTTTGTCTAAGGCTTTAT
GGTATTAATAAATAAACTGTACAAAAATATAGATTTTCCCCTATCCCCTACCCCTGGAAAGTA
ATATACTGAAGTCTCATCATACTGTTTTGGGGATTCCAGTAATTAAATCTCTAGTGAACAAA
GACCTGTTTCAAACAACCTGTGAGCTGACTGGACTATTTAAAGTAATTCTCCTTGTAGTCAC
TTTCAGAGTGAAGACAATGACGAATACTGTCTTTACAAAGGGACTTTTTATTCCACCAACAA
ATTCTGGATTTTGGCATCAGGAAACCACTGTTCAATTTCCAACACTATATCCAAGTTGTTTG
AGAAATTATTTAAACTCTTTAACTTAGAGGGTTTTCTTTCTCCTTTACTTGTTAAAGTGACT
ATATTACAGAGTCACTTTAAGGATTAAATTTATTGCATGCAAAGTTTCTAGATCACTGTCTAG
AAGTCAGTTAGAGTAAGTTCTTTAGTTGTCAATCAAGCATTTAGTAAGGCCCTGCTTTGTGCC
CAGTGTTGACCTCAACAAAGTTGGGGATATCAGAATATTCTAAGATACAGTCGTTGTTCCCAA
GAATCTTGTCTTTCACATACAAGAGGTGTTGCGTTTCATTTTGGCGCTAATGTCCAAACGCTG
GCCTCAGCCATTTACCTTGAAGATTGCAGTTGGCTTCCAACCTGGCCTCTAACTCTAATCTA
GCATTTTCCAGTCCATTGTGACAAAGTCTGCCTTCCCCAGCTACTCCAGCTGTTGGACCTGC
TGCCTTAGAACACAGATTGGTACCTCGTGCC

516/615

FIGURE 512

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA107443
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19353, pI: 10.97, NX(S/T): 0
MAGLWLGLVWQKLLWGAASALSLAGASLVLSLLQRVASYARKWQQMRPIPTVARAYPLV
GHALLMKPDGRGKGRRSSWSATGSAAPFPPSDQPGTRCLWRWPQERGACHPVENALPVLV
VAPWHPPTLLVPHPKVSIFFVCSTGCGISKPLPSVFSLTLTAQLSKPCRFLLPWLGKP
```

Important features of the protein:**Signal peptide:**

Amino acids 1-25

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 75-79

N-myristoylation sites:

Amino acids 3-9;17-23;145-151

Amidation site:

Amino acids 73-77

Leucine zipper pattern:

Amino acids 8-30

517/615

FIGURE 513

GGCGGCTGGACGAGGACGCTCAGAGCCCAGCTCTCGAGAGTTCAAGCAACCGACGGTTCC
CCTACTGCTCCCAGGAGCGGTTACCTGGGCACTCTGTGCCCCCTCCTTCCTGTTCCGGGCCCA
GGCCGAGGACCTGCCAGTAGGGCTCAGTTGCCTGGAGCCCGTTAGCCCCATCCCCAGTT
CACTTTGCTTGTGGGATCTCCCCGTTGCTCCTGCCCGTGGACTGAGTGGCAGGCCATCCT
ACAAGCACCCGGACACTTGACATCAGTGGTGTCAAGACAACCTCTAAGAAGGTTTTCCGTG
ATCCTGCAAGCCCTGCCTTCCTTCCTGGGATCCTGCCTTCAATTTGATTGCACAGGTACC
ACAGCAAGCCAGTGCTGTGTGCTCCGAGTTCCAGGGCGTCCTCCAGCTCAGCCACTGCAC
TGAGAACAATGGACTCTCTGTGGGGCCCAGGAGCCGGGAGTCACCCCTTTGGGGTCCACAA
CACCCGGCTGTCCCCAGACTTGTGTCCAGGGAAGATAGTGTTGAGGGCCCTCAAGGAGAG
CGGGGCAGGGATGCCTGAGCAGGACAAGGACCCTAGAGTCCAAGAGAATCCTGGTGATCA
GAGAAGGGTCCCCGAGGTACCCGGGGATGCACGGTCTGCATTTCCGGCCCCCTGCGGGACAA
TGGAGGCCTCTCTCCCTTTGTGCCCGGGCCCCGGGCCTCTGCAGACAGACCTCCATGCCCA
GAGGTCAGAAATCAGATATAACCAGACATCCCAGACCTCCTGGACGAGCTCCTGCACCAA
CCGAAATGCCATCTCCAGCTCCTACAGCTCCACGGGAGGCTTGCTGGGGCTAAAGCGGAG
GAGGGGGCCAGCCTCATCCCAGTGCAGCTGACCCTCAGTTCCTCAAAGACAGTGAGTGA
GGACAGGCCTCAGGCTGTCTCTTCAGGTACACCCAGTGTGAAAAGGCAGCAGATATAGC
ACCAGGGCAGACACTCACCTCAGGAATGACTCCTCCACATCCGAGGCCTCTAGGCCAG
TACACACAAGTTTCCCTGCTGCCACGCAGGCGAGGGGAGCCTTTGATGCTGCCACCTCC
CTTAGAGCTGGGGTACCGGGTCACTGTTGAAGACCTGGACCGGGAGAAGGAGGCGGCCTT
CCAGCGCATCAACAGTGCACTGCAGGTTGAGGACAAGGCCATCTCGGACTGCAGACCTC
ACGGCCTTCCCACACTTTGTCTCACTTGCAACAGGGGCTTCTGGTCTGCCTGCCGTTTC
TAAAGCACCCAGTATGGATGCACAGCAGGAGACACACAAGTCCCAAGACTGCCTGGGCCT
ACTGGACCCCTTAGCATCTGCTGCAGGGGTCCCCTCTACAGCTCCCATGTCTGGGAAGAA
GCACAGACCACCAGGCCCCCTGTTCTCCTCCTCAGATCCCCTTCTGCCACCTCTTCTGA
TTCACAGGACTCAGCCCAGGTACCTCGCTGATTCTCCTGCCCCCTTCCCAGCTGCAAGCAT
GGATGCGGGCATGAGAAGAACAAGGCATGGCACTTCTGCTCCTGCAGCTGCCGCAGCAGC
CCCTCCCCGCTCCACATTGAACCCACAGTTGGGGTCACTACTGGAGTGGATGGAGGCCCT
TCACATTTCTGGGCCTCAGCCACAGCTGCAGCAGGTGCCCAGAGGTGAGAACCAGAGATC
CCAGACCTCCTGGACCAGCTCGTGCCCCAAATGAATGCCATCTCGAGCCCCCTACAGCTC
TACGGGAGGCCTCCCGGAACAAAAGCGGAAGAGGGGCCAGCCTCATCCCAGTGCAGCTG
ACCCTCAGTTCCTCAAACACAGTGAGTGAGGACGGACCTCAGGCTGTCTCTTCGGGTAC
ACCCAGTGTGAAAAGACGGCAGATACAGCACAGGGCAGACACTCGCCTCCAGGGGTGGC
TCCCCCAGATCCCAGGCCTCTAGGCCCCGTATATGCAAGTTTCCCCTGCTGCCACGCAGG
CGAGGGGAGCCTTTGATGCTGCCACCTCCCTTAGAGATGGGGTACCGGGTCACTGCTGAA
GACCTGGACCGGGAGAAGGAGGAGGCATTCCAGCGCATCAACAGTGCACTGCAGGTTGAG
GACCAGGCCATCTAGGACTGCAGACCTCACGGCCTTCCCACACTTTGTCTCACTTGCA
ACAGGGGCTTCTGGTCTGCCTGCCGTTTCTAAAGCACCCAGTATGGATGCACAGCAGGAG
ACACACAAGTCCCAAGACTGCCTGGGCCTAGTGGCCCCCTGCATCTGCTGCACAGGCCT
GTAGTCCCAGCTACTTGGGAGGCTGAGGCAGGAGAACGGCATAAACCCGGGAGGCAGAGC
TTGCAGTGAGCTGAGATCGCGCCACTGCACTCCAGCCTGGGTGACAGAGCGAGACTCCGT
CTC

518/615

FIGURE 514

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA107786
><subunit 1 of 1, 428 aa, 1 stop
><MW: 45450, pI: 9.28, NX(S/T): 3
MDSLWGPAGSHPFVGHNTLSPDLCPGKIVLRALKESGAGMPEQDKDPRVQENPGDQRR
VPEVTGDARSAFRPLRDNGGLSPFVPGPGPLQTDLHAQRSEIRYNQTSQTSWTSSCTNRN
AIISSYSSTGGLLGLKRRRGPASSHCQLTLSSSKTVSEDRPQAVSSGHTQCEKAADIAPG
QTLTLRNDSSSTSEASRPSTHKFPLLPRRRGEPLMLPPPPELGYRVTVEDLDREKEAAFQR
INSALQVEDKAISDCRPSRPSHTLSSSLATGASGLPAVSKAPSMDAQQETHKSQDCLGLLD
PLASAAGVPSTAPMSGKKHRPPGPLFSSSDPLPATSSSDSQDSAQVTSIIPAPFPAASMDA
GMRTRHGTSAPAAAAAAPRSTLNPTLGSLLWMEALHISGPQPQLQQVPRGQNQRSQT
SWTSSCPK

Important features of the protein:**N-glycosylation sites:**

Amino acids 105-109;187-191

Glycosaminoglycan attachment site:

Amino acids 38-42

N-myristoylation sites:

Amino acids 15-21;130-136;180-186;307-313;361-367

Amidation site:

Amino acids 315-319

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 106-117

519/615

FIGURE 515

GTCAGGGCCAGGGTGAGCGCCCGACTCCGAGCTGTCCCCGCTCCCGGCGCGGGCGCTCCGCTCT
CAGCCACCTCACGGCTGCCAGGAGTGCGCGGGAGTTTGCCCCGGAGCGCGGGGAAGTTTCCTC
CGAAGCTGCGCTCCTGGAACAGCAGCACCTGCAAGCGCCCGGCAGCGGCCCGCGAGGTTACTT
TATGGAATTGGGCTCTTAGAGAACAAGAAAAGACTGAAGTTTACGGGAAAACAAATCATGTG
GTCTTCAGATTCTGAAATAAGGAGAAATGAGCCATCTGAAATGGTCATGAACCCCAACAAG
TCTTCCTCTCTGTGCTGATATTTGGAGTAGCTGGGCTACTCCTCTTCATGTATTTGCAAGTCTGG
ATTGAAGAACAACATACAGGGAGAGTGGAGAAGAGAAGAGAACAAAAAGTAACTTCAGGATGG
GGACCAGTGAAGTACTTGCGGCCTGTACCCAGAATCATGAGTACAGAAAAAATCCAGGAACAT
ATCACCAACCAGAACCCCAAGTTTCACATGCCTGAGGATGTACGAGAAAAAAGGAAAAATCTT
CTACTCAATTCTGAGAGATCTACTAGGCTCTTAACAAAGACCAGTCATTACAAAGGAGGGGAT
CAAGCTTTAAGTAAGTCCACAGGGTCACCAACAGAGAAGTTGATTGAAAAACGTCAAGGAGCT
AAGACTGTTTTTAAACAAGTTCAGCAACATGAATTGGCCAGTGGACATTCACCCTTTAAACAAA
AGTTTAGTCAAAGATAATAAATGGAAGAAAAGTGGAGAGACCAAGAGAAACGAAGGTCTTTC
CTTCAGGAGTTTTGCAAGAAATACGGTGGGGTGAGTCATCATCAGTCACATCTTTTTTCATACA
GTATCCAGAATCTATGTAGAAGATAAACACAAAATCTTATATTGTGAGGTACCTAAGGCTGGC
TGTTCCAATTGGAAGAAATCTGATGGTACTAAATGGATTGGCTTCCTCTGCATACAACATC
TCCACAATGCTGTCCACTACGGGAAGCATTGGAAGAAGCTAGATAGCTTTGACCTAAAAGGG
ATATATACCCGCTTAAATACTTACACCAAAGCTGTGTTTGTTCGTGATCCCATGGAAAGATTA
GTATCAGCCTTTAGGGACAAATTTGAACACCCCAATAGTTATTACCATCCAGTATTCGGAAAG
GCAATTATCAAGAAATATCGACCAAATGCCTGTGAAGAAGCATTAAATTAATGGATCTGGAGTC
AAGTTCAAAGAGTTTATCCACTACTTGCTGGATTCCCACCGTCCAGTAGGAATGGACATTCAC
TGGGAAAAGGTGAGCAAACTCTGCTATCCGTGTTTGATCAACTATGATTTTGTAGGGAAATTT
GAGACTTTGGAAGAAGATGCCAATTACTTTTTACAGATGATCGGTGCTCCAAAGGAGCTGAAA
TTTCCCAACTTTAAGGATAGGCACCTCTCCGATGAAAGAACCAATGCTCAAGTCGTGAGACAG
TATTTAAAGGATCTGACTAGAAGTGAAGACAATTAATCTATGACTTTTATTACTTTGGACTAT
TTAATGTTTAAATTATACAACCTCCACTTTTGTAGTTTGCATTCAATTTTCTAAAACCTGTATAT
ACTTAATGATGATAAGTTCAAATCAGCTGTAATTTTTCTATAATTCTCTGTATGACAGAAATT
TAACCAAGTGCAAGTTGTCTTGATTTAATGTAGATTTTTTACCAAATAGTATGACACCAATTGGC
ACAAAGTTATAGGAAAATCACCTACAGGAGATGTAAACAACTTGAGTTGCTCTAAAATGTTTG
GAAAAGAGCTGCTTTTGCATTATGAATTATATTGTTGAAGCAATAACCTAGCCAGCTGTTGCA
TTAGCTAAAGCAGCCTCTTGCAATGGTAGGAAAAAAGGATCTCAAATAGCATGAGTGTATGTC
TATATCCTGAAATTTATTGTCTAAAATGCATGAATATATTTTTAGCAGTCTGTGGCATATTAA
TCAAAGTGTGAATTGTTTCTTACACCTGGAAATCTTCTATCAACTATAATGATAAATCC
ATTTTGAAGTGATATTTGGACTTAGGCATTTTACTTTAGATTGGAAGGCATTATGTGATTTACA
ATATGAGAATATAGCAGAAAAACCA

520/615

FIGURE 516

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108682
><subunit 1 of 1, 443 aa, 1 stop
><MW: 52021, pI: 9.63, NX(S/T): 4
MQPSEMVMNPKQVFLSVLIFGVAGLLLFMYLQVWIEEQHTGRVEKRREQKVTSGWGPVKY
LRPVPRIMSTEKIQEHITNQNPKEHMPEDVREKKENLLLNSERSTRLLTKTSHSQGGDQA
LSKSTGSPTEKLEKQGAKTVENKFSNMNWPVDIHPLNKSLVKDNKWKKTEETQEKRRS
FLQEFCKKYGGVSHHQSHLFHTVSRIVYEDKHKILYCEVPKAGCSNWKRIIMVLNGLASS
AYNISHNAVHYGKHLKKLDSFDLKGITYTRLNTYTKAVFVRDPMERLVSAFRDKFEHPNSY
YHPVFGKAIKKYRPNACEEALINGSGVKFKEFIHYLLDSHRPVGMDIHWEKVSCLKCPC
LINYDFVGKFETLEEDANYFLQMGAPKELKFPNFKDRHSSDERTNAQVVRQYLKDLTRT
ERQLIYDFYYLDYLMFNYYTTPLL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-24

N-glycosylation sites:

Amino acids 159-163;243-247;324-328;437-441

Glycosaminoglycan attachment site:

Amino acids 53-57

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 177-181

Tyrosine kinase phosphorylation site:

Amino acids 329-337

N-myristoylation sites:

Amino acids 116-122;236-242

521/615

FIGURE 517

GGAAGTTCAGGACACCTGTGTGGCCGCACTGCTCCCTCTGGCCCAACCAATGCTCTGTCCAGCCACCTGCTGC
CCGCTTGGTCTCTTCTGGCAGGGTCTCAGGCTGGGCTGGGTCCCCAACCCTGCAGGAGCCCTGGCCAGG
CCGTGTGCAACTTCGTGTGTGACTGCAGGGACTGCTCAGATGAGGCCAGTGTGTTACCACGGGGCTCGCCCA
CCCTGGGCGCCCCCTTCGCTGTGACTTCGAGCAGGACCCCTGCGGCTGGCGGGACATTAGTACCTCAGGCTACA
GCTGGCTCCGAGACAGGGCAGGGGCCGCACTGGAGGGTCTGGGCTCACTCAGACCACACACTGGGCACCGACT
TGGGCTGGTACATGGCCGTTGGAACCCACCGAGGGAAAGAGGCATCCACCGCAGCCCTGCGCTCGCCAAACCCTGC
GAGAGGCAGCCTCCTCTTGCAAGCTGAGGCTCTGGTACCACGCGGCTCTGGAGATGTGGCTGAAGTGCAGGCTGG
AGCTGACCCATGGCGCAGAGACCTGACCTGTGGCAGAGCACAGGGCCCTGGGGCCCTGGCTGGCAGGAGTTGG
CAGTGACCCAGGCGCATCCGGGGTGAATTCGAGTGACCTTCTCTGCCACCCGAAATGCCACCCACAGGGGCG
CTGTGGCTCTAGATGACCTAGAGTTCTGGGACTGTGGTCTGCCACCCCCAGGCCAACTGTCCCCGGGACACC
ACCATGCCAGAACAAGGTCTGCGTGGAGCCCCAGCAGCTGTGCGACGGGGAAGACAAGTGCAGGGGACCTGTCTG
ATGAGAACCCACTCAGCTGTGGCCGCCACATAGCCACCGACTTTGAGACAGGCTGGGGCCATGGAACCGCTCGG
AAGGCTGGTCCCGAACCACCGTGTGTGGTCTGAGCGCCCTCTGGCCACGCCGTGACCACAGCCGGAACA
GTGCACAGGGCTCCTTCTGGTCTCCGTGGCCGAGCCTGGCACCCTGCTATACTCTCCAGCCCCGAATTCGAAG
CCTCAGGCACCTCCAAGTGTCTGGTCTTCTATCAGTACCTGAGTGGGTCTGAGGCTGGCTGCCCTCAGCTGT
TCTGACAGACTCTGGGGCCCGGGCCCCCGGGCCCCCGTCTGCTGCGGAGGGCGCCGAGGGGAGCTGGGGACCG
CCTGGGTCCGAGACCGTGTGACATCCAGAGCGCCTACCCCTTCCAGATCCTCCTGGCCGGGCGAGACAGGCCCGG
GGGGCGTGTGGGTCTGGACGACCTCATCTGTCTGACCACTGCAGACCACTCTCGGAGGTGTCCACCTGCAGC
CGCTGCCTCCTGGGGCCCCGGGCCCCAGCCCCCAGCCCTGCGGCCAGCTCGCGGCTCCAGGATTCCTGCAAGC
AGGGGCATCTTGCCTGCGGGGACCTGTGTGTGCCCCGGAACAAGTGTGTGACTTCAGGAGCAGTGCAGGGG
GCGAGGACGAGCAGGCTGTGGCACCACAGACTTTGAGTCCCCGAGGCTGGGGGCTGGGAGGACGCCAGCGTGG
GGCGGCTGCAGTGGCGGCTGTCTCAGCCAGGAGAGCCAGGGGTCCAGTGCAGCTGCTGCTGGGCACCTTCTGT
CTCTGCAGCGGCTGGGGGCGAGCTAGGCGCTGAGGCCCGGGTCTCACACCCCTCCTTGGCCCTTCTGGCCCCA
GCTGTGAAGTCCACTGGCTTATTATTACAGAGCCAGCCCCGAGAGGTCTCCTGTAAGTTTGAAGCGGACACAT
GCAGCTGGTACCCAGGCCACCTCTCAGACACACACTGGCGCTGGGTGGAGAGCCGCGGCCCTGACCACGACCACA
CCACAGGCCAAGGCCACTTTGTGCTCCTGGACCCACAGACCCCTGGCCTGGGGCCACAGTGGCCACCTGCTCT
CCAGGCCCCAGGTGCCAGCAGCACCACGGAGTGTCTCAGCTTCTGGTACCACCTCCATGGGCCCCAGATTGGGA
CTCTGCGCCTAGCCATGAGACGGGAAGGGGAGGAGACACACCTGTGGTTCGCGGTGAGGCACCCAGGGCAACCGCT
GGCAGGAGGCTGGGCCACCTTTCCACACAGCCTGGCTCCCATGCCAGTACCAGCTGCTGTTGAGGGCCTCC
GGGACGGATACACGGCACCATGGCGCTGGACGATGTGGCGTGGCGGCCGGGCCCTGCTGGGCCCTAATTACT
GCTCCTTTGAGGACTCAGACTGCGGCTTCTCCCTGGAGGCCAAGGTCTCTGGAGGCGGACGGCAATGCCTCGG
GCCATGCTGCCTGGGGCCCCCAACAGACCATAACCTGAGACAGCCCCAAGGGCACTACATGGTGGTGACACAA
GCCAGACGCACTACCCCGGGGCCAGACGGCCTCCCTGACCTCCAAGGAGCACAGGCCCTGGCCAGCCTGCTT
GTCTGACCTTCTGGTACCACGGGAGCCTCCGCGAGCCAGGCACCTGCGGGTCTACCTGGAGGAGCGCGGGAGGC
ACCAGGTGCTCAGCTCAGTGCACGGCGGGCTTGCCTGGCGCCTGGGCAGCATGGACGTGCAGGCCGAGCGAG
CCTGGAGGGTGGTGTGAGGAGTGGCGCAGGCGTGGCACACTCCTACGTGGCTCTGGATGATCTGCTCCTCC
AGGACGGGCCCCGCTCAGCCAGGTTCTGTGATTTTGAAGTCTGGCCTGTGTGGCTGGAGGCCACCTGGCCGGGC
CCGGCCTGGGCGGATACAGCTGGGACTGGGGCGGGGAGCCACCCCTCTCGTTACCCCGAGCCCCCTGTGGACC
ACACCCCTGGGCACAGAGGACAGGCCACTTTGCCTTCTTTGAAACTGGCGTGTGGGGCCCGGGGGCGCGCCT
GGCTGCGCAGCGAGCCTCTGCCGGCCACCCAGCCTCCTGCCTCCGCTTCTGGTACCACATGGGTFTTCTGAGC
ACTTCTACAAGGGGAGCTGAAGTACTGCTGCACAGTGTCTCAGGGCCAGCTGGCTGTGTGGGGCGCAGGGGGC
ATCGGGCGCACCACTGGCTGGAGGCCAGGTGGAGGTAGCCAGTGCCAAGGAGTCCAGATCGTGTGGAAGCCA
CTCTGGGCGGCCAGCCAGCCCTGGGGCCCATTTGCCCTGGATGACGTGGAGTATCTGGCTGGGCAGCATTTGCCAGC
AGCCTGCCCCAGCCCGGGGAACACAGCCGACCCGGGTCTGTGCCAGCTGTGGTTGGCAGTGCCTCCTATTGC
TCATGCTCCTGGTGTCTGGGACTTGGGGGACGGCGCTGGCTGCAGAAGAAGGGGAGCTGCCCCCTCCAGAGCA
ACACAGAGGCCACAGCCCTGGCTTTGACAACATCCTTTCAATGCGGATGGTGTCAACCTCCCGGCATCTGTCA
CCAGTGATCCGTAGACCAACCCAGACAAGGCCCGCTCCTCAGTGACATCCAGCACTTGGTCAGACCTAGCC
AGGGACCGGACACCTGCCCCGCCAGGCTGGGACAGGCTGCAGGTCTCAGGATATGCTGAGGCTGGGGCTTCCC
TGCCCTGTGCTGACTCTGTGTCTGTGAATAAACACCTGGCCCATGAGGGCGCCCCAAAAA

522/615

FIGURE 518

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108684
><subunit 1 of 1, 1137 aa, 1 stop
><MW: 122776, pI: 6.00, NX(S/T): 4
MPLSSHLLPALVLFLAGSSGWAVPNHCRSPGQAVCNFVCDRCDSDEAQCQYHGASPTL
GAPFACDFEQDPCGWRDISTSGYSWLRDRAGAALEGPGPHSDHTLGTDLGWYMAVGTHRG
KEASTAALRSPTLREAASSCKLRLWYHAASGDVAELRVELTHGAETTLWQSTGPWGPWG
QELAVTTGRIRGDFRVTFSATRNATHRGAVALDDLEFWDCGLPTPQANCPPGHHHCQNKV
CVEPQQLCDGEDNCGDLSDENPLTCGRHIATDFETGLGPWNRSEGWSRNRHRAGGPERPSW
PRRDHSRNSAQGSFLVSVAEPGTPTAILSSPEFQASGTSNCSLVFYQYLSGSEAGCLQLFL
QTLGPGAPRAPVLLRRRRRRELGTAWVRDRVDIQSAYPFQILLAGQTGPGGVVGLDDLILS
DHCRPVSEVSTLQPLPPGPAPAPQPLPSSRLQDSCKQGHLAGDLCVPPEQLCDFEEQ
CAGGEDEQACGTTDFESPEAGGWEDASVGRQLQWRRVSAQESQGSSAAAAGHFLSLQRAWG
QLGAEARVLTPLLGPSPGSCSELHLYLQSQPREVSCNFERDTCWYPGHLSDTHWRWVE
SRGPDHDHTTGQGHFVLLDPTDPLAWGHSALLSRPQVPAAPTECLSEFWYHLHGPFQIGTL
RLAMRREGEETHLWSRSGTQGNRWHEAWATLSHQPGSHAQYQLLFEGLRDGYHGTALDD
VAVRPGPCWAPNYCSFEDSDCGFS PGQGLWRRQANASGHAAWGPPTDHTTETAQGHYMV
VDTSPDALPRGQTASLTSKEHRPLAQPACLTFWYHGSLRSPGTLRVYLEERGRHQVLSLS
AHGGLAWRLGSMQVQAEARWRVFEAVAAGVAHSYVALDDLLQDGPQPFGSCDFESGL
CGWSHLAGPGLGGYSWDWGGGATPSRYPPPPVDHTLGTGAGHFAFFETGVLGPGGAAWL
RSEPLPATPASCLRFWYHMGFPPEHFYKGLKVLHSAQGLAVWGAGGHRHQWLEAQVE
VASAKEFQIVFEATLGGQPALGPALDDVEYLAGQHCQAPSPGNTAAPGSVPVAVGSA
LLLLMLLVLLGLGRRWLQKKGSCPFQSNTEATAPGFDNILENADGVTLPASVTS DP
```

Important features of the protein:**Signal peptide:**

Amino acids 1-20

Transmembrane domain:

Amino acids 1075-1092

N-glycosylation sites:

Amino acids 203-207;281-285;339-343;756-760

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 514-518;1100-1104

N-myristoylation sites:Amino acids 32-38;55-61;61-67;106-112;116-122;336-342;350-356;409-415;
523-529;540-546;678-684;707-713;791-797;870-876;921-927;
937-943;954-960;1036-1042;1071-1077**Amidation site:**

Amino acids 1093-1097

Cell attachment sequence:

Amino acids 191-194

523/615

FIGURE 519

GCAGGGGAGCTCCGAGTGTCCACAGGAAGGGAACATATCAGCTCCTGGCATCTGTAAGGATGCT
GTCCATGCTGAGGACAATGACCAGACTCTGCTTCCTGTTATTCTTCTCTGTGGCCACCAGTGG
GTGCAGTGCAGCAGCAGCCTCTTCTCTTGAGATGCTCTCGAGGGAATTCGAAACCTGTGCCTT
CTCCTTTTCTTCCCTGCCTAGAAGCTGCAAAGAAATCAAGGAACGCTGCCATAGTGCAGGTGA
TGGCCTGTATTTTCTCCGCACCAAGAATGGTGTGTGTCTACCAGACCTTCTGTGACATGACTTC
TGGGGGTGGCGGCTGGACCCTGGTGGCCAGCGTGCACGAGAATGACATGCGTGGGAAGTGCAC
GGTGGGTGATCGCTGGTCCAGTCAGCAGGGCAACAAAGCAGACTACCCAGAGGGGGATGGCAA
CTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCGATGACTACAAGAACCC
TGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCATGTGCCCAACAAGTCCCCCAT
GCAGCATTGGAGAAACAGCGCCCTGCTGAGGTACCGCACCAACACTGGCTTCCTCCAGAGACT
GGGACATAATCTGTTTGGCATCTACCAGAAATACCCAGTGAAATACAGATCAGGGAAATGTTG
GAATGACAATGGCCCAGCCATACCTGTGGTCTATGACTTTGGTGATGCTAAGAAGACTGCATC
TTATTACTCACCGTATGGTCAACGGGAATTTGTTGCAGGATTTCGTTTCAGTTCCGGGTGTTTAA
TAACGAGAGAGCAGCCAACGCCCTTTGTGCTGGGATAAAAGTTACTGGCTGTAACACTGAGCA
TCACTGCATCGGTGGAGGAGGGTTCTTCCCACAGGGCAAACCCCGTCAGTGTGGGGACTTCTC
CGCCTTTGACTGGGATGGATATGGAACACGTTAAGAGCAGCTGCAGTCGGGAGATAACGGA
GGCGGCTGTACTCTTGTTCTATAGATTGAGACAGAGCTCTGCGGTGTCAGGGCGAGAACCCATC
TTCCAACCCCGGCTATTTGGAGACGGAAAACTGGAATCTAACAAGGAGGAGAGGAGACTAA
ATCACATCAATTTGCA

524/615

FIGURE 520

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108701
><subunit 1 of 1, 325 aa, 1 stop
><MW: 36212, pI: 8.68, NX(S/T): 1
MLSMRLRTMTRLCFLLFFSVATSGCSAAAASSLEMLSREFETCAFSFSSLPRSCKEIKERC
HSAGDGLYFLRTKNGVVYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGNKA
DYPEGDGNWANYNTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSALLR
YRTNTGFLQRLGHNLFGIYQKYPVKYRSGKCWNDNGPAIPVVYDFGDAKKTASYYSYGQ
REFVAGFVQFRVFNNERAANALCAGIKVTGCNTEHHCIGGGGFFPQ GKPRQCGDFAFDW
DGYGTHVKSSCSREITEAAVLLFYR
```

Important features of the protein:**Signal peptide:**

Amino acids 1-26

Glycosaminoglycan attachment site:

Amino acids 86-90

N-myristoylation sites:

Amino acids 23-29;88-94;127-133;136-142;265-271

525/615

FIGURE 521

GATCAGTGTGTGAGGGAACTGCCATC**ATG**AGGTCTGACAAGTCAGCTTTGGTATTTCTGCTCCTGCAGCTCTTCT
GTGTTGGCTGTGGATTCTGTGGGAAAGTCCTGGTGTGGCCCTGTGACATGAGCCATTGGCTTAATGTCAAGGTCA
TTCTAGAAGAGCTCATAGTGAGAGGCCATGAGGTAACAGTATTGACTCACTCAAAGCCTTCGTAAATTGACTACA
GGAAGCCTTCTGCATTGAAATTTGAGGTGGTCCATATGCCACAGGACAGAACAGAAAGAAATGAAATATTTGTTG
ACCTAGCTCTGAATGTCTTGCCAGGCTTATCAACCTGGCAATCAGTTATAAAATTAAATGATTTTTTTGTTGAAA
TAAGAGGAACTTTAAAAATGATGTGTGAGAGCTTTATCTACAATCAGACGCTTATGAGAAGCTACAGGAAACCA
ACTACGATGTAATGCTTATAGACCCTGTGATTCCCTGTGGAGACCTGATGGCTGAGTTGCTTGCAGTCCCTTTTG
TGCTCACACTTAGAATTTCTGTAGGAGGCAATATGGAGCGAAGCTGTGGGAACTTCCAGCTCCACTTTCCTATG
TACCTGTGCCTATGACAGGACTAACAGACAGAATGACCTTTCTGGAAAGAGTAAAAAATTCAATGCTTTCAGTTT
TGTTCCACTTCTGGATTGAGGATTACGACTATCATTTTTGGGAAGAGTTTTATAGTAAGGCATTAGGAAGGCCCA
CTACATTATGTGAGACTGTGGGAAAAGCTGAGATATGGCTAATACGAACATATTGGGATTTTGAATTTCCCTCAAC
CATACCAACCTAACTTTGAGTTTGTGGAGGATTGCACTGTAAACCTGCCAAAGCTTTGCCTAAGGAAATGGAAA
ATTTTGTCCAGAGTTCAGGGGAAGATGGTATTGTGGTGTCTCTGGGGTCACTGTTTCAAATGTTACAGAAG
AAAAGGCTAATATCATTGCTTCAGCCCTTGCCAGATCCACAGAAGGTGTATGGAGGTACAAAGGAAAAAAC
CATCCACATTAGGAGCCAATACTCGGCTGTATGATTGGATACCCAGAAATGATCTTCTTGGTCATCCAAAAACCA
AAGCTTTTATCACTCATGGTGAATGAATGGGATCTATGAAGCTATTTACCATGGGGTCCCTATGGTGGGAGTTC
CCATATTTGGTGATCAGCTTGATAACATAGCTCACATGAAGGCCAAAGGAGCAGCTGTAGAAATAAACTTCAAAA
CTATGACAAGCGAAGATTTACTGAGGGCTTTGAGAACAGTCATTACCGATTCCCTCTATAAAGAGAATGCTATGA
GATTATCAAGAATTCACCATGATCAACCTGTAAAGCCCTAGATCGAGCAGTCTTCTGGATCGAGTTTGTCATGC
GCCACAAAGGAGCCAAAGCACCTGCGATCAGCTGCCCATGACCTCACCTGGTCCAGCACTACTCTATAGATGTGA
TTGGGTTCTGCTGACCTGTGTGGCACTGCTATATTTGTTTCAAAAATGTTTTTATTTTCTGTCAAAAAT
TTAATAAACTAGAAAGATAGAAAAGAGGGAA**TAG**ATCTTTCCAAATTCAGAAAAGACCTGATGGGGTAATCCTG
TTAATTCAGCCACATAGAATTTGGTGAAAACCTTGCTATTTTCATATTATCTATTCTGTTATTTTATCTTAGCT
ATATAGCCTAGAATTCATGATCATGAGGTTGTGAGTATATCTCATTTCTTCGTTGTATTTTCTAGGTGTCTTT
ACTCTCTTCTCTCACTTTGTGACACAAGGACATGAATACATCTAAATTTTCTATTTCTGATATGACTGTTTTGA
TGATGTCATTACTTCTATAACCTTAAGTGATAGGGTGACATGCAATATGATTATTCCTGGTGTGCCCCAAACAC
ATGGATATAAAGAGGTAAAAAACTTAAATTCACAAAATTCAGTAAACCACACAAATCAGGTAAGTGTCTATGA
GATTAGCTGGCTATGAGAAACATAATGATGTTTCTTTTCAATTTAAATAAGCCTTTCTACATAGCCAGCATCAG
TGATCTCAGAAAATAAATTGCTAATAATGATGACATGGCATTATGCTTAGAAAAGTTTGCTGTATTTCCATAGAC
CTCATCTAGATGTCATGGCCTACATTTCTGCCATCACTCAACCAATACTTTTTTCTGTTTTCTTGATGATAAAAA
GACCTTTCTCATGATTGCCATCAAATAACAAAAGAACTATTTTTTTCTCACATAGAGAACATGTCAGTAAGAT
ATTCAAGGTGAACAGATATTTTTGGGATTAGTAACATTTTGAATATGTGGTGATAATTACTGAGTTTATAAAAT
TTATTTGATAGTACACTTAAAGAAGATTATATGTTTATTTCTTTAAAAATGATGAATACTCATAATTTCTTATCTC
TATAATCAAAAGTATAATTTACTGTAGAAAATAAAGAGATGCTTGTTCTGAAAGTAAGATCAGTGAAGTCTTT
TCAGTCTCAATCTTTGAGAATTGTAAATTCATCAAATAATTGCTTACATAGTAAAAATTTAAGGTATTAGAAAAC
CTGCATAACAAATAGTATTATATATTAAATATTTTGATATGTAAAGCTCTACACAAAGCTAAATATAGTGTAATA
ATGTTTACACTAGTAAGCAAATATGTTAATCTTCTCATTTTTTACTGTCAATAATCTTAGTGATATGCCTATT
AATAGTTTTAAATAAATAAATTGGCTTATCTGGCTTTTTGAAAATTTTGAAATTTCTACAGATGTTGATTAGGTA
TATCTACAAATTAATTTCAATTTTAAATGATGATATAAAAAATAAATATAAGTATTTTCTTGTGTATGTATACA
ATAAATATAAATAAATAATTGTTTACTGTTTTGAAAGTTTCTTAAGTTTAA

526/615

FIGURE 522

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108720
><subunit 1 of 1, 527 aa, 1 stop
><MW: 60284, pI: 8.31, NX(S/T): 3
MRSDKSALVFLLLQLFCVGCFCGKVLVWPCDMSHWLNVKVILEELIVRGHEVTVLTHSK
PSLIDYRKPSALKFEVVHMPQDRTEENEIFVDLALNVLPGLSTWQSVIKLNDFFVEIRGT
LKMMCESFIYNQTLMKKLQETNYDVMLIDPVI PCGDLMAELLAVPFVLTLRISVGGNMER
SCGKLPAPLSYVPVPM TGLTDRMTFLERVKNSMLSVLFHFWIQDYDYHFWEEFYSKALGR
PTTLCETVGKAEIWLIRTYWDFEFPQPYQPNFEFVGGHLCKPAKALPKEMENFVQSSGED
GIVVFSLSLGFQNVTEEKANIIASALAQIPQKVLWRYKGKKPSTLGANTRYDWIPQNDL
LGHPKTKAFITHGGMNGIYEAIYHGVP MVGVPIFGDQLDNIAHMKAKGA AVEINFKTMTS
EDLLRALRTVITDSSYKENAMRLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRSA AHD
LTWFQHSYSDVIGFLLTCVATAIFLFTKCF LFSCQKFNKTRKIEKRE

Important features of the protein:**Signal peptide:**

Amino acids 1-21

Transmembrane domain:

Amino acids 489-510

N-glycosylation sites:

Amino acids 131-135;313-317;518-522

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 67-71;340-344

Tyrosine kinase phosphorylation sites:

Amino acids 122-131;136-144

N-myristoylation sites:

Amino acids 19-25;276-282;373-379;377-383

Amidation site:

Amino acids 338-342

527/615

FIGURE 523

GGCTGCGGGGTGCGGCACGGAAGATGCACGCGAGGCTCCTGGGGCTCTCGGGCCCTGCTGCAGGC
GGCCGAACAGAGCGCGCGCCTTTACACCGTGGCTTACTACTTCACCACAGGACGGCTTCTGTG
GGGGTGGCTGGCCCTTGCTGTCTCCTGCCCGGGTTCTTGGTCCAGGCCCTGAGCTACCTGTG
GTTCCGAGCAGACGGGCATCCAGGGCATTGCTCCTTGGTGATGCTGCACCTCCTACAGCTTGG
TGTTTTGGAAGCGGCACTGGGACGCTGCACCTGACCAGTCTGCAGAAGGAACTGGAGGCTCCCCA
CCGAGGCTGGCTGCAGCTGCAGGAGGCCGACCTGTGCGCCCTTCGACTCTTGGAGGCCCTGCT
GCAGACTGGGCCCCACCTGCTGCTTCAGACATATGTTTTTCTAGCCTCAGACTTCACAGATATT
GTGCCAGGGGTGAGCACCCCTGTTTTCTGGTCTCCTACTCTCCTGGGCCTGGTGTCTTACACT
CGCTTCATGGGCTTCATGAAGCCAGGCCACCTGGCCATGCCATGGGCCGCCCTCTTCTGCCAG
CAGCTCTGGAGGATGGGCATGTTGGGAACCCGCGTGCTGAGTCTGGTCTGTTCTACAAAGCC
TACCACTTTTGGGTTTTTGTGGTTGCAGGTGCCACTGGCTGGTGATGACATTCTGGCTTGTG
GCCCAGCAGAGTGACATCATCGACAGCACCTGCCACTGGAGGCTGTTCAACCTGCTCGTGGGG
GCCGTGTACATCCTCTGCTACCTCAGCTTCTGGGACAGCCCTTCTAGAAATAGGATGGTCACG
TTCTACATGGTCATGCTGTTGGAGAACATCATCCTGTTGCTGTTGGCCACCGACTTTCTCCAG
GGGGCATCGTGGACCAGCCTGCAGACCATAGCTGGGGTCTGTCTGGATTTCTGATTGGCAGT
GTCTCACTGGTAATTTATTACAGCCTGCTGCATCCAAAATCCACAGACATCTGGCAGGGCTGC
CTAAGGAAGTCTGTGGCATTGCAGGAGGTGATAAAACAGAGAGAAGAGATTCTCCCCGGGCC
ACAGATCTAGCTGGGAAGAGAACCGAGAGCTCAGGCTCATGCCAAGGGGCAAGTTATGAACCA
ACCATTTTAGGGAAGCCCCCTACCCCTGAGCAGGTCCCCCAGAGGCTGGGCTGGGGACCCAG
GTTGCTGTGGAGGACTCTTTCCTCAGTCATCACCCTGGCTGTGGGTGAACTTGCCCTAAAA
ACAGGAAATGTGTCTAAGATCAATGCCGCTTTGGAGATAACAGTCTGCCTATTGTCCACCT
GCATGGGGGTGTGAGTCAACAGGACTACCTGCAGAGAAAGGCCTTGTCTGCCCAGCAAGAGCTC
CCATCCTCATCCCGTGACCCCTCAACCTTAGAGAACAGCTCTGCGTTTGAAGGTGTCCCTAAA
GCAGAGGCCGACCCATTGGAAACCTCAAGTTACGTATCTTTTGCCAGCGATCAGCAGGATGAA
GCACCTACCCAGAACCCAGCAGCCACGCAGGGGGAGGGCACCCCAAAGGAAGGAGCTGACGCT
GTTTCTGGGACACAGGGGAAGGGGACAGGTGGGCAGCAGAGAGGAGGGGAAGGACAGCAGAGT
TCCAGTTGTACTTCAGCGCCACTGCAGAAGTGGCCACATCCTCACAACAAGAAGGCAGCCCA
GCTACTCTGCAAACGGCCCACTCTGGAAGGAGGCTGGGAAAGAGCAGCCCTGCCCAGCCTGCA
TCGCCCCACCCAGTGGGCTTGGCGCCCTTCCCCGACACCATGGCCGACATTAGCCCCATCCTA
GGCACAGGCCCATGTAGAGGCTTCTGCCCCAGTGCAGGCTTCCCTGGAAGAACCCTCAGTATC
TCAGAGCTAGAGGAGCCGCTGGAGCCCCAAAGGGAGCTAAGTCACCATGCAGCTGTTGGTGTG
TGGGTGTCTATTGCCACAGCTGAGGACTGCCCATGAGCCCTGCCTCACGTCCACCCCTAAGTCT
GAGTCTATCCAAACGGACTGCAGCTGCAGGGAACAGATGAAGCAAGAGCCGAGTTTTTTCATC
TGACCACAGTCATGGTGGGATAAGACAACAGGCTGACAAACCAAGCTGGCCATTTGGTACCGT
GAGAAAGGAAATCCCCTTCTGACACCTGTGTCCTTGGGCACATCACTGTCACCTCTGAATCT
CCATCTGCATCCCTGAAAAATGAAGAAACAGGGCTGGATGATTTTGCAGGTCCAATGCAAACA
TCACAGACCCACCCATGCATAGGAGAGACTCTAACATACTTTAGAGGAGGAGAAAGAGATT
CAGTCAAAATTTGTCTGCTACCTTTTATGAGCTGTAGGTTCCCTTATTTTATCTTTTGTGCTG
GCTTCTAGGAAACACAAAGGTAACCCAGATTCTTATTTTATTTGAGGTTCTTGTACAAAT
AGCTTTGCCTCACATTTAGCGGTTATGAATCTCATTTTAATATATTCTAACTGTATTATGTTA
TGAAATCTCTTGGTAAGATAATTTGCATGCTTTCTGGGAGTAGGTAAGGCCTGTGTGCTTGTA
ATAACTAACATAACTGAAAGTGCAAATGTCA

528/615

FIGURE 524

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108726
><subunit 1 of 1, 686 aa, 1 stop
><MW: 74981, pI: 6.60, NX(S/T): 2
MHARLLGLSALLQAAEQSARLYTVAYYFTTGRI LLWGWLALAVLLPGFLVQALS YLWFRAD
GHPGHCSLVMHLHLQLGVWKRHWDAALTS LQKELEAPHRGWLQLQEADLSALRLLLEALLO
TGPHLLLQTYVFLASDFTDIVPGVSTLFSWSSLSWALVSYTRFMGFMKPGHLAMPWAALF
CQQLWRMGMLGTRVLSLVLFYKAYHFWVFVAGAHWLVMTFWLVAQQSDIIDSTCHWRLE
NLLVGAVYILCYLSFWDSPSRNRMVTFYVMMLLENIILLLLATDFLQASWTS LQTIAGV
LSGFLIGSVSLVIYYSL LHPKSTDIWQGCLRKSCGIAGGDKTERRDSPRATDLAGKRTE
SGSCQGASYEPTILGKPPTPEQVPPEAGLGTQVAVEDSFLSHHHWLWVKLALKTGNVSKI
NAAFGDN SPAYCPPAWGLSQQDYLQRKALSAQQELPSSSRDPSTLENSSAFEGVPKAEAD
PLETSSYVSFASDQQDEAPTQNPAAQTQEGTPKEGADAVSGTQKGKTGGQQRGGEGQQSS
TLYFSATAEVATSSQQEGSPATLQTAHSGRR LGKSSPAQPASPHVGLAPFPDTMADISP
ILGTGPCRGFCPSAGFPGRTLSISELEEPLEPKREL SHHAAGVWVSLPQLRTAHEPCLT
STPKSESIQTDCSCREQMKQEPSFFI
```

Important features of the protein:**Signal peptide:**

Amino acids 1-17

Transmembrane domains:

Amino acids 35-50;269-287;293-313

N-glycosylation sites:

Amino acids 416-420;467-471

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 344-348

N-myristoylation sites:Amino acids 188-194;288-294;299-305;335-341;338-344;362-368;
390-396;473-479;529-535;536-542;558-564;603-609;
643-649**Amidation sites:**

Amino acids 354-358;568-572

Leucine zipper pattern:

Amino acids 112-134

529/615

FIGURE 525A

AGTGCCTCTGTTCATTTAATCTCCACGGAGTCTGAAGGTGCTTCCCAGGTTTGTCCCCATCACACAGATGAGGC
AATCGTTCTGTAAAGACTGTCCTTGGGTCATTATGTGTCAGCAATGAAATCGGTGCTGCCATTACTAAACCCCTTACT
GTGTGCTGGCATTGTGTATGCATGCATGTGTGTGCGTGACACGCTGTGTGTTGCGTGTACATGTGCATGTGTGTG
TTGTGTGCTGTGTGTGCACATGTAGAAAGAAAGTGATGTGTGGGAATGGAGAATTCCAACCCAGGAGGAGACTG
TGCCTGGGGCTGCCACGAGAAGTGGTGACACTTCGAGAAACGGGTTCCAAATGCACGTTGCCTTCCAGTTCTCTG
TGTGACCTTGGGCAAGTCACTTCAGCTCCCTGAGCTTTGTTTTTAAAAATATTTTTTAAATGTATAAAACCATGG
ACCATTACATATGAAGAGAAATGTGTGTGCAAAACATTAGTTAATAATCACAAGGTGGAGGAGTGCCTGCTCAGA
CCCAGAGCTGACACAGGGAACCTCTCCAGAAGGCTGCAGGGCTTCCCTCCCAACCCCTCCAACGGCCCACTTGCTG
AGCCCGTGCTTATCTGTTTCAGTGGAATGCCATGTGCCAGCTTCCCTCAGAAGTAAAGCCACTAGGTAAAGTGTGAC
ACTCTGTGCCAGCTTGGTGCAAAGCCCCCTTGTGTGTGCTATCTTATTGACCTCCCAATAGCATGGTAAGGTCA
GTACTGTCACTTCCCCACTTTGAAGATGAGGAGAGACAAATTCTAGATGGAATGGAGGTACGCAGTGGA
TAGGATCCAGACAGATTAATCCAATCTCAAGCCTGAATTCTTCCATTCCACGCTACGCTTGAAGCTCAATCTCTC
TTCTGTGTTGATTCTCCCCACTTCCCCACCCCAAGATATATCCCATCGCTGCTTGGTGGACAGTAGCCATGACTG
GGTTTTGGTAAAGGTGCTGAATAATCAGGCTGCTGGTTAGTTTTTACATTTACCTTTCCAGTGAAATGGGGC
CCCATGAAAAGGCGAGCTCAAGTTGTAAATTAACAAAGGAAGGACAGAAAGGTCTTCTGTTTGCACCTACCCCTA
AGGATTTGGGGTAGACACTGGGAATTTACTAATTATGAATTCAGTGCTTTCTTGTGTAAGAGAGGCGTGGAA
TCAACGCTGAGTGAAGGCATCAAGTTTAAGCTGCTAATTCTTCTGATCATGCAGAATAAAAGCTACGTCCTT
GAAATACACCAGGCGACTAAACATAATCTTTGCGTTTCCGTAGTGTTGGTTAAGGAATCCAGATGTTACTGCAAT
AACCCTCCATAAACAAGGAACACCCAGCTGTGAGAACTGGCTTCTCAGCATTCTGTCAGCAGAGGCTCTTC
CGGGGCCAGCCCTGGAGAACCCTCAGGGTCTGATGGTTGCCCTGTTTCAGCACAGCCCTTATTGCGAGGCAG
ACGGCTACGGGCACAGCCACAGGCTGAAGGTGAGTCCAGCACACAACCTTCTGACAGTGAACAGGAGTAAACATG
GGACCCACCCGAAACCTTTGCTGTGTTGACTTCTTAGCAATGGAGGCAGCTCTAGGCTCTGGAGAGTTCGGGTAT
AGGAGACCATGACTTGAGCAGACTGATATAAGTGAATGCAAAACATATTTAGATGGCACAACCTTAATTTAGATTT
ATCAGTGCTAATATAGAAAAGCTAGTATTTATTGGGGCTTATTAGATTTTTAGTCTGAATCCTCACAACCTTACG
AGGGGGTTCTGTTTACAGACTATGATCTTGATGATTTCCCAAGATGCTCATTAAGTATATGGTGAAGTAGA
ATTTGAATACAGAAGACCTGGTTCTGCTACTTTCTGTGTTTCTATTGGTTCAAACAGCCTTTCTTCTTTCAA
ACAACCTTCAGTGCAATTCATGGTTTTGGAAAATAAACTTGATTTTGAGATTGAGACAATAAGTGCATTTTAAATG
TTTATTCTTTTATCTTGAAAACCTGATATATTTATGAAATGATATGTGCTCACTCAGTGTCAACACTTCAAACAA
CACAGACAGTACAATGACAAATGGAGATCAGCTCTAATCTCGGCCCCCAATTTAATGCATTGCTGAATATTCTT
CTGAACATAGTCCATCCACACTGTCCCATGACACAAGACGCTCCAAGGGCTGAAGATAGAGGGACTTCTGCAG
TCAAGAGAGCTGGGAACTCTTGACAGTCACAATGTGCATTTGGGTATTAAAGGCTCTGCAAGTTCTGCACCA
AATAAACCCCTTGGATTGGCTTGATCCAATGCCATGTTTCCAAAACCTACTTGCCCGTGGGACACCTTAGTCCATA
ACACAGGTTGGCATTCTTCTAGAGAGTGTGCTGTGAAAACACTGGTCTCACAGCACCGTGCATTCACTCCAGCA
GGTATTTACCAAGCAGGGACTTTGGGCCAGGTCCGTGCTAGGCTCTGCAGGTGGACCAGCCAGCCCTGACCTCCA
TGGTGTCTCTTCTCATGGGAGAGGCTGCACAGCAGTCATTGAGAAAACGAGAAAACACACAGGTACTTTCAGATG
CTGATAATGACTACCATGTGCTAAAAGAGCTCCAGGTGTTGTCTGTTTTGAGACAATCTTCTCGACAATGAGATA
GAATGAACCATGCAAACTTTGGGGGCTACGATGGTTTTAGGAAAGAGCTAGAGTGAAAATCCTTTGACATATAT
ACATACAAATAAAGATACATGTGTATAATTTTATGTAATTGACATCACATTATATGCTGGCACCTGCTTTTTTG
CTTAATGAAAATGTCAAAGGTAATATTACCAATCAATCAATATATTTACCATCGTGTTTAATTTCTGCAGAGCA
CTTATTTCAAGCACATACTGCATTTTCTTAGTCACTCACTGGTGGGAATAGAAAGTTTTCTCAGGCATGCATTTT
TCCCACTTCTGAAATGATCTCCTTAGAATAAATCCCCAAATTTGATTGCTGGGTCAAAGGCATGAACATTTTA
CATTTTTATACAATAATGTCAAACCTTCCGGAAATGATGCTCACTTTACTTTCCCTCCAAGACTGTGTGAAA
ATGCCATTTTCTAAATGCTTACTATGACTGGTTTCCAACCTACATTTTAATTTCTGTTCAATCTGATAGGCCAAA
AAATGATATTTAATTTTTATTTGATTGATAATGACCTTGAACGTGCCATTAGCCTTTTGCATGTATTCTTTTAT
GAAACATCTGTTCTATCCTTCGTAATGTTCTCTCATATGTTAACTTTTCTTATTGATTTGTTAGAGCACTT
TGTATATTGTGAATATTAGCTTTTGTGATCAGAATTATGGAATTGTTGTTGCTTTAGTTTTGCTTATCAAGTTT
AAAGCCATTGAGATGTTGTAATGTGTATGTTGTTAAATTTATGCTTATTTTGTGTTTTCTGATGCTCATAT
GTTTAGAATGGTCAAGCAATCCCACTTATGATTACATAAATATTCTCCCATATTGCTCTTAGCATTTTTTTTCT
TTTTCATGTAACCCCTTTGTTCTTTTCCAGGAATTTACTTTGCGGTAAGAAATGGGCTGGCTTCCAGTTTATGTTT
CCAAATGGTGATTGAGCTGTTCCATTTCCATATTCTCCCTTATTAGAAATGACCACTATATTATGTTCTAAAATA
TCTGCGTACTTGTGTCCTTCTATAATCTCAGTTCATCTTTTGGAGCTATCTTTTGATTCCTTTTCAAACCCAC
ACTGCTTTTACTGAAGTGTATCATCTTATACATTTTAACTACTCAGCAAGACAAGTTTCTCAATGCCACTCTTTT
TCAGAGTTTTTCTGGTGGTTGTAAGATGTTTATTTCTTGGATAACTTTAGAACTCTTTTGTCCAAGGTA
AAATATATCCACATTGAGATCACTGAATATACAGACTAATTGAGAAAAATGTATGCTTTTATTGCATTGA
GTCTTCTTATCCAATAAAAAAGATATGAATTTCCATGTATTGAAATCTTCACTGAGACTATTTTTGGCTTTTCA

530/615

FIGURE 525B

CATGTCCTGCAAATGTATTGTTAAATTTATTTTTAGGTATTTAGGGGAAATGATTTCTAAAGTTTGTATTTTC
TAGCTTGTTATAATTTACATATGAGATAGTCATTGTTGTATATTATTTATAACTGATCATATTACTGTATTTGTA
TTGTTTAAATAGTTTTCTATTATTTGGGTTTTCCTGGAATACAACTTATTATCTACAAATTATGATTGTTTT
GCCTTTCCAATGTTTCATAACTGTTTTTATATTCTTGTCTGATTGCTTTGTTTCAGCACTTCTAGAATAAAGTCAT
GCAATACTAATGA

531/615

FIGURE 526

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108728
<subunit 1 of 1, 100 aa, 1 stop
<MW: 10922, pI: 8.81, NX(S/T): 0
MSAMKSVLPLLNPYCVLAFVYACMCVRAHVCVCVYMCMCVLCACVCTCRKKVMCGNGEFQ
PRRRLCLGLPREVVTLRETGSKCTLPSSSLCDLGQVTSAP

Important features of the protein:**Signal peptide:**

Amino acids 1-28

N-myristoylation sites:

Amino acids 80-86;94-100

Prokaryotic membrane lipoprotein lipid attachment sites:

Amino acids 13-24;34-45

532/615

FIGURE 527

GTGAGACTTCTTTCTTCATTGTGGCTAGCTTTGAAAAGACCCTCTGAACTTCCTAAAGATATC
AAGATGATATCACCAGACTTGCCCTTTTGGACAATTGTCTTGATCATAGTTAGTTGGACAAC
TGTGGAGCACTAGCCATACTTCTTTCTTATCTTTACTATGTGTTTAAGGTTGTTTCATCTGCAA
GCCAGCTTAACAACCTTTAAGAATAGCCAGCCTGTGAATCCCAAACACTCTAGAAGAAGTGAA
AAGAAATCCAATCATCATAAAGACTCCTCAATACACCATCTTCGTTTATCTGCCAACGATGCT
GAAGATAGCCTTCGCATGCACAGTACTGTGATTAACTTACTAACATGGATTGTATTACTCAGC
ATGCCTTCTCTAATTTATTGGCTAAAGAATCTTAGGTATTATTTTAAACTTAATCCTGATCCA
TGTA AACCTTTGGCATTTATCCTTATTCGACTATGGCAATTCTTGGAATACTTACACTGTT
TCAATAAAATCAAGTAAATTGTTGAAGACTACTTCACAATTTCCACTTCCTCTGGCTGTTGGT
GTGATTGCTTTTGGGTCAGCACATTTATATAGGCTTCCATGCTTTGTCTTCATTCCCTCTTTTA
CTCCATGCATTATGCAACTTTATGTAAGATTGGACTTAAGGAATGATGAAGATAATTTATGTG
TTTAGGGCCAGTGATAAGAGGGAACACACAGATCCATCAGTATGGACAGCAAGATCCTTTGGA
GAAGACAAGTCTATTTTACAATATTGAAAATAGGAAATTAGTTTTGTAATGTTTGAGGGAAG
TAGTTGAAGCATGGTTTTGTTTTGTGGTGTGGAATCCATGTACTAATCATTTTTGAAAAATTC
ATGAAGGGATATATGGTGATCACTATCATTGAGGACTCCTGTGCATATAAAATAGTCTGTTTT
ATCAACTGTAAA

533/615

FIGURE 528

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108738
><subunit 1 of 1, 196 aa, 1 stop
><MW: 22225, pI: 9.90, NX(S/T): 0
MISPDLPFLTIVLIIVSWTTCGALAILLSYLYYVFKVVHLQASLTTFKNSQPVNPKHSRR
SEKKSNNHHKDSSIHHLRLSANDAEDSLRMHSTVINLLTWIVLLSMPSLIYWLKNLRYEFK
LNPDPCKPLAFILIPTMAILGNTYTVSIKSSKLLKTTSQFPLPLAVGVIAFGSAHLYRLP
CFVFIPLLLHALCNFM
```

Important features of the protein:**Signal peptide:**

Amino acids 1-25

Transmembrane domains:

Amino acids 91-108;128-143;167-186

N-myristoylation site:

Amino acids 141-147

534/615

FIGURE 529

GCGAGCCGGGTCCCACCAATGGCCGCGAATTATTCCAGTACCAGTACCCGGAGAGAACATGTCA
AAGTTAAACCAGCTCCCAGCCAGGCTTCCTGGAACGGCTGAGCGAGACCTCGGGTGGGATGT
TTGTGGGGCTCATGGCCTTCCTGCTCTCCTTCTACCTAATTTTCACCAATGAGGGCCGCGCAT
TGAAGACGGCAACCTCATTGGCTGAGGGGCTCTCGCTTGTGGTGTCTCCCGACAGCATCCACA
GTGTGGCTCCGGAGAATGAAGGAAGGCTGGTGCACATCATTGGCGCCTTACGGACATCCAAGCTT
TTGTCTGATCCAACTATGGGGTCCATCTTCGGGCTGTGAACTGCGGAGGCACGTGGAGATG
TACCAATGGGTAGAACTGAGGAGTCCAGGGAGTACACCGAGGATGGGCAGGTGAAGAAGGAG
ACGAGGTATTCCTACAACACTGAATGGAGGTGAGAAATCATCAACAGCAAAAACCTTCGACCGA
GAGATTGGCCACAAAAACCCAGTGCCATGGCAGTGGAGTCATTCATGGCAACAGCCCCCTTT
GTCCAAATTGGCAGGTTTTTCCTCTCGTCAGGCCTCATCGACAAAGTCGACAACTTCAAGTCC
CTGAGCCTATCCAAGCTGGAGGACCCTCATGTGGACATCATTGCGCGTGGAGACTTTTTCTAC
CACAGCGAAAATCCCAAGTATCCAGAGGTGGGAGACTTGCGTGTCTCCTTTTCTATGCTGGA
CTGAGCGGCGATGACCCTGACCTGGGCCCAGCTCACGTGGTCACTGTGATTGCCCGGCAGCGG
GGTGACCAGCTAGTCCCATTTCTCCACCAAGTCTGGGGATACCTTACTGCTCCTGCACCACGGG
GACTTCTCAGCAGAGGAGGTGTTTCATAGAGAACTAAGGAGCAACTCCATGAAGACCTGGGGC
CTGCGGGCAGCTGGCTGGATGGCCATGTTTATGGGCCTCAACCTTATGACACGGATCCTCTAC
ACCTTGGTGGACTGGTTTTCTGTTTTCCGAGACCTGGTCAACATTGGCCTGAAAGCCTTTGCC
TTCTGTGTGGCCACCTCGCTGACCCTGCTGACCGTGGCGGCTGGCTGGCTCTTCTACCGACCC
CTGTGGGGCCCTCCTCATTGCCGGCCTGGCCCTTGTGCCCATCCTTGTTGCTCGGACACGGGTG
CCAGCCAAAAAGTTGGAGTGAAGAACCCCTGGCACCCGCCGACACCTGCGTGAGCCCTGAGG
CTGGTTGTACAATGCCCACGCCTGCCTGGCTGCTTTACCTGGGAGTGCTTTTCGATGTGGGCA
CCTGGGCTTCCTAGGGCTGCTTCTGAGTGGTTCTTTACGTGTTGTGTCCATAGCTTTAGTCT
TCCTAAATAAGATCCACCCACACCTAAGTCACAGAATTTCTAAGTTCCCCAACTACTCTCACA
CCCTTTTAAAGATAAAGTATGTTGTAACCAGGACGTCTTAAATGATTCTTTGTGTACCTTTTC
TGTCATATTCAGAAACCGTTCTGTGCCTGCTGGGAGTAATTCCTTTAGCAATTAAGTATTTGG
TAGCTGAATAAGGGGTGAGAACTTCTGAAACCAGAGATCTGTAATCATCTCTATTGGCCTGGG
GTGCCTGTGCTATAAATGAGTTTCTTCACATGAAAAACACAGCCAGCCCCAAGATGACTTATCT
GGGTTTAGGATTCAATAGTATTCATAACTGCTTATTACATGAGCAATTTTCATCAAATCTCCA
AACTCTTAAAGGATGCTTTCGGAACACGCTGTATACCTAGATGATGACTAAATGCAAAATC
CTTGGGCTTTGGTTTTTTTCTAGTAAGGATTTTAAATAACTGCCGACTTCAAAGTGTTCTTA
AAACGAAAGATAATGTTAAGAAAAATTTGAAAGCTTTGGAAAACCAAATTTGTAATATCATTG
TATTTTTTATTAAAGTTTTGTAATAAATTTCTAAATTATCA

535/615

FIGURE 530

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108743
><subunit 1 of .1, 400 aa, 1 stop
><MW: 44876, pI: 8.32, NX(S/T): 2
MAANYSSSTSTRREHVKTSSQPGFLERLSETSGGMFVGLMAFLLSFYLIFTNEGRALKT
ATSLAEGLSLVVSPDSIHSVAPENEGRLVHIIGALRTSKLLSDPNYGVHLPVAVKLRRHVE
MYQWVETTESREYTEDGQVKKETRYSYNTEWRSEIINSKNFDREIGHKNPSAMAVESFMA
TAPFVQIGRFFLSSGLIDKVDNFKSLSLSKLEDPHVDIIRRGDFFYHSENPKEVVDLR
VSFSYAGLSGDDPDLGPAHVTVIARQRGDQLVPFSTKSGDTLLLLLHHGDFSAAEEVFHRE
LRSNSMKTWGLRAAGWMAMFMGLNLMTRILYTLVDWFPVFRDLVNIGLKAFACVATSLT
LLTVAAGWLFYRPLWALLIAGLALVPILVARTRVPAKKLE

Important features of the protein:**Transmembrane domains:**

Amino acids 34-53;365-388

N-glycosylation site:

Amino acids 4-8

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 140-144

Tyrosine kinase phosphorylation sites:

Amino acids 99-107;220-227

N-myristoylation sites:

Amino acids 35-41;93-99;310-316

Cell attachment sequences:

Amino acids 221-224;268-271

536/615

FIGURE 531

AAAAAAAAAAAAAAAAAGAAGCTCTTATGCCAGGAACCTGGAATGGAGACCAATATATATTG
GTTATATCATAGTATCACAGGGTTACTTTGGCATTGAGAGAAATGGGCAATAA
CTGTTACTTTAAAAGCTTGGGTGCTGTGATTCTGCCTTCAGCCTCAGCCACTTTTGTGGTGCT
TTGCGTGGCATCAGTACCTCCACTGATTCTTCTGTCTTTCCTCTCTCTCTTCCCCCTCTTT
CCCTTCTGTTTTTCTCAGATCTAAGGGTTATAATGGAGGGGCAAACTGCCTGGCTATTTCAGA
TAAGACTTCACTGAGTGACTGTTTCAGCCCATGATTTACCCTGCAGTTTAACAGGCTCAGGAAT
TAGGTCGCATCAGTTGAGCGCGGGTCACTTAGGCCTATAATCATCATCAGACGGCAATTAAAG
GACCATTTCTGCCTTTTTCACTATTACATCCCCGCCTGTAGCCCAGCCTGCCATACAGTAGA
TACTCAATAAATATTTGCTGAATGATAACCAATAA

537/615

FIGURE 532

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108758
<subunit 1 of 1, 100 aa, 1 stop
<MW: 10316, pI: 8.52, NX(S/T): 0
MGNNCYFKSLGAVILPSASATFVVLCVASVPPLILLSFLSLFPSPFSPVFLRSKGYNGGA
NCLAISDKTSLSDCSAHDLPCLTGTSGIRSHQLSAGHLGL

Important features of the protein:**Signal peptide:**

Amino acids 1-47

N-myristoylation site:

Amino acids 58-64

538/615

FIGURE 533

CGGGGTGTACGAAAGAGAAACCCGGAGGGCGCCGGGGACTGGGCCGGGGTCTGCAGGGCTCAG
CTGAGCCCATGAGCTCCCAGAGCTAACCCCTGAACACCCAGGCGGGCAAAGGGCTGATGTCGG
TAGTCCCCATCCTGGAGGGGAGGCTCTGCGCATCTGCTCCTGGCATGGCGCTGCGGCACCTC
GCCCTCCTGGCTGGCCTTCTCGTGGGAGTGCAGCAAGTCCATGGAGAACACGGCCAGCTG
CCCGAGTGCTGTGTGGATGTGGTGGGCGTCAACGCCAGCTGCCCAGGCGCAAGTCTGTGTGGT
CCAGGCTGTTACAGGCGCTGGAACGCGGACGGGAGCGCCAGCTGCGTCCGCTGTGGGAACGGA
ACCCTCCCAGCCTACAACGGCTCCGAGTGTAGAAGCTTTGCTGGCCCGGGTGCGCCATTCCCC
ATGAACAGAAGCTCAGGGACCCCCGGGCGGCCACATCCTGGGGCTCCGCGCGTGGCCGCCTCC
CTCTTCTGGGCACGTTCTTCATTAGCTCCGGCCTCATCCTCTCCGTAGCTGGGTTCTTCTAC
CTCAAGCGCTCCAGTAAACTCCCCAGGGCCTGCTACAGAAGAAACAAAGCTCCGGCCCTGCAG
CCTGGCGAAGCCGCTGCAATGATCCCCCGCCACAGTCCTCAGACGTGGGGTCTGCAGGAAAG
GAGGACCCACCACGACAGGGCAGACCCCCAATACCTGCTCCTCCTTGAAGTCCAGCTCCACCC
GAGGACAGACGCAGCCGGCCTCCGCCAGGGCCTCCTGAGCAGCCATCGCTTCAGTGGTGTGG
GTCAGGCGGACCCAAGAGTCAGCCCGTACGGAAGCCGCGCTACGTGAGGCGGGAGCGGCCCT
GGACAGGGGCCACGGATCCCGCTGCCTTCCCGGGGGAGGCCCGTATCAGCAATGTCTGACCTGG
AGGCCGAGACCACGCCACGCACTTGGCGGCAGGGACCCGGAGGCCGACCCCTTGGCGGGAACC
AGCACAAAGTGTTGGCATCGCCCGGCGCCCGGGACAGTCCTGGGCACAGCCTCGGCTCTGGGT
CCCTCCGCCTCCCAGCGACGGACGCCAAAGGTCCCGGGCCGCCTGAGGCTCCTCCCCACCAC
AGCCATCTCGTTTTATCGGACCAGGAGCAGGCATCCATGAGACCTCAGAGCTTCAGATCGAGGC
CTTGGGGGGTCCGGGCCCCCCCCAGGAAACACGGTGAGGCCCCAGCGCCTGCAGCCAAAGCTGG
CACGATCTATGGGGCAGGTGCCGCTCTGCCTAGAAAAGCCAGGGGCTCTGCTGCCGTGCCCTC
CAGAGCCCACAGCGGGCAGGACTCCTCCAGCACCACCACACCCAGTGGCCCGAGACCCCTCTG
AGAACAGTGAGGCTGGTCCTCGTGCCGTTCCAGCCGGTGCCCGGCCAGTGGGGAGGACACAGC
CTAGGAACCAGCTGCCTGAGACCAGGGTGCCTCTGGGCTGTCTCCCGCTGGCGGAGACCCC
AAGCACGCAGCCACCCATTTCCGGAGCTGCAGGATAGAGCTTCCTCTTGATCTCTGTTTTTAAG
CAGAAATTCATTGTGCAGAAAAGTCCTCCAGAGCTCTGTGGCCCCGCTCGGATCCGCTGGACC
CCCATGCCTGGCTGATCCCTGCCCACGTGGGGCAGGCCACATCTAACCCCCACAAGTCACTG
CCTCACTGCACCTGCCAAGGCTGCCCTGGCGCTGAGTCCTGGGGTCCCTCCCGGAGTTCCTGG
GAGAAAGGCGCCGTCGTGGCCGCCTCCCGCACGCCAGGCCCGGGCTCCACCGTGGGTCTCAGA
CGCCCTGCGGCACCGGCACCGTCTGCTTTAGCATGGGACCCCATCTGAGGGGTGGCCTGGCC
TTCGGGGTCCCCACGCTCCTTTGCGAAGTCCACTGTGGGTGCCATCATGGTCTCCGGGACCTG
GGCCAGCGGGAACGTGGGGGCACTGGGTGTGCTGATATAAAGTCGGCATTACTCAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

539/615

FIGURE 534

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108765
><subunit 1 of 1, 189 aa, 1 stop
><MW: 19464, pI: 9.60, NX(S/T): 4
MALRHLALLAGLLVGVASKSMNTAQLPECCVDVVGVNASCPGASLCGPGCYRRWNADGS
ASCVRGNGTLPAYNGSECRSFAGPGAPFPMNRSSGTPGRPHPGAPRVAASLFLGTFFIS
SGLILSVAGFFYLKRSSKLPRACYRRNKAPALQPGEEAAMIPPPQSSDVGSAGKEDPPRQ
GRPPIAPP

Important features of the protein:**Signal peptide:**

Amino acids 1-18

Transmembrane domain:

Amino acids 111-129

N-glycosylation sites:

Amino acids 38-42;68-72;75-79;92-96

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 134-138

N-myristoylation sites:

Amino acids 11-17;36-42;43-49;59-65;69-75;122-128

540/615

FIGURE 535

TGGATCTGCGGGAATGTGGGCTGGAGAGGTCCTGCCGTGGTACCAGCCTCCAGCCTGCCCCCA
GGACTGCCCCCTGACCCAGGCGCGCCCGCTGCTCGGTGGCAGGAGGGCCGGCGGAGCGCC**ATGG**
CCTGCATCCTGAAGAGAAAAGTCTGTGATTGCTGTGAGCTTCATAGCAGCGTTCCTTTTCCTGC
TGGTTGTGCGTCTTGTAATGAAGTGAATTTCCCATTGCTACTAAACTGCTTTGGACAACCTG
GTACAAAGTGGATACCATTCTCCTACACATACAGGCGGCCCTTCGAACTCACTATGGATACA
TAAATGTGAAGACACAAGAGCCTTTGCAACTGGACTGTGACCTTTGTGCCATAGTGTCAAAC
CAGGTCAGATGGTTGGCCAGAAGGTGGGAAATGAGATAGATCGATCCTCCTGCATTTGGAGAA
TGAACAATGCCCCCACCAAAGGTTATGAAGAAGATGTCGGCCGCATGACCATGATTTCGAGTTG
TGTCCCATACCAGCGTTCCTCTTTTGCTAAAAAACCTGATTATTTTTTCAAGGAAGCGAATA
CTACTATTTATGTTATTTGGGGACCTTTCCGCAATATGAGGAAAGATGGCAATGGCATCGTTT
ACAACATGTTGAAAAAGACAGTTGGTATCTATCCGAATGCCCAAATATACGTGACCACAGAGA
AGCGCATGAGTTACTGTGATGGAGTTTTTAAGAAGGAACTGGGAAGGACAGTACAGAG**TGAC**
CATGCAGTGTTGATTGATCGAACAGCAACCACCACATACATGTCCTGCCCCACCACAAAAGGA
AGGAAGGAATAAAAGAAAGAAAGAAAGAAACAAACAAACAAACAAACAAACTAAGCAAGACA
AAACAAATACCCATGTCAGTGGTTCAAAGATTAAGATTGTGGCTTTGTGTAAAGTTCTTTCCC
TTTGTAGACTTGCTGCATAATTATTCAGGTATGATGGTTACAGTTTTTAAAAAGGAAGGGAAA
TTGTGGTATGTGGTATGTAAATATTTTTAAATGTTGTCTCTCTGTTTTGATCAGTTTTTGTTT
TATTCAATTTGTCTTTATTAAATCTTATCAAAGCA

541/615

FIGURE 536

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108783
><subunit 1 of 1, 210 aa, 1 stop
><MW: 24022, pI: 9.51, NX(S/T): 1
MACILKRKSVIAVSFIAAFLLVVRVNEVNFPLLNCFGQPGTKWIPFSYTYRRPLRT
HYGYINVKTQEPLQLDCDLCAIVSNSGQMVGQKVGNEIDRSSCIWRMNNAPTKEYEEDVG
RMTMIRVVSHTSVPLLLKNPDYFFKEANTTIYVIWGPFNRMRKDGNGIVYNMLKKTVGII
PNAQIYVTTEKRMSYCDGVFKKETGKDSTE

Important features of the protein:**Signal peptide:**

Amino acids 1-27

N-glycosylation sites:

Amino acids 148-152

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 6-10;191-195;201-205

N-myristoylation sites:

Amino acids 41-47;87-93;91-97;167-173;178-184

542/615

FIGURE 537

GT TTTAT T GACAATACATGCATCATATCTTTT GACTTTTGAAGGATATCTCATGTCAAAGGAAT
CAAGTTATGATTTATAGAGGATTCAGCTGGAATACCTTGTGGGTGCTGGCTGAGGGTGGCAAA
ACGCCTACCGAGACATGAAGGTTTTAGCCACTAGTTTTGTCTTGGGAGCCTGGGGTTGGCCT
TCTACCTGCCTTTGGTGGTGACTACACCTAAAACACTGGCCATCCCTGAGAAGCTGCAAGAAG
CTGTGGGGAAAGTTATCATCAATGCCACAACCTGTACTGTCACTGTGGCCTTGGCTATAAGG
AGGAGACCGTCTGTGAGGTGGGCCCTGATGGAGTGAGAAGGAAATGTCAGACTCAGCGCTTAGAA
TGTCTGACCAACTGGATCTGTGGGATGCTCCATTTACCATTCTCATTGGCAAGGAATTTGAG
CTTAGCTGTCTGAGTTCAGACATCTTGGAGTTTGGACAGGAAGCTTTCCGGTTCACCTGGAGA
CTTGCTCGAGGTGTCATCTCCACTGACGATGAGGTCTTCAAACCTTTCAAGCCAACTCCCAC
TTTGTGAAGTTTAAATATGCTCAGGAGTATGACTCTGGGACATATCGCTGTGATGTGCAGCTG
GTAAAAA ACTTGAGACTTGTCAAGAGGCTCTATTTTGGGTTGAGGGTCCTTCTCCTA ACTTG
GTGAATCTGAATTTCCATCAGTCACTTACTGAGGATCAGAAGTTAATAGATGAGGGATTGGAA
GTTAATCTGGACAGCTACTCCAAGCCTCACCACCCAAAGTGGA AAAAGAGGTGGCGTCAGCC
TTGGGAATAGGAATTGCCATTGGAGTGGTTGGTGGCGTGTTGGTGAGGATTGTCCTCTGTGCG
CTAAGGGGGGGCCTGCAGCAGTGA CAGCTTCAAGAACTTAACAGCCTTGCTCCTGAAGAACTG
GCTGCCCAGGAAGCCAAGCTAGCTTTTTAGGGGAGTGTTCCAGCTGCTGGTAGTGGATCAGCT
TAGAGGGAACACTCCCACAGCCAAAAGAATGAGTGGGAGAAATGGAGGGGACAATCTCCTGGG
AGCTATGCGCAGTAACCTAACTTCCTTATGTCCCATGGATCTCTCCTGATCTTCCCTGCCCA
TTGGGTACCCAGGAACTGCAAGCATTGCCTGTGTTCTTGGGAAGAGTTCTAAGAAGCTTGCA
TTCATTTTCTACCCTTTATGACTTGGATGCCTCCCCACCTCCATTTCCCCTCTTCTGAGCTGT
GTATTCATGTAGAGGGATGTATTCAGCCTTTTTAGTGAACATTTTTTTTCAATAAAAGTAATT
CACAGTAA

543/615

FIGURE 538

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108789
><subunit 1 of 1, 255 aa, 1 stop
><MW: 28440, pI: 8.92, NX(S/T): 1
MKVLATSEVLGSLGLAFYLPVVTPKTLAIPEKLQEAVGKVIINATTCTVTCGLGYKEE
TVCEVGPDPGVRRCQQRLECLTNWICGMLHFTILIGKEFELSCLSSDILEFGQEAFFRT
WRLARGVISTDDEVFKPFQANSHFVKFKYAEYDSGTYRCDVQLVKNLRLVKRLYFGLRV
LPPNLVNLNFHQSLTEDQKLIDEGLEVNLDYSKPHHPKWKKKVASALGIGIAIGVVGGV
LVRIVLCALRGGLQQ

Important features of the protein:**Signal peptide:**

Amino acids 1-30

Transmembrane domain:

Amino acids 225-244

N-glycosylation site:

Amino acids 45-49

N-myristoylation sites:

Amino acids 126-132;156-162;204-210;229-235;231-237;235-241

544/615

FIGURE 539

GCGCTCATCACTGGCTGGGGACAGAGCCGGGCACCAAGGAGCGACAGGATCCCGAAGAGAGAG
AGAGAAGGCAGCGAGGGAAGGAGGACCCCGGCAGGCAGCAGCATGAAATTCAGCCCAGCGCAC
TACCTGCTGCCTCTCCTGCCTGCGCTGGTCCTCAGCACCAGACAGGACTATGAAGAGCTAGAA
AAGCAGCTGAAAGAAGTCTTTAAGGAGCGAAGCACCATTCTTCGTCAGCTGACAAAGACATCA
AGAGAACTTGATGGAATTAAAGTCAATCTTCAGTCCTTAAAAAACGATGAGCAGTCTGCCAAA
ACTGATG TTCAGAACTTCTGGAATTAGGACAGAAACAAAAGAGAAGAAATGAAGTCTCTTCAG
GAGGCCCTGCAAAATCAGCTTAAGGAGACATCAGAGAAAGCAGAAAAACACCAGGCTACTATT
AATTTTTTAAAGACTGAAGTTGAAAGAAAGAGCAAAATGATCCGAGACCTCCAGAATGAGGAT
TCAAGGAAGAGACCAAGAGATCTCCAGTGGAGATAGTCTCCATGAGGACCATGTCAATATAC
TTATTGATGTATCTCTTAGTACCTAGAATAGTGGAGATTATATTAGATACAAAATAAATATGT
GTGGAATTAATTAATAA

545/615

FIGURE 540

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108806
><subunit 1 of 1, 159 aa, 1 stop
><MW: 18865, pI: 9.76, NX(S/T): 0
MKFSPAHYLLPLLPALVLSTRQDYEELEKQLKEVFKERSTILRQLTKTSRELDGIKVNLO
SLKNDEQSAKTDVQKLELGQKQREEMKSLQEALQNQLKETSEKAQKHQATINFLKTEVE
RKSKMIRDLQNEQSRKRPRDLQWKIVSMRTMSIYLLMYL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-22

N-myristoylation site:

Amino acids 54-60

FIGURE 541

[illegible]

547/615

FIGURE 542

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108936
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19472, pI: 5.71, NX(S/T): 0
MSPSGRLCLLTIVGLILPTRGQTLKDTTSSSSADSTIMDIQVPTRAPDAVYTELQPTSPT
PTWPADETPQPQTQTQQLGTDGPLVTDPEETHKSTKAAHPTDDTTTLSERPSPSTDVQTD
PQTLKPSGFHEDDPFFYDEHTLRKRGLLVAAVLFITGIIILTSGKCRQLSRLCRNRCR

Important features of the protein:**Signal peptide:**

Amino acids 1-21

Transmembrane domain:

Amino acids 147-162

Tyrosine kinase phosphorylation site:

Amino acids 45-52

N-myristoylation site:

Amino acids 146-152

548/615

FIGURE 543

CGGCTCGAGGTGAGAAGGAACTGCAAGAGTGGGGCAGAGAACCAGAGTGTGAGAGCAAAACC
TCCTCTATCTGCACATCCTGGGGACGAACCGGGCAGCCGGAGAGCTGCGGCCGGCCAGTCCC
GCTCCGCCTTTGAAGGGTAAAACCCAAGGCGGGGCCTTGTTCTGGCAGAAGGGACGCT**ATGA**
CCGCAGAATTCCTCTCCCTGCTTTGCCTCGGGCTGTGTCTGGGCTACGAAGATGAGAAAAAGA
ATGAGAAACCGCCCAAGCCCTCCCTCCACGCCTGGCCCAGCTCGGTGGTTGAAGCCGAGAGCA
ATGTGACCCTGAAGTGTGAGGCTCATTCCCAGAATGTGACATTTGTGCTGCGCAAGGTGAACG
ACTCTGGGTACAAGCAGGAACAGAGCTCGGCAGAAAACGAAGCTGAATTCCCCTTCACGGACC
TGAAGCCTAAGGATGCTGGGAGGTACTTTTGTGCCTACAAGACAACAGCCTCCCATGAGTGGT
CAGAAAGCAGTGAACACTTGCAGCTGGTGGTCACAGATAAACACGATGAACTTGAAGCTCCCT
CAATGAAAACAGACACCAGAACCATCTTTGTGCGCCATCTTCAGCTGCATCTCCATCCTTCTCC
TCTTCCTCTCAGTCTTCATCATCTACAGATGCAGCCAGCACGGTTCATCATCTGAGGAATCCA
CCAAGAGAACCAGCCATTCCAACTTCCGGAGCARGAGGCTGCCGAGGCAGATTTATCCAATA
TGGAAGGGTATCTCTCTCGACGGCAGACCCCCAAGGAGTGACCTATGCTGAGCTAAGCACCA
GCGCCCTGTCTGAGGCAGCTTCAGACACCACCCAGGAGCCCCCAGGATCTCATGAATATGCGG
CACTGAAAGTGT**TAG**CAAGAAGACAGCCCTGGCCACTAAAGGAGGGGGGATCGTGCTGGCCAAG
GTTATCGGAAATCTGGAGATGCAGATACTGTGTTTCCTTGCTCTTCGTCCATATCAATAAAAT
TAAGTTTCTCGTCTTA

549/615

FIGURE 544

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119510
><subunit 1 of 1, 236 aa, 1 stop
><MW: 26079, pI: 5.05, NX(S/T): 3
MTAEFLSLLCLGLCLGYEDEKKNEKPPKPSLHAWPSSVVEAESNVTCLKQAHSQNVTFVL
RKVNDSGYKQEQSSAENEAEFPFTDLKPKDAGRYFCAYKTTASHEWSESSEHLQLVVTDK
HDELEAPSMKTDTRTIFVAIFSCISILLFLSVFIIYRCSQHGSSSEESTKRTSHSKLPE
QEAAEADLSNMERVSLSTADPQGVTYAELSTSALSEAASDTTQEPPGSHEYAALKV
```

Important features of the protein:**Signal peptide:**

Amino acids 1-16

Transmembrane domain:

Amino acids 135-153

N-glycosylation sites:

Amino acids 44-48;55-59;64-68

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 171-175

Tyrosine kinase phosphorylation sites:

Amino acids 61-69;87-95

N-myristoylation sites:

Amino acids 12-18;203-209

550/615

FIGURE 545

GGCGGCCCGGAGCTGGGAGCGCGGGGAAGGCGGTTGGGGTTCTGACAGCTGCGCGCGATCCTG
CTCTCTCTCAGCCGCCTGTGGACATGCGCAAAGGGCCCTCTCCTGAGTCCAGATGATGCTCAT
ACCAATGGCTTCAGTGATGGCGGTGACTGAACCGAAATGGGTCTCGGTCTGGAGCCGCTTCCT
CTGGGTGACGCTGCTGAGCATGGTGCTGGGGTCCCTGCTGGCCCTGCTGCTGCCGCTGGGGGC
TGTGGAGGAGCAGTGCTTGGCTGTGCTCAAAGGCCTCTACCTGCTCAGGAGCAAACCGGACAG
GGCGCAGCATGCCGCCACCAAGTGCACCGCCCGTCCACGGAGCTCAGCATCACCTCCAGGGG
CGCGACGCTGCTGGTGGCCAAGACCAAGGCCTCTCCAGCGGGTAAGTTGGAAGCCAGAGCTGC
CCTGAACCAAGGCCCTGGAGATGAAGCGCCAGGGCAAGCGGGAAAAAGCCCAAAGCTCTTCAT
GCACGCCCTCAAGATGGACCCGGACTTCGTGGACGCGCTCACCGAGTTTGGCATCTTCTCGGA
AGAAGACAAGGACATCATCCAGGCGGACTACTTGTACACCAGAGCATTGACCATCTCACCTA
CCATGAGAAAGCACTGGTCAACCGCGATCGGACACTGCCTCTTGTGGAAGAGATCGACCAGAG
GTATTTTCAGCATCATCGACAGCAAAGTGAAGAAGGTCATGTCCATCCCCAAGGGGAACCTCAGC
TCTGCGCAGGGTCATGGAGGAGACCTACTACCATCACATCTACCACACAGTGGCCATCGAGGG
CAACACCCTCACCTCTCGGAAATCAGGCACATCCTGGAGACCCGCTACGCCGTGCCCGGGAA
GAGCCTGGAGGAGCAGAACGAGGTCATAGGCATGCATGCAGCCATGAAGTACATCAACACGAC
TCTGGTTTCGCGCATCGGCTCCGTACCATCAGCGACGTGCTGGAGATCCACAGGCGGGTGCT
GGGCTACGTGGACCCCGTGGAAGCCGGCAGGTTTCGGACAACACAGGTCCTGGTCCGACACCA
CATCCCTCCCCATCCGCAGGATGTGGAAAAGCAGATGCAGGAGTTTGTACAGTGGCTCAACTCC
GAGGAAGCCATGAACCTGCACCCAGTGGAGTTTGCAGCCTTAGCCATTATAAACTCGTTTAC
ATCCACCCTTTTATTGATGGCAACGGGAGGACCTCCCGTCTGCTCATGAACCTCATCCTCATG
CAGGCGGGCTACCCGCCCATCACCATCCGCAAGGAGCAGCGGTCCGACTACTACCACGTGTTG
GAAGCTGCCAACGAGGGCGACGTGAGGCCTTTCATTTCGCTTCATCGCCAAGTGTACTGAGACC
ACCCTGGACACCCTGCTTTTTTGCCACAACCTGAGTACTCGGTGGCACTGCCAGAAGCCCAACCC
AACCCTCTGGGTTCAAGGAGACGCTTCCTGTGAAGCCCTTAACCCTAGAAATCCTCAGTGACA
AAGGCTGTCCTGAGGTAGGAAA

551/615

FIGURE 546

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119517
><subunit 1 of 1, 458 aa, 1 stop
><MW: 51778, pI: 7.81, NX(S/T): 2
MMLIPMASVMAVTEPKWVSVWSRFLWVTLLSMVLGSLALLLPLGAVEEQCLAVLKGLYL
LRSKPDRAQHAATKCTSPSTELSITSRGATLLVAKTKASPAGKLEARAALNQALEMKRQG
KREKAQKLFMHALKMDPDFVDALTEFGIFSEEDKDIIQADYLYTRALTISPYHEKALVNR
DRTLPLVEEIDQRYFSIIDSKVKKVMSIPKGNLRRVMEETYYHHIYHTVAIEGNTLTL
SEIRHILETRYAVPGKSLEEQNEVIGMHAAMKYINTTLVSRIGSVTISDVLEIHRRVLGY
VDPVEAGRFRRTTQVLVGHHIPPHQDVEKQMGEFVQWLNSEEAMNLHPVEFAALAHYKLV
YIHPFIDGNGRTRSRLMLNLILMQAGYPPITIRKEQORSYYHVLEAANEGDVRPFIRFIK
CTETTLDTLLFATTEYSVALPEAQPNHSGFKETLPVKP
```

Important features of the protein:**Signal peptide:**

Amino acids 1-46

N-glycosylation sites:

Amino acids 275-279;446-450

Tyrosine kinase phosphorylation sites:

Amino acids 216-225;217-225;244-232

N-myristoylation sites:

Amino acids 35-41;235-241;266-272;368-374

Amidation site:

Amino acids 119-123

552/615

FIGURE 547

CCTCTGTCTGTGCTCCCATCCCAGGGAGTATAGGTGGAGCCTCCAGAGCCCATGGACAGGGCA
TGCTGGGGCTGGGCCAGCCCCAGCGGTGTCTCTAAGGCACCCCTGGGATCCCCACTGAGCTGG
CCTACTTCAGACAGCCAGGGCCCACCCCTCTGGCCCCCTTAGTGTCCAGCTCGTGGCCCCCTTG
GCATTTCCACAAGACGCCAAGATGAGATTCCCATGGGGACCCAGGGCTGCTTCTCAAAGAGC
CTCCTGCTCTCAGCCTCAATCCTGGTCCTCTGGATGCTCCAAGGCTCCCAGGCAGCTCTCTAC
ATCCAGAAGATTCCAGAGCAGCCTCAAAGAACCAGGACCTTCTCCTGTCTCAGTCCAGGGTGT
CCAGACACCTTCCAGGACTTCAACTGGTACCTGGGGGAGGAGACGTACGGAGGCACGAGGCTA
TTTACCTACATCCCTGGGATACAACGGCCTCAGAGGGATGGCAGTGCCATGGGACAGCGAGAC
ATCGTGGGCTTCCCCAATGGTTCCATGCTGCTGCGCCGCGCCAGCCTACAGACAGTGGCACC
TACCAAGTAGCCATTACCATCAACTCTGAATGGACTATGAAGGCCAAGACTGAGGTCCAGGTA
GCTGAAAAGAATAAGGAGCTGCCCAGTACACACCTGCCACCAACGCTGGGATCCTGGCGGCC
ACCATCATTGGATCTCTTGCTGCCGGGGCCCTTCTCATCAGCTGCATTGCCTATCTCCTGGTG
ACAAGGAAGTGGAGGGGGCCAGAGCCACAGACTGCCTGCTCCGAGGGGGCCAGGGATCTCTGTCC
ATCTTGCTGCTCGGCTGTATCCCCAGTGCCTTCAGTGACGCCCAGCACATGGATGGCGACCACA
GAGAAGCCAGAATTGGGCCCTGCTCATGATGCTGGTGACAACAACATCTATGAAGTGATGCCC
TCTCCAGTCCTCCTGGTGTCCCCCATCAGTGACACAAGGTCCATAAACCCAGCCCGGCCCTG
CCCACACCCCCACACCTGCAGGCGGAGCCAGAGAACCACCAGTACCAGCAGGACCTGCTAAAC
CCCGACCCTGCCCCCTACTGCCAGCTGGTGCCAACCTTCCATGGGTCTGGGCCAGGCCAGC
CAGGGAGAAGACAAGGCCCCAGCCCTCCTCTGGGAGCCTCACACCTGAGACCAGCAGGACAAG
GCCATTGGGGGCTGTGGGGCCGATGAGGTGGACTCAGCCAAAGACTCAGCAGCACATGGGGCA
GGTGTCTGGCAGGGGGACAGGAGACTGTAACAGGCCCAGGTCTTGTGCAGCCCCTGAATGC
ACGCCCCGCTTCGGTCTGTTCTTCAAGCAAGCTGGCCTGGGCCATGTGCCTGTGAAAGGCAG
GCTCTGGCCCCCTTCCATGCCAAAGTCCCCAAGATCTGGATATCTGGGGACAAGATGGTGGC
CTCAGGCCTGCCTCCCAGGCAGTTGGCTGGGCTCCCAACTGTCTGTCTCAATGCCCTACCCC
AACTCCACTAGTGACCCTCAGAGTCTTCTCCCCCTTAGGACAAGGCAGACACCCACCATGCGG
GCCTCAGGTGGCAGAGAGGCCAGCCTCACAGGCCTGTGGCCCCACACACCAGTCCCAGCAAG
GTGACCACGGCTGCTGGACCCCTTCCCTGTTTCAAGCAGGCCCAGCCCCTCTCAGAACCTGCTG
CCAGCTGCTGGTCTTGGCCCCCACCCTGAATCTTACTGAGTCCCTCTGGGCAGCAGCTCCCTT
CTCCACCCCACCCCAGCACCCGTCCCAATGTGGCCTCAGCTTGTCTCTCCCTTCCCCAACT
ATGCATTTCATTAGCAATAAATGAGCCTTTGCTGCA

553/615

FIGURE 548

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119535
><subunit 1 of 1, 300 aa, 1 stop
><MW: 32638, pI: 6.02, NX(S/T): 1
MEIPMGTTQGCFSKSLLLSASILVLWMLQGSQAALYIQKIPEQPQKNQDLLLLSVQGVDPDTF
QDFNWYLGEEYGGTRLFTYIPGIQRPQRDGSAMGQRDIVGFPNGSMLLRRRAQPTDSGT
QVAITINSEWTMKAKTEVQVAEKNKELPSTHLPSTNAGILAATIIGSLAAGALLISCIAYL
LVTRNWRGQSHRLPAPRGQGSLSILCSAVSPVPSVTPSTWMATTEKPELGPAGHDAGDNNI
YEVMPSPVLLVSPISDTRSINPARPLPTPPHLQAEPENHQYQQDLLNPDPAPYCQLVPTS

Important features of the protein:**Signal peptide:**

Amino acids 1-32

Transmembrane domain:

Amino acids 159-178

N-glycosylation site:

Amino acids 104-108

N-myristoylation sites:

Amino acids 6-12;29-35;55-61;91-97;157-163;165-171

554/615

FIGURE 549

GCCACTCACACCATCTGCTAATGGGACAGCTCACTCTTCCCTCCAAACCATGGCCTTGGCTCA
AGAGCTTCCTTGTCTTCTGGAATGTTCTTTCTCCAGCTCCAGGTGTTGAAATTCTGCCTGGTC
TGGGTCTCCTGTTGAAGGACGCCCTCCACTGGGAAGGATCCTCTTGCCTTCACCACTTGTCTT
CACCAGCCCCCTGCTCCCCCTCTTCTTCTTGGGGCTGTTGTCGTTGTTGATACTTTTTTTTTTGT
GTGTTTGACACACATCTTCTTCTCACCCCTCTAACACAGTTCTCAACCACAGCACTTTTGTCCC
TGGAGATGTTGGCAGTGTCCAGAGGCGTGTTGATGGTCCCCTGAGGGTGGGGGTGCTGCTGGCA
CCAGATGGTAGGGAGATGCCAGGGGTGCTGCTCCACACCCTATGGGACACTGCACAGTACACC
TGGCCTGTGTCCCCACAGCGAGAGCTGGCCCTGGGCAGGCGTGCTCCCTGCGGTGTGTGTTG
GTTGGGATCCTCCACAGTGACAGACGGTGCGCTCTGCCACGTTTCCACACAGCTCTTTTGCT
TGTGGAGCTACCCCTTTGCGAGAGAGCTCATTTCCCTGCGGTCTTTGGCCTGCAGAAGTAAAA
TGAAGGGTGGTGAATTACACCCCTGCTGGTTACACATGGAAAACCTCAGGAGTGAGAATTTTGT
GGAGAGCAAGAGAGGTGAGACTGGGGTGCTGGCTGCCAGCCAGGCGGTCCCTCAGCCCCCTGGA
GAAGCGGGGTGGGGCCTGCACACCGAGTCCTTCCAGTGAGTCCAGTGATGCTCTCTCCTCTTC
CTCCCAGTCACCTTTCTCTCCAGTGCCACTACTGCGCTTTTCGATGCAGAATAATTCAGTATTT
GGCGACTTGAAGTCGGACGAGATGGAGCTGCTCTACTCAGCCTACGGAGATGAGACAGGCGTG
CAGTGTGCGCTGAGCCTGCAGGAGTTTGTGAAGGATGCTGGGAGCTACAGCAAGAAAGTGGTG
GACGACCTCCTGGACCAGATCACAGGCGGAGACCCTCTAGGACGCTCTTCCAGCTGAAGCAG
AGAAGAAATGTTCCCATGAAGCCTCCAGATGAAGCCAAGGTTGGGGACACCCTAGGAGACAGC
AGCAGCTCTGTTCTGGAGTTCATGTGATGAAGTCCATCCCGACGTTTCTGTGGATATCTCC
ATGCTCAGCTCTCTGGGGAAGGTGAAGAAGGAGCTGGACCCTGACGACAGCCATTTGAAGTTG
GATGAGACGACGAAGCTCCTGCAGGACCTGCACGAAGCACAGGCGGAGCGCGGCGGCTCTCGG
CCGTCGTCCAACCTCAGCTCCCTGTCCAACGCCTCCGAGAGGGACCAGCACCCCTATGAGTTTCTTCAG
TCTCCAGAGCCTGCGGCCTCTGCCAAGACCTAACTCTAGACCACCTTCAGCTCTTTTATTTTA
TTTTTTTAGTTTTATTTTGCACGTGTAGAGTTTTTGTATCAGACAAGGACTTTGATCCTGTC
CCCTTTGGCATGCGGGAAGCAGCCGCGGGGAGGTAATGAATTGTCTGTGGTATCATGTCAGCA
GAGTCTCCAAGCCCCACGAACCTGAGGAGTGGAGTCATACGCGAAGGCCATATGGCCATCGT
GTCAGCAGAGAGAGTCTCTGTACACAGCCCCGTGAACCCTGAGGAGTGGAGTCATACACGAAG
GGCGTGTGGCCATCGTGTGTCAGCAGAGAGAGTCTCTGTACACAGCCCCGTGAACCCTGAGGAGTGG
AGTCATACGCGAAGGGTGTGTGGCCAGGCTGCAGAGCTGCGTGCCGTTTGTGTCCGAGCATCA
CGTGTGGCTCCAGCCCTTGTCTTCTGCCAGTGTAGACACCTCTGTCTGCCCCACTGTCTTGGGG
TCGCTCTTGGGAGGCACAGGCATGGGTGTGTCTGGCCTCATTCTGTATCAGTCCAGTGTGTTT
CTGTATAGTTTGTGTCTCCCAGGCAGGCCATGGTAGGGGCCCTCGCAGGGGCCATTGGGGAGC
ACAGGGCCAGGCTGGGGTGAAGGAGAGCTCCCTGTTTTCTGTTTAATTGATGAGCCTGGGAAA
GGAGTGTGTTCTGCCTGCCCCGTACAGTGGAGCGTCCGTGTCCATAAAACGTTTCTAACTG
GGAA

555/615

FIGURE 550

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119537
><subunit 1 of 1, 104 aa, 1 stop
><MW: 11136, pI: 8.20, NX(S/T): 0
MLAVSRGVLMVPLGLGVLLAPDGREMPGVLLHTLWDTAQYTWPVSPPTARAGPGQAWSLRC
VLVGILHSDRRCALPTFPHSSFACGAHPFAESSFPCGLWPAEVK

Important features of the protein:**Signal peptide:**

Amino acids 1-20

N-myristoylation sites:

Amino acids 53-59;64-70;97-103

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 74-85

556/615

FIGURE 551

CGCCCTTAGCATGGGTTTCTGCCGAGCGCCCTGCACCCGCTGTCTCTCCTGGTGCAGGCCATCATGCTGGCCAT
GACCTGGCCCTGGGTACCTTGCCTGCCCTTCTACCTGTGAGCTCCAGCCCCACGGCCTGGTGAAGTGAACCTG
GCTGTTCTGAAGTCTGTGCCCCACTTCTCCATGGCAGCACCCTGGCAATGTACCAGCCTTTCTTGTCTCTC
CAACCGCATCCACCACCTCCATGATTCTGACTTTGCCACCTGCCAGCCTGCGGCATCTCAACCTCAAGTGGAA
CTGCCCCGCGGTTGGCTCAGCCCCATGCACTTCCCCTGCCACATGACCATCGAGCCCAGCACCTTCTTGGCTGT
GCCACCCCTGGAAGAGCTAAACCTGAGCTACAACAACATCATGACTGTGCCTGCGCTGCCAAATCCCTCATATC
CCTGTCCCTCAGCCATACCAACATCCTGATGCTAGACTCTGCCAGCCTCGCCGGCCTGCATGCCCTGCGCTTCCCT
ATTATGGACGGCAACTGTTATTACAAGAACCCTGCAGGCAGGCACTGGAGGTGGCCCCGGGTGCCCTCCTTGG
CCTGGGAGCCTCACCACCTGTCACTCAAGTACAACAACCTCACTGTGGTGGCCGCAACCTGCCTTCCAGCCT
GGAGTATCTGCTGTTGTCTACAACCGCATCGTCAAACCTGGCGCCTGAGGACCTGGCCAATCTGACCGCCCTGCG
TGTGCTCGATGTGGCGGAAATTGCCGCGCTGCGACACGCTCCCAACCCCTGCATGGAGTGCCCTCGTCACTT
CCCCAGCTACATCCCGATACCTTCAGCCACCTGAGCCGTCTTGAAGGCCTGGTGTGAAGGACAGTTCTCTCTC
CTGGCTGAATGCCAGTTGGTTCGCTGGGCTGGGAAACCTCCGAGTGTGACCTGAGTGAGAATCTCTCTACAA
ATGCATCACTAAAACCAAGGCCCTCCAGGGCCTAACACAGCTGCGCAAGCTTAACCTGTCTTCAATTACCAAAA
GAGGTGTCTTTGCCACCTGTCTCTGGCCCTTCTTGGGAGCCTGGTGCCTGGAAGGAGCTGGACATGCA
CGCATCTTCTTCCGCTCACTCGATGAGACCAGCTCCGGCCACTGGCCCGCTGCCATGCTCCAGACTCTGCG
TCTGCAGATGAACCTTCATCAACCAGGCCAGCTCGGCATCTTCAAGGCCTTCCCTGGCCTGCGCTACGTGGACCT
GTCGGACAACCGCATCAGCGGAGCTTCGGAGCTGACAGCCACCATGGGGGAGGCAGATGGAGGGGAGAAGGTCTG
GCTGCAGCCTGGGGACCTTGTCTCCGGCCCCAGTGGACACTCCAGCTCTGAAGACTTCAGGCCCAACTGCAGCAC
CCTCAACTTCACCTTGGATCTGTACGGACAACCTGGTGACCGTGCAGCCGGAGATGTTTGGCCAGCTCTCGCA
CCTGCAGTGCCTGCGCTGAGCCACAACCTGCATCTCGCAGGCACTCAATGGCTCCAGTTCTTCCGCTGACCGG
TCTGCAGGTGCTAGACCTGTCCCAATAAGCTGGACCTTACCACGAGCACTATTACGGAGCTACCACGACT
GGAGGCCCTGGACCTCAGCTACAACAGCCAGCCCTTTGGCATGAGGGCGTGGGCCACAACCTTCAGCTTCGTGGC
TCACCTGCGCACCTGCGCCACCTCAGCCTGGCCACAACAACATCCACAGCCAAGTGTCCCAGCAGCTCTGCAG
TACGTGCTGCGGGCCCTGGACTTCAGCGGCAATGCACTGGGCCATATGTGGGCCGAGGGAGACCTCTATCTGCA
CTTCTTCCAAGGCCTGAGCGGTTTGATCTGGCTGGACTTGTCCAGAACCCTGTCACACCCTCCTGCCCCAAAC
CCTGCGCAACCTCCCAAGAGCCTACAGGTGCTGCGTCTCCGTGACAATTACCTGGCCTTCTTTAAGTGGTGGAG
CCTCCACTTCTGCCCCAACTGGAAGTCTCGACCTGGCAGGAAACAGCTGAAGGCCCTGACCAATGGCAGCCT
GCCTGCTGGCACCCGCTCCGGAGGCTGGATGTGAGCTGCAACAGCATCAGCTTCGTGGCCCCCGGCTTCTTTTC
CAAGGCCAAGGAGCTGCGAGAGCTCAACCTTAGCGCCAACGCCCTCAAGACAGTGGACCACTCCTGGTTTGGGCC
CCTGGCGAGTGCCCTGCAAATACTAGATGTAAGCGCCAACCTCTGCACTGCGCCTGTGGGGCGGCCTTTATGGA
CTTCTGCTGGAGGTGAGGCTGCCGTGCCCGTCTGCCAGCCGGGTGAAGTGTGGCAGTCCGGGCCAGCTCCA
GGCCTCAGCATCTTTGCACAGGACCTGCCCTCTGCTGGATGAGGCCCTCTCCTGGGACTGTTTCGCCCTCTC
GCTGCTGGCTGTGGCTCTGGGCTGGGTGTGCCATGCTGCATCACCTCTGTGGCTGGGACCTCTGGTACTGCTT
CCACCTGTGCCTGGCCTGGCTTCCCTGGCGGGGGCGGCAAGTGGGCGAGATGAGGATGCCCTGCCCTACGATGC
CTTCGTGGTCTTCGACAAAACGAGAGCGCAGTGGCAGACTGGGTGTACAACGAGCTTCGGGGGAGCTGGAGGA
GTGCCGTGGGCGCTGGGCACTCCGCTGTGCTGGAGGAACGCGACTGGCTGCCGCAAAACCTCTTTGAGAA
CCTGTGGGCTCGGTCTATGGCAGCCGCAAGACGCTGTTTGTGCTGGCCCAACGAGCCGGGTGAGTGTCTCTT
GCGGCCAGCTTCTGCTGGCCAGCAGCGCTGCTGGAGGACCGCAAGGACGTCGTGGTGTGTTGATCTCTGAG
CCCTGACGGCCGCGCTCCCGCTACGTGCGGCTGCGCCAGCGCCTCTGCCGCCAGAGTGTCTCTCTGGCCCCA
CCAGCCAGTGGTCAGCGCAGCTTCTGGGCCAGCTGGGCATGGCCCTGACCAGGGACAACCACCACTTCTATAA
CCGGAACCTTCTGCCAGGGACCCACGGCCGAATAGCCGTGAGCCGGAATCTGCACGGTGCCACCTC

557/615

FIGURE 552

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119714
><subunit 1 of 1, 1032 aa, 1 stop
><MW: 115799, pI: 8.61, NX(S/T): 12
MGFCRSALHPLSLLVQAIMLAMTLALGTLPAFLPCELQPHGLVNCNWLFLKSVPHFMSMAA
PRGNVTSLSLSSNRIHHLHDSDEFAHLPSLRHLNLKWNCPVGLSPMHFPCHMTIEPSTFL
AVPTLEELNLSYNNIMTVPALPKSLISLSLSHTNILMLDSASLAGLHALRFLFMDGNCY
KNPCRQALEVAPGALLGLGSLTHLSLKYNLTVPVPRNLPSSLEYLLLSYNRIVKLAPEDL
ANLTALRVLDVGGNCRRCDHAPNPCMECPRHFPQLHPDTFSHLSRLEGLVLKDSSLSWLN
ASWFRGLGNLRVLDLSENFYKCIITKTKALQGLTQLRKLNLSFNYQKRVSFAHLSLAPSF
GSLVALKELDMHGIFFRSLDETTLRPLARLPMLOTLRLQMNFINQAQLGIFRAFPGLRYV
DLSNDRISGASELTATMGADGGEKVWLQPGDLAPAPVDTPSSEDFRPNCSTLNFTLDLS
RNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQVLDLSHNKLDLYHEHS
FTELPRLEALDLSYNSQPFMGQGVGHNFSEVAHLRTLRLSLAHNNIHSQVSQQLCSTSL
RALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLDSLQNRHLTLPLQTLRNLPKSLQVLR
RDNYLAFFKWWSLHFLPKLEVLDLAGNQLKALTNGSLPAGTRLRRLDVSCNSISFVAPGF
FSKAKELRELNLNLSANALKTVDHWSWFGPLASALQILDVSANPLHCACGAAFMDFLLEVQAA
VPGLPSRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCFALSLLAVALGLGVPMLHHLCG
WDLWYCFHLCLAWLPWRGRQSGRDEDALPYDAFVVFDDKTQSAVADWVYNELRGQLEECRG
RWALRLCLEERDWLPGKTLFENLWASVYGSRKTLFVLAHTDRVSGLLRASFLLAQQRLLE
DRKDVVVLVILSPDGRRSRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGMALTRDNHFF
YNRNFCQGPTAE

Important features of the protein:

Signal peptide:

Amino acids 1-30

Transmembrane domain:

Amino acids 818-835

N-glycosylation sites:

Amino acids 64-68;129-133;210-214;242-246;300-304;340-344;
469-473;474-477;513-517;567-571;694-698;731-735

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 347-351

Tyrosine kinase phosphorylation site:

Amino acids 863-871

N-myristoylation sites:

Amino acids 27-33;41-47;63-69;193-199;361-367;409-415;
563-569;607-613;695-701;794-800;929-935;945-951;
1010-1016

Amidation site:

Amino Acids 974-978

Leucine zipper patterns:

Amino acids 204-226;644-666;814-836

558/615

FIGURE 553

GGCGTGGGACGTGCTGCGGCGTCCTAGCTGGCTTACAGGGCGGCGGGGGTGTGTGTCCTCT
GTTAAGAGTGCTACTCGCCCGGGGTGATCTGTGCATGCCACTCCTGGGTGAGACGGTGAGGT
CGGCGTCTGCGAGGACGCGGCGGTGGAGTAGAAGGGCAGCCGGAGACAGGCCCGGCCCTT
CCGAGGCTAGACGGCCCCAGCTTCGCGGGGATCATGGCATTGCTGGTGGACCGAGTGCGGGGC
CACTGGCGAATCGCCGCCGGGCTCCTGTTCAACCTGCTGGTGTCCATCTGCATTGTGTTCCCTC
AACAAATGGATTTATGTGTACCACGGCTTCCCCAACATGAGCCTGACCCTGGTGCACCTTCGTG
GTCACCTGGCTGGGCTTGTATATCTGCCAGAAGCTGGACATCTTTGCCCCAAAAGTCTGCCG
CCCTCCAGGCTCCTCCTCCTGGCCCTCAGCTTCTGTGGCTTTGTGGTCTTCACTAACCTTTCT
CTGCAGAACAACACCATAGGCACCTATCAGCTGGCCAAGGCCATGACCACGCCGGTGATCATA
GCCATCCAGACCTTCTGCTACCAGAAAACCTTCTCCACCAGAATCCAGCTCACGCTGATTCT
ATAACTTTAGGTGTAATCCTAAATTCTTATTACGATGTGAAGTTTAATTTCCCTTGAATGGTG
TTTGCTGCTCTTGGTGTTTTAGTTACATCCCTTTATCAAGTGTGGGTAGGAGCCAAACAGCAT
GAATTACAAGTGAACCTCAATGCAGCTGCTGTACTACCAGGCTCCGATGTCATCTGCCATGTTG
CTGGTTGCTGTGCCCTTCTTTGAGCCAGTGTTTGGAGAAGGAGGAATATTTGGTCCCTGGTCA
GTTTCTGCTTTGCTTATGGTGCTGCTATCTGGAGTAATAGCTTTCATGGTGAACCTTATCAATT
TATTGGATCATTGGGAACACTTCACCTGTCACCTATAACATGTTCCGACACTTCAAGTTCTGC
ATTACTTTATTCGGAGGATATGTTTTATTTAAGGATCCACTGTCCATTAATCAGGCCCTTGGC
ATTTTATGTACATTATTTGGCATTCTCGCCTATACCCACTTTAAGCTCAGTGAACAGGAAGGA
AGTAGGAGTAACTGGCACAACGTCCTTAATTGGGTTTTTGTGGAGAAAAGAATGTTGTCCCA
AGAAGATAAAAAATATTGTTAAGTGTGCAAGTTATTA

559/615

FIGURE 554

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125170
><subunit 1 of 1, 313 aa, 1 stop
><MW: 35066, pI: 9.39, NX(S/T): 5
MALLVDRVRGHWRIAAGLLFNLLVSICIVFLNKWIYVYHGFPNMSLTLVHFVVTWLGLYI
CQKLDIFAPKSLPPSRLLLLALSFCGFVVFTNLSLQNNITIGTYQLAKAMTTPVIIAIQTF
CYQKTFSTRIQLTLIPITLGVILNSYYDVKFNFLGMVFAALGVLVTSLYQVWVGAKQHEL
QVNŞMQLLYYQAPMSSAMLLVAVPFFEPVFEQGGIFGPWSVSALLMVLLSGVIAFMVNLS
IYWIIGNTSPVTYNMFGHFKFCITLFGGYVLFDPLSINQALGILCTLFGILAYTHFKLS
EQEGSRSKLAQRP
```

Important features of the protein:**Signal peptide:**

Amino acids 1-27

Transmembrane domains:

Amino acids 46-60;75-90;153-167;192-208;221-237

N-glycosylation sites:

Amino acids 43-47;92-96;97-101;238-242

N-myristoylation sites:

Amino acids 17-23;57-63;140-146;155-161;162-168;283-289

560/615

FIGURE 555

GTTAGGCAGAGCCAAGGTGGTTGCAGACCTGGAATCAGAACAGCTTTTAGACCAACCTGAAAG
CAGGAATGTAAGCACTGTTTCACAGAGATTTTCGTCTTTGGCTTATTGTGCCTGCAGAGTCTAG
TGCTTCTTTGCCAGCTGTGCTGACTCAGCACTCC**ATG**CCTGTTTTCTGGAACCACTCCCTGGA
GCTGGGCCATGTTTTGATTGACAGTGTGGAGCTAGCCCAGCAAGTACTCTACATGCAACCCCC
CAGCCAGGCACTACCTCTGCTCCTCCTCCATGGCCTCCTGCTACACCGGCAGCTCTATGGAAC
AAGGCTGCAGGCACACAGGGGGCGCTGGAGTCAAGTGACTCTAACCAGGTTCTTCAGACCCA
AGACCAGCTGTGGGCAAGTCTTAGCAATCCCCGTGCTGCCATGCAAGAGCTGGCTGCTTCAGT
TTTCTACGGGGGTCTCTGGGGGACACTGAGGACAGGGAGGCCCTGATTAGCCTCACACAAGC
CTGCCTGAGCCCCAGTAGTGGGAGCTGGGTCCAGCCACACACACCTCAGTCTTTGCTGGCCAC
GCTCATGCCCTCCAGCTAAGGGAGCTGGATGCAATGGCAGAGTGCAAGGCCAGATGCACC
TACTGCCCTCACCACC**TGA**ACCCCGGCTCTGCGGACTGAGTGAGGGCCCCCAAGCCTGGCTGT
TGCGACGCCAGAGTCGCGCTCTCTTGAGTGCCTGTCAGCGGAGTTCACCCGTGTGGGTTCTCTG
AGTCTCGAAGAGGCGCCAGCTTGCGGAAAGGCGACTGCGGCAACGCCTAGTGCAAGTCAACCG
GAGGCTGGAGTCACTGCAGGATCTGCTGACCCACGTGATTGCGCAAGACGAGTCCGACGCCCC
GTGGTCAGTGCTGGGGCCAAATGCACGGCGGCCTCTGGAGGGCGTCTTAGAGACCGAGGCTCT
AGAACTGAGCCAGTTGGTGGGCACGCTACAACGCGACCTTGATTGCCTGTTGCAGCAGCTGAA
GGGCGCACCCCGTGGCCCTCCCGCCGCTGTGCTGCGGTGGCCACGCTCTCTGGACTGGCCG
CCTACCCCTGCCTTGCGGACCTCATGCGCCGGCCGGTCCGCAGCCGCCCTGGCACTGGCTGCG
ACAGTTGTCGCGCCGTGGGCAACTGTTGGTTCGTTACTTGGGCGTGGGCGCGGACGCGAGCAG
TGATGTACCAGAGCGCGTCTTCCACCTGTCAGCCTTTCGCCACCCGCGCCGCTGCTGCTGGC
ATTGCGTGGGGAAGCTGCCCTGGACCAGAATGTGCCAGCTCGAATTTCCCTGGTAGCCGAGG
CTCGGTCTCAGTCAGCTCCAGTATAAACGTCTGGAGATGAACAGCAACCCTCTGCACTTCAG
GGTGGAGAATGGTCCAAATCCACGGTTCCAGAGAGAGGGCTGCTGCTGATCGGGCTACAGGT
CCTACATGCGGAGTGGGACCCAATAGCTGGAGCCTTGCAAGACAGTCCTTCCAGCCAACCCAG
CCCTCTGCCTCCCGTCAGCATCAGCACACAGGCCCGGGCACCAGTGACCTGCCAGCCCCAGC
CGACCTGACTGTGTACTCGTGTCTGTGTACATGGGAGGGCCCCCTTGGCACCGCTAAGCTGCA
GAGCAGGAACATCGTGATGCATCTGCCTTTACCCACCAAGCTCACCCCCAACACCTGTGTCCA
AAGGAGGGTCCATGTGTGCAGCCACCCCTGTCTTGAGCCCGTCTACCAAATAAAGTTGTAG
TGATTCCA

561/615

FIGURE 556

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA129594
><subunit 1 of 1, 162 aa, 1 stop
><MW: 17598, pI: 6.58, NX(S/T): 1
MPVFWNQSLGHLIDSVELAQQVLYMQPPTQALPLLLHGLLLHRQLYGTRLQAHGR
WSQVTLTQVLQTQDQLWASLSNPRAAMQELAASVFYGGPLGDTEDREALISLTQACLSPS
SGSWVQPHTPQSLLATLMPLPAKGAGCNGRVQGPDAPTALT
```

Important features of the protein:**Signal peptide:**

Amino acids 1-45

N-glycosylation site:

Amino acids 6-10

N-myristoylation sites:

Amino acids 97-103;144-150

562/615

FIGURE 557

GACCTTGAGCCCTCGAAAGCGACATGGCGGTTCTCTTAAAGCTGGGCGTTCTCTGCAGTGGCC
AAGGAGCTCGAGCTCTCCTACTCCGAAGCCGGGTGGTCAGACCCGCTTATGTGTCAGCATTTTC
TCCAGGACCAGCCTACCCAAGGACGGTGTGGTACCCAGCACATTACCTGTCACCAAGCCACC
ACTCTGGTTCCAAGGCTGCATCTCTCCACTGGACCAGTGAGAGGGTTGTAGTGTCTGCTCT
TGGGGCTGATCCCTGCTGGGTACTTGAATCCCTGCTCTGTGGTGGACTACTCTCTGGCTGCAG
CCCTCACCCCTGCACAGTCACTGGGGCCTTGGACAAGTGGTTACCGACTACGTTTCATGGGGACA
CCCTGCCGAAGGCTGCCAGGGCAGGCCTCTTGGCACTCTCAGCTTTGACCTTTGCTGGGCTTTGC
TACTTCAATTACCACGATGTCGGCATCTGCAGAGCGGTTGCCATGCTGTGGAAGCTCTGACCT
GGGTGCAGCACTTTGATTGTGTGCCTCCTTGCCTCTGCTTTACCAATGCCGTTACCTCGCAG
TGAGGGGGGATGAAGGATAAGCCATTGGTGGGCAGAATGTCTTCTAATTACATGGTTATTTT
CAGAATTTATTTGTTGAGGAAGAGGTTTGAGGAGTTAGGTTTCGACCATTTCGTGAGTCTGTGTT
CCATACTCCACTGAGTGTGGGCACTAGCTCACAGCCTCGCGGTGAGACTGAACATTTTCATGAG
CTCATGTTGCCCTTTGACCACCATTTCTTAAGGAGAGCCAGCTGATTGCTGTCAGGATAAGAGC
ATCTCTTCAGCCAGGAGGGAGGCCTGTTCCCTCCTGAGTTAGACTTTGCATGAAGCTCGAAAG
TATTCCCTTTGGAACCTCCCATTTCTTGTTTCAGGTGACACCAGCTCTGTTGATGGCTCTGCTTC
TAGGGAACATTTAATCAGGAGATGCTCTCAATGACTAATTTGTCTAAGTCTTAGGAAGGAGGT
TGAGGAAAGCTGGATTTAGACAAGTTCAATTTAGGGAGTTCTCCTTGTTTGTGGATTAAAATA
TGACAGATTGCAAACAGACTACTCTTCAAATGTATCTCAATTGTGCAGAAGTGAGCTGTCCAA
AAGTATAAGACTAAGTGATAAACTGTCTTCCCACCGTGGGAGTTGTTAATGAGAAAGAAAGTG
TACTCTGAAAAAACAAGGGGG

563/615

FIGURE 558

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA129793
><subunit 1 of 1, 159 aa, 1 stop
><MW: 17014, pI: 9.38, NX(S/T): 0
MAVLLKLGVLCSGQGARALLRSRVVRPAYVSAFLQDQPTQGRCGTQHIHLSPSHHSGSK
AASLHWTSERVVSVLLGLIPAGYLNPCSVVDYSLAAATLHSHWGLGQVVTDYVHGDTL
PKAARAGLLALSALTFAGLCYFNYHDVGICRAVAMLWKL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-15

Transmembrane domains:

Amino acids 71-88;126-140

Glycosaminoglycan attachment site:

Amino acids 12-16

N-myristoylation sites

Amino acids 8-14;58-64;78-84;108-114;148-154

564/615

FIGURE 559

CCCAGCCCCGCGTTTCGGCTGCTCTCGAGGAGGCCGGAGTCCCCGGAGACGATGCGCCCCGCGC
AGCCGCCTGCGCCTGCGGGAGCCGGCTGCCCTTGAGATGGAGTTGCTGCCTCTTTGGCTCTGC
CTGGGTTTTCACTTCTGACCGTGGGCTGGAGGAACAGAAGCGGAACAGCCACAGCAGCCTCC
CAAGGAGTCTGCAAGTTGGTGGGTGGAGCCGCTGACTGCCGAGGGCAGAGCCTCGCTTCGGTG
CCCAGCAGCCTCCCCCCCCACGCCCGGATGCTCACCTGGATGCCAACCTCTCAAGACCCTG
TGGAATCACTCCCTCCAGCCTTACCCTCTCCTGGAGAGCCTCAGCCTGCACAGCTGCCACCTG
GAGCGCATCAGCCGCGGCGCCTTCCAGGAGCAAGGTCACCTGCGCAGCCTGGTCCTGGGGGAC
AACTGCCTCTCAGAGAACTACGAAGAGACGGCAGCCGCCCTCCACGCCCTGCCGGGCTGCGG
AGGCTGGACTTGTCAGGAAACGCCCTGACGGAGGACATGGCAGCGCTCATGCTCCAGAACCTC
TCCTCGCTGCGGTCCGTGTCCTGGCGGGGAACACCATCATGCGGCTGGACGACTCCGTCTTC
GAGGGCCTGGAGCGTCTCCGGGAGCTGGATCTGCAGAGGAACTACATCTTCGAGATCGAGGGC
GGCGCTTTCGACGGCCTGGCTGAGCTGAGGCACCTCAACCTGGCCTTCAACAACCTCCCCTGC
ATCGTGGACTTCGGGCTCACGCGGCTGCGGGTCTCAACGTGAGCTACAACGTCTGGAGTGG
TTCCTCGCGACCGGGGGAGAGGCTGCCTTCGAGCTGGAGACGCTGGACCTGTCTACAACCAG
CTGCTGTTCTTCCCGCTGCTGCCCCAGTACAGCAAGTTGCGGACCCTCCTGCTGCGCGACAAC
AACATGGGCTTCTACCGGGACCTGTACAACACCTCGTCGCCGAGGGAGATGGTGGCCCAGTTC
CTCCTCGTGGACGGCAACGTGACCAACATCACCACCGTCAGCCTCTGGGAAGAATTCTCCTCC
AGCGACCTCGCAGATCTCCGCTTCTGGACATGAGCCAGAACCAGTTCAGTACCTGCCAGAC
GGCTTCTGAGGAAAATGCCTTCCCTCTCCACCTGAACCTCCACCAGAATTGCCTGATGACG
CTTCACATTCGGGAGCACGAGCCCCCGGAGCGCTCACCGAGCTGGACCTGAGCCACAACCAG
CTGTGCGAGCTGCACCTGGCTCCGGGGCTGGCCAGCTGCCTGGGCAGCCTGCGCTTGTTCAAC
CTGAGCTCCAACCAGCTCCTGGGCGTCCCCCTGGCCTCTTCGCCAATGCTAGGAACATCACTAC
ACTTGACATGAGCCACAATCAGATCTCACTTTGTCCCCCTGCCAGCTGCCTCGGACCGGGTGGG
CCCCCTAGCTGTGTGGATTTTCAGGAATATGGCATCTTTAAGGAGCCTGTCTCTGGAGGGCTG
TGGCCTGGGGGCAATTGCCAGACTGCCCATTCCAAGGGACCTCCCTGACCTACTTAGACCTCTC
AAGCAACTGGGGGGTTCTGAATGGGAGCCTCGCCCCACTCCAGGATGTTGCCCCCATGTTACA
GGTCTGTCTCTCAGGAACATGGGCCTCCACTCCAGCTTTATGGCGTTGGACTTCTCTGGGTT
TGGGAATCTCAGGGACTTAGATCTGTGCGGGAATTGCTTGACCACCTTCCCAAGGTTTGGGGG
CAGCCTGGCCCTGGAGACCTGGATCTCCGTAGAACTCGCTCACAGCCCTTCCCCAGAAGGC
TGTGTCTGAGCAGCTCTCGAGAGGTCTGCGGACCATCTACCTCAGTCAGAATCCATATGACTG
CTGTGGGGTGGATGGCTGGGGGGCCCTGCAGCATGGGCAGACGGTGGCCGACTGGGCCATGGT
CACCTGCAACCTCTCCTCCAAGATCATCCGCGTGACGGAGCTGCCCCGAGGTGTGCCTCGGGA
CTGCAAGTGGGAGCGGCTGGACCTGGGCCTGCTCTACCTCGTGCTCATCCTCCCCAGCTGCCT
CACCTGCTGGTGGCCTGCACTGTCATCGTCCTCACTTTTAAGAAGCCTCTGCTTCAGGTCAT
CAAGAGCCGCTGCCACTGGTCTCCTCCGTTTACTGACCTGGCTGTGTGCCAAGACTCGAAATTCTG
GTCCGCACACAACAGGACACTTTCTCTGCCAGCTTTCAAGATGTGATGCAGAGGCCAAGTCTG
ACGAATTGAAGTTTCAATTAAAATTTAATATGTTTCCATTCTCATCGCCACCCACCCCG
CCCCACCACCGCCCAAGTTCTTTTCCATCATTATAATTATCCTTATTATCTTGGTAAAT
ATTTATTAAGTGACTTTTTCAGAAATAAAAGGCAACGTGTCTCATAAATATTTTTTAAAAAA
AAAAAAAAAAAAA

565/615

FIGURE 560

><subunit 1 of 1, 692 aa, 1 stop
><MW: 76366, pI: 6.07, NX(S/T): 11
MELLPLWLCLGFHFLTIVGWRNRSGTATAASQGVCKLVGGAADCRGQSLASVPSSLPPHAR
MLTLDANPLKTLWNHSLQPYLLESLSLHSLCHLERISRGAFQEQGHLRSLVLGDNCLSEN
YEETAALHALPGLRRLDLSGNALTEDMAALMLQNLSSLRSVSLAGNTIMRLDDSVFEG
ERLRELDLQRNYIFEIEGGAFDGLAELRHLNLAFFNNLPCIVDFGLTRLRLVNVSYNVLEW
FLATGGEAAFELETLDLSHNQLLFFPLLPQYSKLRITLLLRDNNMGFYRDLYNTSSPREMV
AQFLLVDGNVTNITTVSLWEEFSSSDLADLRFLDMSQNFQYLPDGFRLKMPSLSHLNLH
QNCLMTLHIREHEPPGALTELDLSHNQSELHLAPGLASCLGSLRLFNLSNQLLGVP
LFFANARNITTLDMSHNQISLCPLPAASDRVGPSCVDFRNMASLRSLSEGCGLGALPDC
PFQGTSLTYLDLSSNWGVNLGSLAPLQDVAPMLQVLSLRNMGLHSSFMALDFSGFGNLRD
LDLSGNCLTTFPRFGGSLALETDLRRNSLTALPQKAVSEQLSRGLRTIYLSQNPYDCCG
VDGWGALQHGQTVADWAMVTCNLSSKIIRVTELPGGVPRDCKWERLDLGLLYLVLIPLSC
LTLLVACTVIVLTFKKPLLQVIKSRCHWSSVY

Important features of the protein:**Signal peptide:**

Amino acids 1-18

Transmembrane domain:

Amino acids 651-672

N-glycosylation sites:Amino acids 21-25;74-78;155-159;232-236;292-296;309-313;
312-316;408-414;427-431;500-504;622-626**Glycosaminoglycan attachment site:**

Amino acids 533-537

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 566-570

N-myristoylation sites:Amino acids 24-30;39-45;45-51;141-147;199-205;245-251;
308-314;396-402;416-422;420-426;471-477;
484-490;497-503;522-528;545-551;555-561;610-616**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 657-668

Leucine zipper patterns:

Amino acids 48-70;492-514

566/615

FIGURE 561

TGGCCTACTGGAAAAAAAAAAAAAAAAAAAAAGTCACCCGGGCCCCGCGGTGGCCACAACAT
GGCTGCGGCGCCGGGGCTGCTCTTCTGGCTGTTTCGTGCTGGGGGCGCTCTGGTGGGTCCCGGG
CCAGTCGGATCTCAGCCACGGACGGCGTTTCTCGGACCTCAAAGTGTGCGGGGACGAAGAGTG
CAGCATGTTAATGTACCGTGGGAAAGCTCTTGAAGACTTCACGGGCCCTGATTGTCGTTTTGT
GAATTTTAAAAAAGGTGACGATGTATATGTCTACTACAACTGGCAGGGGGATCCCTTGAAC
TTGGGCTGGAAGTGTTGAACACAGTTTTTGGATATTTTCCAAAAGATTTGATCAAGGTACTTCA
TAAATACACGGAAGAAGAGCTACATATTCCAGCAGATGAGACAGACTTTGTCTGCTTTGAAGG
AGGAAGAGATGATTTTAAATAGTTATAATGTAGAAGAGCTTTTAGGATCTTTGGAAGTGGAGGA
CTCTGTACCTGAAGAGTCGAAGAAAGCTGAAGAAGTTTCTCAGCACAGAGAGAAATCTCCTGA
GGAGTCTCGGGGGCGTGAACCTTGACCCTGTGCCTGAGCCCGAGGCATTCAGAGCTGATTCAGA
GGATGGAGAAGGTGCTTTCTCAGAGAGCACCGAGGGGCTGCAGGGACAGCCCTCAGCTCAGGA
GAGCCACCCTCACACCAGCGGTCCTGCGGCTAACGCTCAGGGAGTGCAGTCTTCGTTGGACAC
TTTTGAAGAAATTCTGCACGATAAATTGAAAGTGCCGGGAAGCGAAAGCAGAACTGGCAATAG
TTCTCCTGCCTCGGTGGAGCGGGAGAAGACAGATGCTTACAAAGTCCTGAAAACAGAAATGAG
TCAGAGAGGAAGTGGACAGTGC GTTATTCATTACAGCAAAGGATTTTCGTTGGCATCAAAATCT
AAGTTTGT TTTACAAAGATTGTTTTTTAGTACTAAGCTGCCTTGGCAGTTTGCATTTTTTGAGCC
AAACAAAAATATATTATTTCCCTTCTAAGTAAAAAAAAAAAAAAAAAAAAA

567/615

FIGURE 562

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131639
><subunit 1 of 1, 303 aa, 1 stop
><MW: 33900, pI: 4.81, NX(S/T): 2
MAAAPGLLFWLFLVGLGALWWVPGQSDL SHGRRFSDLKVCGDEEC SMLMYRGKALEDFTGPD
CRFVNFKKGDDVYVYYKLAGGSLELWAGSVEHSFGYFPKDLIKVLHKYTEELHIPADET
DFVCFEGGRDDFNSYNVEELLGSLELEDSVPEESKKAEEVSQHREKSPEESRGRELD PVP
EPEAFRADSEDEGEGAFSESTEG LQGQPSAQESH PHTSGPAANAQGVQSSLDTFEEILHDK
LKVPGSESRTGNSSPASVEREKTDAYKVLKTEMSQ RSGQCVIHYSKGFRWHQNLSLFYK
DCF
```

Important features of the protein:**Signal peptide:**

Amino acids 1-22

N-glycosylation site:

Amino acids 294-298

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 30-34

Tyrosine kinase phosphorylation site:

Amino acids 67-76

N-myristoylation sites:

Amino acids 205-211;225-231;277-283

Amidation site:

Amino acids 28-32

568/615

FIGURE 563

GCCAGCCGTGGGATTAGGCTTCGCCGGCTACGATTGCGGCCCCCATCTTCTGACTTTTCCTCG
TGTGACCCATCTTTTCAAATTCCTTACCTGAGGAAGGAGCCCGATTACAAGGATATTTACCT
GCTCCTACCCTGATCTAGGGACGAGGATGGGAAGACCGCCTGTGGCCATGAGCCCTCCCCGGT
GCTCCTGGGGCTAAGGCTGGGGCTGCAGCC**ATG**GGGCTGGGTGAGCCCCAGGCCTGGTTGCTG
GGTCTGCCCACAGCTGTGGTCTATGGCTCCCTGGCTCTCTTCACCACCATCCTGCACAATGTC
TTCCTGCTCTACTATGTGGACACCTTTGTCTCAGTGTACAAGATCAACAAAATGGCCTTCTGG
GTCGGAGAGACAGTGTTTCTCCTCTGGAACAGCCTCAATGACCCTCTCTTCGGTTGGCTCAGT
GACCGGCAGTTCCTCAGCTCCCAGCCCCGCCTGTGTGGAGAGGAGCTGCTTGTGGGCAGTGAG
GAGGCGGACAGCATCACCTTGGGCGCGTATCTCCGGCAGCTGGCACGCCATCGGAACTTCCTG
TGGTTCGTGAGCATGGACCTGGTGCAGGTGCAGTGGCTCACGCCTGTAATCCCAGCACTTCGG
GACGCCAAGGTGGAAAGACCGCTTGAGCCCAGGAGTTCGAGGCTGCAAT**TGA**GTTATGATTGCA
CCTGCACTCCAGCCTGGGCGGCAGAGAAAGGCTCCATCTCTAAAAAAGAAGAGCTAAGTG
CTGTACCTAAAACATGCAGTATATAAACTGGCTGAACTTAGAAATAAACTGTTTTCATGTTAT
GAAAA

569/615

FIGURE 564

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131649
><subunit 1 of 1, 153 aa, 1 stop
><MW: 17603, pI: 7.42, NX(S/T): 0
MGLGQPQAWLLGLPTAVVYGSALFTTILHNVFLLYYVDTFVSVYKINKMAFWVGETVFL
LWNSLNDPLFGWLSDRQFLSSQPRLCGEELLVGSEEADSITLGRYLRQLARHRNFLWFVS
MDLVQVQWLTPVIPALRDAKVERPLEPRSSRLQ
```

Important features of the protein:**Signal peptide:**

Amino acids 1-20

N-myristoylation sites:

Amino acids 4-10;12-18;93-99

Leucine zipper pattern:

Amino acids 102-124

570/615

FIGURE 565

CGGCACGAGTAAAATGGAGATAATATCACCATGCACTCAGCCCTAGCCACTGCATTGCTGTTA
CTGATAACCATTACTGCTGCTACGTCGTTTTTTGATGGCTCAGCCCTTAGGGAAGGGGGATCA
AGGGAGAAGCCCGGACCTTCCCGCAGGAGGTGGGCTGGGCACAGCCCTGAACCATGGAGGTCA
CCCACCCTGAGGTCGGGACCTGGGTTCCCTTCCTATCCACTGGGGGTCCCAGCCTTTGTCTTC
ATCTCTCCAGGTCCCAGCCCTTCACAGTGGGCACTTCCCTGCCTGTGACGGAGGCCCCAGCCA
TCTCC

571/615

FIGURE 566

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131652
><subunit 1 of 1, 89 aa, 1 stop
><MW: 9688, pI: 11.49, NX(S/T): 0
MHSALATALLLLIPLLLLRFFDGSALREGGSREKPGPSRRRWAGHSPEPWRSPTLRSGP
GFPSYPLGVPAFVFISPGSPSQWALPCL

Important features of the protein:**Signal peptide:**

Amino acids 1-18

Glycosaminoglycan attachment site:

Amino acids 58-62

572/615

FIGURE 567

AGTCTAGCAGGAAAGGAGAGGGAGCTTTCCCCGAAGACCCTCCTGGACCAGCCCCAGGCTCCT
GTGCTGGTTGCACGCCAGGGCCTGTACTGACCACCTCCACGTGCCACTGGGGCTGTAAGGAGGA
ATGGCGGCCGTGGGCAGCCTGCTTGGCCTGGCAGCCTCTTCCTGGCTAGGGGGCCAGAACGCC
TCTGACCACAGCCTGTGGCTCCTGAGGAAGCCCCGAGGCTCATCCTGCCCCGGCACGGGTCAC
CAGCTCTGCCGGCTGAGGCAGAGCACCGTGAAGGCCACCGGACCTGCACTCCGCCGCCTGCAC
ACATCCTCCTGGCGAGCTGACAGCAGCAGGGCCTCACTCACTCGTGTGCACCGCCAGGCTTAT
GCACGACTCTACCCCGTGCTGCTGGTGAAGCAGGATGGCTCCACCATCCACATCCGCTACAGG
GAGCCACGGCGCATGCTGGCGATGCCCATAGATCTGGACACCCTGTCTCCTGAGGAGCGCCGG
GCCAGGCTGCGGAAGCGTGAGGCTCAGCTCCAGTCGAGGAAGGAGTACGAGCAGGAGCTCAGT
GATGACTTGCATGTGGAGCGCTACCGACAGTTCTGGACCAGGACCAAGAAG**TGA**ACCGTGGCTC
CAGCCACCCCGGGACATTGCTAAGATGGGAGGGCTGTTCTTAAATCACTCGTTCTTGAAGCTGC

573/615

FIGURE 568

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131658
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18903, pI: 11.08, NX(S/T): 1
MAAVGSLGLAASSWLGGQNASDHSLWLLRKPRGSSCPGTGHQLCRLRQSTVKATGPALR
RLHTSSWRADSSRASLTRVHRQAYARLYPVLLVKQDGSTIHIRYREPRMLAMPIDLDTL
SPEERRARLRKREAQLQSRKEYEQELSDDLHVERYRQFWTRTKK
```

Important features of the protein:**Signal peptide:**

Amino acids 1-18

N-glycosylation site:

Amino acids 20-24

N-myristoylation sites:

Amino acids 5-11;9-15;17-23;18-24

574/615

FIGURE 569

GGTGCCAAAGGGTTTCGGGGGGGAGCACTGAGGCTTTAGCAGCTCTCCTGTATCCTCATTTGTCAT
CCTCCTGTAGCAGCTGGAAAATTCAGATTACAGGTGAAATTCCTGGCTGGCAATCTTCTGTAT
TATGGACACAGTGATGTGCCAGAAGGGCTTTGCATCCCTGAGACTGAAGGAAGCTCCATTTTTT
GGAGCCCTCCCACACCTTGCTCTGTGTGCCTCTCATTCTGATTTGAATTCTTATTTTGCTATA
TGATGAAGCTGTAATCCTAAGTTTAAAAAGGGGAGTAGGTATTGACATCATGGTAGAAATAGG
CTGTCTTATGGAAGTGTAGTTAGGGATCACAGCCTATTGGACCAGCCCCAGCCTTAGCAGCAG
TTCTGTACACTGATTCTTCCAGATTAGTCTACGTTCCCTCGAACAGACCTATGCCATGGGTTA
CAACTACAATTTGTTGTCGATTAGAGTTAACTTACAGACTCTCAAAACCCCATTTCTTTGGGTT
TAGGCAACTTCCAGAAGTAGTCATTTATTTGAATTTTAGTCTAAGATCAACTGAATTAGGGAG
GTTTGAAAGTGTAAGAGCAAATCGTACATTCCAAACACTTTGTAAAGAAGGAATGGGAGTG
TCAACTAAAGGAAATGGTGTGCATCCCAGCAAAGAGAGACCGAAAGCAAAGTCATAAAC
ATGCCACAGCTCAGCTGTCCTGCTCCGTGTCCTCTCCATACCCTTGTTGACTGTGCTCATA
TTAGCCAGAGACCTAAGTGCTCTTGGAGGATGTCCCTGGGGCCCCCTCCCCCTCCGCTGTAC
TGTCTACTTCTGATCCTCTCTTCTGTGCAGGAGAGGTCCAGGCCTTCTATGAGGACCTGAGT
GGCCGGCAGTACGTGAATGAAGTCTTCAACTTCAGCGTGGACAAGCTCTATGACCTCCTCTTC
ACCAACTCGCCCTTCCAGCGGGATTTTCATGGAGCAGCGCGCTTCTCTGATATCATCTTCCAT
CCATGGAAAAAGGAGGAGAATGGAAACCAGAGCCGAGTGATTCTTTACACCATCACCTTACC
AACCCTCTGGCTCCCAAACTGCCACTGTCAGGGAGACACAGACCATGTACAAGGCGAGCCAG
GAGAGTGAATGTTACGTGATAGATGCCGAAGTCTCACCCACGACGTGCCCTACCACGACTAC
TTCTACACAATCAATCGCTACACGCTCACCCGTGTGGCTCGGAACAAGAGCCGACTCAGGGTC
TCCACAGAGCTGCGCTATCGAAAACAGCCCTGGGGGTTAGTGAAAACGTTTCATCGAGAAGAAC
TTCTGGAGTGGGCTGGAGGACTACTTCCGCCATTTAGAGAGCGAGCTGGCCAAAACGGAGAGC
ACTTATTTGGCTGAGATGCACAGACAATCTCCCAAAGAGAAGGCCAGCAAGACTACAACGGTG
CGGAGGAGGAAGCGTCCCCATGCCACCTGCGAGTCCCTCACCTGGAAGAGGTGATGAGCCCG
GTCACCACGCCACAGATGAGGATGTGGGCCACAGGATCAAACATGTGGCAGGTTCCACACAG
ACGCGGCATATCCCGGAGGACACCCCAACGGTTTCCACCTGCAGAGCGTGTCCAAGCTGCTG
CTGGTTATCAGCTGTGTTCTGGTGCTGCTGGTCATCCTTAACATGATGCTCTTCTACAACTC
TGGATGTTGGAATACACCACGCAGACCCCTCACTGCCTGGCAGGGTCTAAGGCTCCAAGAAAGG
TTACCCAGTCTCAGACAGAATGGGCCCAGCTCTTAGAGTCCCAACAAAAGTACCACGATACT
GAGCTCCAAAATGGAGGGAAATCATCAAATCCTCAGTGATGCTCCTTGACCAGATGAAGGAC
TCGCTCATCAACCTTCAGAACGGCATCAGGTCCCGCGACTACACGTCGGAAAGTGAAGAAAAG
AGGAATCGCTATCAT**TGA**CAAGGCAGGAACAGGGTGGCTGCAAGAGGCCTGTGCAATACATGT
ACATAGACCATATAAATATATATATATAAATATATATATATACAGAATATAAATATATATATT
ATATACAGATTTTAAAAAGAGATAATGCCTATGTACCAGGGAGAAGGAGCGGGCCCTCCCGC
GCCCTGTGCTGGCCGGAGCAGCGTTTCTTATGGTGGAGCAGCTGAGGAGGGCAGGAACCGCC
TCTCAGCACCGACCTCCCCTGATCTCCCTCCTCCACCCCTCTGTTCCCCACCCCTTCCCTTGC
TGGCCATTCTTGGCTTTTAGAAGGGAAATGTTGAGCCAAAGTTATGCCTGCGAAGACCCCTAAG
GTCTCAAAAAGAAGTCTTAAGACGGCATTGCTTAAGGTGCTTCATTCCCTAATCCCCTTTTGA
TTTGTTCCTCAAAATAAAAGAGAATCTTTTCTCCCTAAAAAAAAAAAAAAAAAAAAAAAAA

575/615

FIGURE 570

><subunit 1 of 1, 425 aa, 1 stop
><MW: 49786, pI: 8.84, NX(S/T): 3
MPTSSAVLLRLVLSIPLLTVLILARDLSALGGCPWGPLPLRCHCLLPDPLFCAGEVQAFYE
DLSGRQYVNEVFNFSDVKLYDLLFTNSPFQORDFMEQRRFSDIIFHPWKKEENGNSRVIL
YTITLTNPLAPKTATVRETQTMKASQSECEYVIDAEVLTHDVPYHDYFYTTINRYTLTRV
ARNKSRLRVSTELRYRKQPWGLVKTFFIEKNFWSGLEDYFRHLESELAKESTYLAEMHRQ
SPKEKASKTTTIVRRRKRPVPHLEEVMSPTTPTDEDVGHRIKHVAGSTQTRHIPE
DTPNGFHLQSVSKLLLVISCVLVLLVILNMMLFYKLWMLEYTTQTLTAWQGLRLQERLPQ
SQTEWAQLLESQQKYHDTLQKWREIIKSSVMLLDQMKDSLINLQNGIRSRDYSSESEEK
RNRYH

Important features of the protein:**Signal peptide:**

Amino acids 1-28

Transmembrane domain:

Amino acids 312-334

N-glycosylation sites:

Amino acids 73-77;114-118;183-187

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 97-101

Tyrosine kinase phosphorylation sites:

Amino acids 144-153;188-196

N-myristoylation sites:

Amino acids 201-207;291-297

Leucine zipper pattern:

325-347

576/615

FIGURE 571

GTAGAGAGTGAAGCAGCAAGACTGCAGAGCCTCATCAAGAAGTGTGGAGTGAAGGGAAGGCTTCAGATGGACAAT
TTGTGTGCTGGGGAAAAAATGGAATGTGCTGCAAATTCCTGTGGATAAGGGTGGACGGCTGCTCTGTCAACTT
TGACCATTTTTCAGATTCTGCGGGCCATTGGTAAAGGGAGTTTTGGAAAGGTATGCATCGTGCAGAAAGCGAGACAC
TAAGAAAATGTATGCAATGAAGTACATGAACAAGCAGAAAGTGCATCGAGAGGGATGAGGTTCCGGAATGTTTTCCG
GGAGCTGCAGATCATGCAAGGGCTGGAGCACCCCTTCTGGTCAATCTGTGGTACTCCTTCCAGGATGAGGAGGA
CATGTTTCATGGTGGTGGACCTGCTCCTGGGAGGCGACCTGCGCTACCATCTGCAGCAGAATGTGCATTTACAGA
GGGACTGTGAACTCTACATCTGTGAGCTGGCACTGGCCCTGGAGTATCTTCAGAGGTACCACATCATCCACAG
AGACATCAAGCCAGACAATATCCTGTGGATGAACACGGACATGTTTACATTACAGACTTCAACATAGCGACGGT
AGTGAAAGGAGCAGAAAGGGCTTCTCCATGGCTGGCACCAGCCCTACATGGCTCCAGAAGTATTCAGGTTGTA
CATGGACAGAGGCCCCGGATACTCGTACCTGTGCACTGGTGGTCCCTGGGCATCACAGCCTATGAGCTGCTGCG
GGGCTGGAGGCGGTACGAAATCCACTCGGTACGCCCACATCGATGAAATCCTTAACATGTTCAAGTGGAGCGTGT
CCACTACTCCTCCACGTGGTGCAAGGGATGTTGGCCCTGCTGAGGAAGCTCCTGACCAAGGATCCTGAGAGCCG
CGTGTCCAGCCTTCATGACATACAGAGCGTGCCCTACTTGGCCGACATGAACTGGGACGCGGTGTTCAAGAAGGC
ACTGATGCCCCGCTTGTGCCCAATAAAGGGAGGTTGAACTGCGATCCCACATTTGAGCTTGAAGAGATGATTCT
AGAATCCAAGCCACTTCACAAAAGAAGAAGCGATTGGCAAAGAACAGATCCAGGGATGGCACAAGGACAGCTG
CCCGCTGAATGGACACTGCAGCACTGTTTGGAGACTGTCCGGAGGAATTCATCATATTCAACAGAGAGAAGCT
CAGGAGGCAGCAGGGACAGGGCAGCTCTTGGACACCCAGCCGAGGGGGAGGCCAGGCCCAAAGCAAGCT
CCAGGACGGGTGCAACAACAACCTCCTCACCCACACCTGCACCCGTGGCTGCAGCAGCTGAGCCCCACACTTGTTG
CTGCTCAACAGGACTGCACTCGTCTCTGCCCTGCCACCAGAGCCCCCTCTTGTGCCCTGATGGTCCCTGTCTC
ACCCCTGAAAACATCAGATGCAGAAAAGCCCTGGACTTGGAGCTGGGAAGCCTGGGTTCTGGTCCCATCTCCAT
GACTGATTACGTGTGACCTCAGACAAGTCACGCCCTCTCTGTGCCTCCGTTTTCTGCATCTGCCAAAGGGGTTA
AACACTTCTGCCCCACTTCAAATTACAAGATTATGGGGAGAACCCAATTAGGTAGGAAACATGAAAACCTTTGA
TATTTATAAAATCATTTTTACGTGCAAAATATAACCTTAATATTTGAAGTGACCCCCATTCCCCAAAGCAATCAA
ACCGTCATGACTTTTGAATTTGGCACATCCTAGCTTGTAGAGGGCACTTCCGAAAACACAGCCCTGACAGCAA
AATAAAGGTCTGATATGTTGGCCCCCTTCATGGAAACAACGCTGCCAAATCCTGGAGCAAAACCTGAAGTGTCTT
CATGTGCATTCTCTGGCAGGCCACAGTCCTTCTGAGCTTGTAAAGATGGTGCAGCATGCAGACCAGACTTGTCCCC
AAGGTCTCAGCGCTGCGGTCTCACTCCTCCCCCTCATTTAAGAAGACTATCCTTACCTTTTAGTTTTCAGCAGTCCT
CACCACCACCATATCCCCAGTGCTGGGATGGCACACAGGTGTCCATTGAGATGAGAGTTGGGTGCTGAGCATTG
GTTACTCCTGCAGAGTGTAATCAGCACCCCATCCAAGTGGCCCCGAAAGCCAGACCTGCAGCAGAACTCTCCAAC
TCTCTATCAGCTTTCAGGGTTTTCTCTCCTGGGAAGGGTGTAATAACAGCTTGTGATGATTCTTCTTACAGAGAGT
ATCCAATCGGTATTGGTGGAGCGGCTCCCTATTTATACAATAGGAAGCATGGGTGCTTAGAAAGTTTATTTTCAGG
AGGAAAATGGGTTACACACAAAAGCAAATACATTCTGATCTGCTCAGGGAGAAGCTTGCCCTTTGAACTGGAAGA
TGTTGGGATGAGCAGGGAAAGCTTAGACTTTGGAGTCAGGTTTGTGTTTCAAGATCCAGCCCTGCTGGCTACTAAC
TAACCTGGGAGACCTTAGGCAAAGCATGCAATCGCTCTGAATGGCAGTTTCCCTCATTTTTAAACAGGGATAATAAA
ACTAATATTGCAGGGGAGTTACAGGGTTAAATAAGATCCTGTGTGTAACCCCAAGCATTGGATGACTCATAGAAT
GGCCTTTTTTGTGAGCATAATCGTCATCATTTATTTAGATACTTTCTTCTTCACTCACCCAGCAGGTGAGTTTTT
TGTGCAAAACAACCTGTTTAGGATTCTTCCAATGTTCTTCTGGGGTCTTTGATATTTGTTTGTACATCCTGC
TGAAGTTCGACTGTGTTTTATTTTTTATCCAACTTCCATTTTTTCACTTTTTTACATGATTACTCAATCCTTGGG
GCTGTCCATGTCTCTTAGATTTCTTAAAAGACATTTTAAATGTATGGTTAGGTTTTATATTTTTATTTTTTAA
AAAAGAAATAGTCAGTGTTTTCTCCTTTCAACCGAGACTATTTCTGGATTGTGTGCTCCTCGTCAGTTGACTTGT
TTTGACACTTTTTCTTACTTCATGTCCCATCAACAACCGTCCTGCTCCCCACCTCCCCAGGAAATAAGGGGC
CTGCTCCTCTCCCTACTGTGACCTGGAGGCTCTTAAGATGATGATGGTTTTTTTATTGGGCTGAGTTTACGAA
TTAGGGGCAGGAGCTGGAAGTCGCCCTAGGAACACCAGATTTCTGGTTCTGTTCAAGTTGGCATTTCTGTTTG
GAATAAACTATTTCTTGG

577/615

FIGURE 572

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA136110
<subunit 1 of 1, 364 aa, 1 stop
<MW: 42195, pI: 7.40, NX(S/T): 1
MKYMNKQKCIERDEVNRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGDLRY
HLQQNVHFTEGTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNIATV
VKGAERASSMAGTKPYMAPEVFQVYMDRGPVSYVVDWWSLGITAYELLRGWRPYEIHVS
TPIDEILNMFKVERVHYSSWCKGMVALLRKLLTKDPESRVSSLHDIQSVPYLADMNWD
VFKKALMPGFVPNKGRLNCDPTFELEEMILESKPLHKKKKRLAKNRSRDGTDKSCPLNGH
LQHCLETVREEFIIFNREKLRRQQGQGSQQLDTSRGGGQAQSKLQDGCNNNLLTHTCTR
GCSS

Important features of the protein:**N-glycosylation site:**

Amino acids 285-289

N-myristoylation sites:

Amino acids 123-129;290-296;337-343;339-345;348-354

Serine/Threonine protein kinases active-site signature:

Amino acids 92-105

FIGURE 573

[illegible]

579/615

FIGURE 574

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA139592
><subunit 1 of 1, 882 aa, 1 stop
><MW: 98428, pI: 8.89, NX(S/T): 5
MKHVTVGRNMRGCVSRSCSRQRRPQHHLPSAGPASACAAA VAVSVPATVPPKQLPLHG
QVNICGCPLLFFLLFQLLLLLPLPSRSRKPPTQLTLAQLQTVSSAQLYLAPRAPLRHWH
RRVFYFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCALVPLLGSVPPHPPAPSPCCSG
QTMLKMLSFKLLLLAVALGFFEGDAKFGERNEGSGARRRRCLNGNPPKRLKRRDRRMSQ
LELLSGGEMLCGGFYPRLSCLLSDSPGLGRLENKIFSVTNNTTECGKLLLEEIKCALCSPH
SQSLFHSPEREVLERDLVLP LLCKDYCKEFFYTCRGHIPGFLQTTADEFCFYARKDGGL
CFPDFPRKQVRGPASNYLDQMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDG
SQRLFILEKEGYVKILTPEGEIFKEPYLDIHKLVSQGIKGGDERGLLSLAFHPNYKKNGK
LYVSYTTNQERWAIGPHDHILRVVEYTVSRKNPHQVDLRTARVFLEVAELHRKHLGGQLL
FGPDGFLYIILGDGMITLDDMEEMDGLSDFTGSVLRLDVD TDMCNVPYSIPRSNPHFNST
NQPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRSSARILQIIKGKDYSEEP
SLLEFKPFSNGPLVGGFVYRGCQSERLYGSYVFGDRNGNFLT LQQSPVTKQWQEKPLCLG
TSGSCRGYFSGHILGFGEDELGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEECRATV
QPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFC RTAKCEPACRHGGVCVRPNKCLCK
KGYLG PQCEQVDRNIRRVTRAGILDQIIDMTSYLLDLTSYIV
```

Important features of the protein:**Transmembrane domains:**

Amino acids 63-80;186-201

N-glycosylation sites:

Amino acids 152-156;281-285;598-602;629-633;641-645

Glycosaminoglycan attachment site:

Amino acids 417-421

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 856-860

N-myristoylation sites:

Amino acids 12-18;413-419;457-463;698-695;720-726;723-729

EGF-like domain cysteine pattern signatures:

Amino acids 805-817;837-849

580/615

FIGURE 575

CGGCTCGAGAGCGGGGCAAACCTGCTTGGCACCTCTTCAATAGGTGACATTCAATGATAGATCT
CTGGCTTCCTGCTCTGTTTGTCTGGTTGCCCTGGAAAGCCTGCTGCTCAGCCCATGCCCCGG
GACTTCCTCCACCCTCACCAGGACATTCTTTCCATCTCTTGTCTCCTGTGTGCAAGTCCCTTT
CTCCTGGATTCCATGTCTTGAATGTTTCTTAATTTACTTCCTCATTTTGGCAGAGGATGTCCT
CCAGTTGTTTTCTGGGAATGCTAATATGCAAGTGAACCAGTGACCTGCAGTTCTGCCCACACA
GGGTAAATAACCAATCAGATTCTCTCTTTTCAAGATGGTTAACATAACAGACACCAAGAAAGG
GAAGAGGAGCCGACAGCAGAGGGGGAAGCTGAAAAGACGCACAAAGAATGGCCATAAAAGATA
TGAGCAACCCCAGCTTTCCAGACAGTCACTTTTCCCAGTGGTCATACCTGGTCTGGAAGATTCT
CCCATCATCTCGAATAAAGCTGTTGTTGCTTTTAACTCCATGGAGAGACCGAATGGAGTGAGC
CCAGCAGGGCATGCTGGGCAAGAGAGGTCCCCGAGTCCCAAATAAGAATTTCAACTAGTATA
AAACGAGGCAGCGAACCACACGTGGAAGTCTGATACCGCTTGCAAGGGGAATTGAATAGAT
GTCTCCCTATTGGTAAGGATGTGGTTTTATTGACTTGAAATAACAAAGCCCCGCAAGCAACAAC
TGATCATCCGCGGGATGCTGCCACAAGGAATAATTGAGCACTCATTGAGACACAGGGGAAACC
ACTGCCTCTTTCAGTCTTCTCCCAGATTCCAACAGTCAGTGTTACAGCATTTACCTTGTTT
ACCTCCCTGAGAAGACGTTGCAGCTCACTACCCAGTGGGCACTGGGAGCCTCTGCTCAGGT
GGGAGACAGATGCCCCCACATGCACATCTGGTGTATGAAGCAGATACTGGGGCTTCATAA
ACACAGAAGGGGAGGGAAGTAGCCCCAGGGCAGTGTGGGGCCTCCTGACTAAAAGTAGCTT
GCAAACCCCTGCCTATAACAGCCACTTCTGGCAGTCATTGTGCCACTTAGGAGCCCTCCTCA
CCGCTCTTCTTTAGTTCCTTCACTCTGTATAGACCCTGCCAGAGCAGCTCAGGGTGGAGCAG
CTGCAGCCATGGGACCTGCTCCAGGCAAGGCCCTATGCTACACAGTCCCTGGGGGTGAGGATT
CCAGAGGAGTCAATTCCCTACCCGCCCTTCCAGGGGATGGCCGAGATGAGCGTTCCACAGGG
AAAGTGAAAAGTTGCAAGGCTGTTGCGGAAACACCAGGGGTTCATTTAGGTCTTGCTGCTCAT
CTCACAGAAAGCCAGTCACTGAGACAAGTATTGTGAGGGAAGAAGGCTTTATCCAGGTGCTAC
AGACAGGGTGAACAAGAGATCAGTCTCAAATCCATCATCATCAACTGACTAAAATTAGGGGTT
TATATAGCAGGGAAGAAATGTAACATGTGGGAAAACAGGGATTAACGAGGGGCAAGGAAG
AGGAGTTGGCCAACAGGCAGCAGGTGGTCACCTGGGGAATCATGATGGGTGAGGGGTCTGGCT
TCTCACTTTCAGATGTGGGGATCTGGTAAATTTTCACTTCTTGATACCGTCTGGGAGGATTG
CTGGCTGGTTTCTGAGAAAGGAATTCAGATGACATAAATGTAAATTTCTCCTTGGGTTTCAA
GACTGAGAGGGTCAATTTCTAGGTTTATTCAAGAAAACCATAAACATCAGTTCTATGGGACA
ATTGGGCCCATTTCAGGCTCTGAGGATAAGGGTTAATGAGGGGACAGAGTCGCCTGGAGAAG
TTCAGTGGGGCCTACAAGAACTAGAGAGGCTTCTGGCAAAGCTCTATGCTGTCTATCCTCT
CTTCTCTCCTTGCAGGAAGATTCCAGTATAATAGACCCGAGGTGAAAAGGCTTTTGTTCAATA
AGTAGAAAACCTGAAGGGGGTGGGAGGCACATGGATTTGAACCAGAGACCGCTTGGCCCTGCAG
GCAAATGCTGTACCTTCAGTTGCACCCCTCACTTGTTACAGCTGTTTCTGATAAGCACTTGTG
CAGCCCCATCAGCACCTCGATTTCTTCTTGGTGAAGTCCATGGGAACAGCCCCACTGCAAACAA
CCCATTCCTGCTCTCCTCTTCTCTAAACCTCAACCTCCTCCTACCTGGCAGTCCACAGGCC
TACAGCTTCTCCTCAGTGGGAAAGACATCAGCTTGGAAAACCACTTGGAAAGCCAACGTTATC
CTAGAAAAGCTTTTTTAAATGACCCAGCAGGACAAGTCTCCGGATGGCCTTGGCCAACCCGGTG
CTTCCCTCTTTTCTTGGTTGTAGTTCTCAGAATAACTAGAGAATGTACTGGGAGTGTGTCTCT
GAGATAAGGAGGAAGTGTCTAAACCTGGACTCTGTTCCCATCACACCTAGAACAGGATGTCC
TGCAACGCTTTAGCCCAATGATCCAAGTTGCCCTTGGGGTATAAACTTGACAGCAGAGGGCG
TTCAGGGTCCCTCAGCTGCAGTGTGAAGTGGGACACACAGGTGAGACTCCATCTGCCCTGGGC
AGGTTCTGAGCCTTGGGGGACCAGTTCACCTTACATCCCAGGCTTCTGTTGTCCCTTGCCTG
CCTGTAAGGAATAAAGTTGCTTTGCTTA

581/615

FIGURE 576

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA139608
><subunit 1 of 1, 80 aa, 1 stop
><MW: 8927, pI: 3.77, NX(S/T): 0
MIDLWLPALFVLVALESLLLSPCPGTSSTLTRTFFPSLVSCVQVPFSWIPCLECFLIYFL
ILAEDVLQLFSGNANMQVNQ
```

Important features of the protein:**Signal peptide:**

Amino acids 1-29

Transmembrane domain:

Amino acids 47-62

N-myristoylation sites:

Amino acids 25-31

582/615

FIGURE 577

ATCGGTTAGCGCCTTGCCATGATTAATCCAGAGCTGCGGGATGGCAGAGCTGATGGCTTCATA
CATCGGATAGTTCCCAAGTTGATACAAAACCTGGAAGATTGGCCTTATGTGCTTCCTGAGTATT
ATTATTACTACAGTTTGCATTATTATGATAGCCACATGGTCCAAGCATGCTAAACCTGTGGCA
TGTTTCAGGGGACTGGCTTGGAGTGAGAGATAAGTGTTTCTATTTTCTGATGATACCAGAAAT
TGGACAGCCAGTAAATATTTTGTAGTTTGCAGAAAGCAGAACTTGCTCAGATTGATACACAA
GAAGACATGGAATTTTGAAGAGGTACGCAGGAACCTGATATGCACTGGATTGGACTAAGCAGG
AAACAAGGAGATTCTTGGAAATGGACAAATGGCACCACATTCAATGGTTGGCCATCAAACCTCC
AAATGGTCTTGCAACTGGAGCCTCCGACAATGGCTTCTTCTGCTGGGACCCCTTAGATAGGCC
TCTGAGGGAGCTCTGACTGCCGTTTCCCCAAAACAATGTCCCCTGTCAGCAGGAAGCAGTTAA
ATCAGTCTTCATCCTTATCCTTAATATAACGGCAGTTAGATGTACTTCTTTAGAGGGAGTAAA
TTTATCAATTCAGAGCAATTCATCCTCCTCTTTCATCTTTGATTACAGTTAATAGGCTATA
AATTTTGATAATGTAGAATAAACTACAGAAAACCTTCTTG

583/615

FIGURE 578

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA143292
><subunit 1 of 1, 160 aa, 1 stop
><MW: 18576, pI: 9.29, NX(S/T): 3
MINPELRDGRADGFIHRIVPKLIQNWKIGLMCFLSIIITTVCIIIMIATWSKHAKPVACSG
DWLGVRDKCFYFSDTRNWTASKIFCSLQKAELAQIDTQEDMEFLKRYAGTDMHWIGLSR
KQGDSWKWTNGTTFNGWPSNSKWSCNWSLRQWLLLLGPLR

Important features of the protein:**Signal peptide:**

Amino acids 1-42

N-glycosylation sites:

Amino acids 78-82;130-134;146-150

N-myristoylation site:

Amino acids 131-137

584/615

FIGURE 579

TGAAGGCCTGTGAGTGAGGAATGCCTCTCACCAGCTGTGCCTGAGCTGCAGCACTCCAGCCAC
TGCTGTCTCCTTAGCTGCTCACATATGGATACTTTCACAGTTCAGGATTCCACTGCAATGAGC
TGGTGGAGGAATAATTTCTGGATCATCTTAGCTGTGGCCATCATTGTTGTCTCTGTGGGCCTG
GGCCTCATCCTGTACTGTGTCTGTAAGTGGCAGCTTAGACGAGGCAAGAAATGGGAAATTGCC
AAGCCCCTGAAACACAAGCAAGTAGATGAAGAAAAGATGTATGAGAATGTTCTTAATGAGTCG
CCAGTTCAATTACCGCCTCTGCCACCGAGGAATTGGCCTTCTCTAGAAGACTCTTCCCCACAG
GAAGCCCCAAGTCAGCCGCCCGCTACATACTCACTGGTAAATAAAGTTAAAAATAAGAAGACT
GTTTCCATCCCAAGCTACATTGAGCCTGAAGATGACTATGACGATGTTGAAATCCCTGCAAAT
ACTGAAAAAGCATCATTTTGAAGAACAGCCATTTCTTCTTTTTTGGCAAAACTGAAGAGGGTTCAC
ACAACTTATTTTAAAAACAATCAAGAATGGTTGAACTTCAGTAGGTCTCTGGGCCCTGAAAGCC
AGTGGTGATTTTATGAAGCTCTATAAGATAAAGCACTTCCCAAACCTTAGATGAAGACACCCC
TGCGATCGGATGACTGCAGCCAGAGGAGACACATGGGTGCTCGGCTCTGAGGACTTAGAGGGG
TCAGCCTTGTGCTGTTGAGGAACTTTCCATGGGAAGGACCACGGGGCTCCATGGCTCCCACC
TGTGGGAACTACTCATTTCTTGGCATTCCTTCCCCCTTCATTCCCTTTGGTTTGCATGGTTC
TGAGTGATATTAAATCTCAGCATTTGGTTGTGCAAAAAA

585/615

FIGURE 580

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA144844
><subunit 1 of 1, 145 aa, 1 stop
><MW: 16618, pI: 5.26, NX(S/T): 1
MDTFTVQDSTAMSWWRNFWIILAVAIIVSVGLGLILYCVCKWQLRRGKKWEIAKPLKH
KQVDEEKMYENVLNESPVQLPPLPPRNWPSLEDSSPQEAPSQPPATYSLVNKVKNKKTVS
IPSYIEPEDDYDDVEIPANTEKASF
```

Important features of the protein:**Signal peptide:**

Amino acids 1-35

Tyrosine kinase phosphorylation site:

Amino acids 61-70

Amidation site:

Amino acids 48-52

586/615

FIGURE 581

GGCCGCCTCCGCGGGGCTGTGGGAAGCTTGGGCTGTCCCAGGACCGTCAGTCTCCTCCTCTGA
CCCTCCCTTTCCCTTGTGTGTAGGGCCGCCGTCCCACCCACCTCGCCGGAGTCCGGGGCG
GCCCCGGTGTCCCTCCGAGCCTGCTGCACTCCACGTCCCCCTACCAGGGCTCCAGCCCCAG
GGAAATCTCCGACCAGGCCCGCCAGGAGCCAGATCCAGGCTCCTGGAAGAACCATGTCCGGC
AGCTACTGGTCATGCCAGGCACACACTGCTGCCCAAGAGGAGCTGCTGTTTGAATTATCTGTG
AATGTTGGGAAGAGGAATGCCAGAGCTGCCGGCTGAAAATTACCCAACCAAGAGAAATCTGCAGG
ATGGACTTTCTGGTCCTCTTCTTGTCTACCTGGCTTCGGTGCTGATGGGTCTTGTCTTATC
TGCGTCTGCTCGAAAACCCATAGCTTGAAAGGCCTGGCCAGGGGAGGAGCACAGATATTTTCC
TGTATAATTCCAGAATGTCTTCAGAGAGCCGTGCATGGATTGCTTCATTACCTTTTCCATACG
AGAAACCACACCTTCATTGTCCTGCACCTGGTCTTGCAAGGGATGGTTTATACTGAGTACACC
TGGGAAGTATTTGGCTACTGTCAGGAGCTGGAGTTGTCCTTGCATTACCTTCTTCTGCCCTAT
CTGCTGCTAGGTGTAAACCTGTTTTTTTTTACCCTGACTTGTGGAACCAATCCTGGCATTATA
ACAAAAGCAAATGAATTATTATTTCTTCATGTTTATGAATTTGATGAAGTGATGTTTCCAAAG
AACGTGAGGTGCTCTACTTGTGATTTAAGGAAACCAGCTCGATCCAAGCACTGCAGTGTGTGT
AACTGGTGTGTGCACCGTTTCGACCATCACTGTGTTGGGTGAACAACCTGCATCGGGGCCTGG
AACATCAGGTACTTCCTCATCTACGTCTTGACCTTGACGGCCTCGGCTGCCACCGTCGCCATT
GTGAGCACCACTTTTCTGGTCCACTTGGTGGTGATGTCAGATTTATACCAGGAGACTTACATC
GATGACCTTGGACACCTCCATGTTATGGACACGGTCTTTCTTATTTCAGTACCTGTTCTGACT
TTTCCACGGATTGTCTTCATGCTGGGCTTTGTCTGTTCTGAGCTTCCTCCTGGGTGGCTAC
CTGTTGTTTGTCTGTATCTGGCGGCCACCAACCAGACTACTAACGAGTGGTACAGAGGTGAC
TGGGCCTGGTGCCAGCGTTGTCCCTTGTGGCCTGGCCTCCGTCAGCAGAGCCCCAAGTCCAC
CGGAACATTCACCTCCCATGGGCTTCGGAGCAACCTTCAAGAGATCTTTCTACCTGCCTTTCCA
TGTCATGAGAGGAAGAAACAAGAA**TGA**CAAGTGTATGACTGCCTTTG

587/615

FIGURE 582

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA144857
><subunit 1 of 1, 344 aa, 1 stop
><MW: 39787, pI: 7.44, NX(S/T): 2
MDFLVLFLEYLASVLMGLVLICVCSKTHSLKGLARGGAQIFSCIPECLQRAVHGLLHYL
FHTRNHTFIVLHLVLQGMVYTEYTWEVFGYCQELELSLHYLLLPLYLLLGVNLFFFTITCG
TNPGIITKANELLFLHVEYEFDEVMFPKNVRCSTCDLRKPARSKHCSVCNWCVHRFDHHCV
WVNNCIGAWNIRYFLIYVLTLTASAATVAIVSTTFLVHLVVMSDLYQETYIDDLGHLHVM
DTVFLIQYLFLLTFPRIVFMLGFVVVLSFLLGGYLLFVLYLAATNQTTNEWYRGDWAWCQR
CPLVAWPPSAEPQVHRNIHSHGLRSNLQEIFLPAFPCHERKKQE
```

Important features of the protein:**Signal peptide:**

Amino acids 1-29

Transmembrane domains:

Amino acids 100-116;201-217;256-275

N-glycosylation sites:

Amino acids 65-69;284-290

N-myristoylation sites:

Amino acids 32-38;77-83;120-126;322-328

Cell attachment sequence:

Amino acids 292-298

DHHC zinc finger domain:

Amino acids 140-204

588/615

FIGURE 583

CCGCGGAAGTGGCAGGCGTTTCAGAGCGTTCAGAGGCTGCGGATGAGCAGACTTGGAGGACTCCAGGCCAGAGACT
AGGCTGGGCGAAGAGTTCGAGCGTGAAGGGGCTCCGGGCCAGGGTGACAGGAGGCGTGCTTGAGAGGAAGAAGTT
GACGGGAAGGCCAGTGCACGGCAAATCTCGTGAACCTTGGGGGACGAATGCTCAGGATGCGGGTCCCCGCCCTC
CTCGTCTCTCTCTCTGCTTCAGAGGGAGAGCAGGCCCCGTGCCCCATTTCTGCAACAGCCAGAGGACCTGGTG
GTGCTGCTGGGGGAGGAAGCCCGGCTGCCGTGTGCTCTGGGCGCCTACTGGGGGCTAGTTCACTGGAGTAAGAGTGGG
CTGGCCCTAGGGGGCCAAAGGGACCTACCAGGGTGGTCCCGGTACTGGATATCAGGGAATGCAGCCAATGGCCAG
CATGACCTCCACATTAGGCCCCGTGGAGCTAGAGGATGAAGCATCATATGAATGTCAGGCTACACAAGCAGGCCCTC
CGCTCCAGACCAGCCCAACTGCACGTGCTGGTCCCCCAGAAGCCCCCAGGTGCTGGGCGGCCCTCTGTGTCT
CTGTTGCTGGAGTTCTGCGAACCTGCATGTGCGAGCGTGGGGATGCCGCCCTACCCCTGAATTGCTGTGG
TTCCGAGATGGGGTCTGTTGGATGGAGCCACCTTTTCATCAGACCCTGCTGAAGGAAGGGACCCCTGGGTCACTG
GAGAGCACCTTAACCTGACCCCTTTTCAGCCATGATGATGGAGCCACCTTTGTCTGCCGGGCCGGAGCCAGGCC
CTGCCCCACAGGAAGAGACACAGCTATCACACTGAGCCTGCAGTACCCCCCAGAGGTGACTCTGTCTGCTTCGCCA
CACACTGTGCAGGAGGGAGAGAAGGTCATTTTCTGTGCCAGGCCACAGCCAGCCTCCTGTACAGGCTACAGG
TGGGCAAAGGGGGCTTCCGGTGTCTGGGGCCCCGGGGCCAAAGGTTAGAGGTCGTGGCAGACGCTCGTTCTCTG
ACTGAGCCCGTGTCTGCGAGGTTCAGCAACGCCGTGGGTAGCGCCAACCGCAGTACTGCGCTGGATGTGCTGTTT
GGGCGGATTCTGCAGGCAAAGCCGGAGCCCGTGTCCGTGGACGTGGGGGAAGACGCTTCTTCAGTGCAGCCTGG
CGCGGGAACCCGCTTCCACGGGTAACCTGGACCCCGCCGCGGTGGCGCGCAGGTGCTGGGCTCTGGAGCCACACTG
CGTCTTCCGTCCGTGGGGCCCCGAGGACGCGAGGCGACTATGTGTGCAGAGCTGAGGCTGGGCTATCGGGCCTGCGG
GGCGGCGCGCGGAGGCTCGGCTGACTGTGAACGCTCCCCAGTAGTGACCGCCCTGCACTCTGCGCCTGCCTTC
CTGAGGGGCCCTGCTCGCTCCAGTGTCTGGTTTTCGCCTCTCCCGCCCCAGATGCCGTGGTCTGGTCTTGGGAT
GAGGGCTTCTTGAGGCGGGGTGCGAGGGCCGGTTCTGTTGGAGACATTCCTGCCCCAGAGAGCCGCGGGGGA
CTGGGTCCGGGCTGATCTCTGTGCTACACATTTCCGGGACCCAGGAGTCTGACTTTAGCAGGAGCTTTAACTGC
AGTGCCCGGAACCGCTGGGCGAGGGAGGTGCCAGGCCAGCCTGGGCGTAGAGACTTGCTGCCCACTGTGCGG
ATAGTGGCCGAGTGGCCGCTGCCACCACAACCTCTCCTTATGGTCATCACTGGGGTGGCCCTCTGCTGCTGGCGC
CACAGCAAGGCCTCAGCCTCTTTCTCCGAGCAAAAGAACCTGATGCGAATCCCTGGCAGCAGCGACGGCTCCAGT
TCAGGAGGTCTGAAGAAGAGGAGACAGGCAGCCGCGAGGACCGGGGCCCATTTGTGCACACTGACCACAGTGAT
CTGTTCTGGAGGAGGAAGGGACTCTGGAGACCAAGGACCCCAACCAACGTTACTACAAGGTCCGAGGAGTCAGT
GTGAGCCTGAGCCTTGCGGAAGCCCTGGAGGAGGTCTCTTCTGCCACCACCCTCCCCCTTGGGCCCCAGGG
ACCCCTACCTTCTATGACTTCAACCCACACCTGGGCATGGTCCCCCCTGCAGACTTTACAGAGCCAGGGCAGGC
TATCTCACCACACCCACCCCTCGAGCTTTCACCAGCTACATCAAACCCACATCCTTTGGGCCCCCAGATCTGGCC
CCCGGGACTCCCCCTTCCCATATGCTGCCCTTCCCCACACCTAGCCACCCGCTCTCCAGACTCAGGTGTGACAT
CTTTCCAATGGAAGAGTCTTGGGATCTCCAACCTTGCCATAATGGATTGTTCTGATTTCTGAGGAGCCAGGACAAG
TTGGCGACCTTACTCTCCAAAACCTGAACACAAGGGGAGGGAAAGATCATTACATTTGTGAGGAGCATTGTATA
CAGTCAGCTCAGCCAAAGGAGATGCCCAAGTGGGAGCAACATGGCCACCCAATATGCCACCTATTTCCCGGTG
TAAAGAGATTCAAGATGGCAGGTAGGCCCTTTGAGGAGAGATGGGGACAGGGCAGTGGGTGTTGGGAGTTTGGG
GCCGGGATGGAAGTTGTTTCTAGCCACTGAAAGAAGATATTTCAAGATGACCATCTGCATTGAGAGGAAAGGTAG
CATAGGATAGATGAAGATGAAGAGCATACCAGGCCCCACCCTGGCTCTCCCTGAGGGGAACCTTGTCTCGGCCAAT
GGAAATGCAGCCAAGATGGCCATATACTCCCTAGGAACCCAAATGGCCACCATCTTGATTTTACTTTTCTTAA
GACTCAGAAAGACTTGGACCCAAGGAGTGGGGATACAGTGAGAATTACCACTGTGGGGCAAATATTGGGATAA
AAATATTTATGTTTAATAATAAAAAAAGTCAAAGAGAAAAAAA

589/615

FIGURE 584

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA145841
><subunit 1 of 1, 708 aa, 1 stop
><MW: 75093, pI: 6.65, NX(S/T): 3
MLRMRVPALLVLLFCFRGRAGPSPHFLQQPEDLVVLLGGEARLPCALGAYWGLVQWTKSG
LALGGQRDLPGWSRYWISGNAANGQHDHIRPVELEDEASYECQATQAGLRSPAQHLHVL
VPPEAPQVLGGPSVSLVAGVPANLTCRSRGDARPTPELLWFRDGVLLDGATFHQTLLKEG
TPGSVESTLTLPFSSHDDGATFVCRARSQALPTGRDTAITLSLQYPPEVTLSPHTVQE
GEKVIFLCQATAQPPVTGYRWAKGGSPVLGARGPRLEVVDASFLTEPVSCEVSNVAGSA
NRSTALDVLFGPILQAKPEPVSVVDVGEDASFSCAWRGNPLPRVTWTRRGAQVLGSGATL
RLPSVGPEDAGDYVCRAEAGLSGLRGGAEEARLTVNAPPVVVTALHSAPAFLRGPARLQCL
VFASPADAVVWSWDEGFLEAGSQGRFLVETFPAPESRGGLGPGGLISVLHISGTQESDFS
RSFNCSARNRLGEGGAQASLGRRDLLPTVRIVAGVAAATTTLLMVITGVALCCWRHASKA
ASFSEQKNLMRIPGSSDGSRRGPEEEETGSREDRGPVHTDHSIDLVEEEGTLETKOPT
NGYYKVRGVSVSLSLGEAPGGGLFLPPPSPLGPPGTPTFYDFNPHLGMVPPCRLYRARG
YLTTPHPRAFTSYIKPSTFGPPDLAPGTPFFPYAAFTPSHPRLQTHV
```

Important features of the protein:**Signal peptide:**

Amino acids 1-20

Transmembrane domain:

Amino acids 511-531

N-glycosylation sites:

Amino acids 143-147;301-305;484-488

N-myristoylation sites:

Amino acids 48-54;60-66;79-85;139-145;180-186;183-189;355-361;383-389;
387-393;460-466;473-479;494-500;495-501;514-520;528-534;
554-560;592-598;608-614

Amidation site:

Amino acids 500-504

Cell attachment sequence:

Amino acids 149-152

Multicopper oxidases signature 1:

Amino acids 445-466

Immunoglobulin domain:

Amino acids 326-377

590/615

FIGURE 585

GCCCGCCTGAGGAAGCCGTGTGCCTGGGATGCCAAGAGCCAGAGAATGGATCTTCTCCGAGTG
GGGACATTGCTGACAATCCCGGCTTCCCGAGGCGGCTAAGAACAGGCAGTTTGTGTGCGGCTGG
CTGCAGATACCCAGAGGCACAAAGAGACCGAAGCCACCCGGAGGGACCCACGGACGGACAGAT
GGTAGGCGCGAACC CGAGAGGACCGGCGGAGGCTGAGCACCGAGAGCCGCCAAGGAAGAGAAA
CTAACCACAGCCAAGTTACCCCGCCGGCTTTCCTTCGCTGCGCTAAGGAATGAACCCCTTCCA
GCTCGATCTGCTCTTCGTCTGCTTCTTCTCTTCAGTCAAGAGCTGGGCCTCCAGAAGAGAGG
ATGCTGTCTGGTGTGCTGGGCTACATGGCCAAGGACAAGTTTCGGAGAATGAATGAAGGCCAAGT
CTATTCTTCAGCCAGCAGCCCCAGGACCAGGTGGTGGTGTGCGGACAGCCAGTGACGCTACT
TTGCGCCATCCCCGAATACGATGGCTTCGTTCGTGGATCAAGGACGGCTTGGCTCTGGGTGT
GGGCAGGGACCTCTCAAGTTACCCACAGTACCTGGTGGTAGGGAACCACTGTGAGGGGAGCA
CCACCTGAAGATCCTGAGGGCAGAGCTGCAAGACGATGCGGTGTACGAGTGCCAGGCCATCCA
GGCCGCCATCCGCTCCCGCCCCGCACGCCTCACAGTCTGGTGGCGCCTGATGACCCCGTCAT
CCTGGGGGGCCCTGTGATCAGCCTGCGTGCGGGGGACCCCTCTCAACCTCACCTGCCACGCAGA
CAATGCCAAGCCTGCAGCCTCCATCATCTGTTGCGAAAGGGAGAGGTCATCAATGGGGCCAC
CTACTCCAAGACCCTGCTTCGGGACGGCAAGCGGGAGAGCATCGTCAGCACCCCTCTTCATCTC
CCCTGGTGACGTGGAGAATGGCCAGAGCATCGTGTGTGCGTACCACCAACAAAGCCATCCCCGG
AGGAAAGGAGACGTCGGTCACCATTTGACATCCAGCACCCCTCCACTGGTCAACCTCTCGGTGGA
GCCACAGCCAGTGCTGGAGGACAACGTCGTCACCTTCCACTGCTCTGCAAAGGCCAACCCAGC
TGTCACCCAGTACAGGTGGGCCAAGCGGGGCCAGATCATCAAGGAGGCATCTGGAGAGGTGTA
CAGGACCACAGTGGACTACACGTACTTCTCAGAGCCCCGTCTCCTGTGAGGTGACCAACGCCCTG
GGCAGCACCAACCTCAGCCGCACGGTTGACGTCTACTTTGGGGCCCCGGATGACCACAGAACCC
CAATCCTTGCTCGTGGATCTGGGCTCTGATGCCATCTTCAGCTGCGCCTGGACCGGCAACCCA
TCCCTGACCATCGTCTGGATGAAGCGGGGCTCCGGAGTGGTCTGAGCAATGAGAAGACCCCTG
ACCCTCAAATCCGTGCGCCAGGAGGACGCGGGCAAGTACGTGTGCCGGGCTGTGGTGGCCCGT
GTGGGAGCCGGGGAGAGAGAGGTGACCCTGACCGTCAATGGACCCCCCATCATCTCCAGCACC
CAGACCCAGCACGCCCTCCACGGCGAGAAGGGCCAGATCAAGTGCTTCATCCGGAGCACGCCG
CCGCCGGACCGCATCGCCTGGTCTTGAAGGAGAACGTTCTGGAGTCGGGCACATCGGGGCGC
TATACGGTGGAGACCATCAGCACCGAGGAGGGCGTCATCTCCACCCTGACCATCAGCAACATC
GTGCGGGCCGACTTCCAGACCATCTACAACCTGCACGGCCTGGAACAGCTTCGGCTCCGACACT
GAGATCATCCGGCTCAAGGAGCAAGGTTTCGGAATGAAGTCGGGAGCCGGGCTGGAAGCAGAG
TCTGTGCCGATGGCCGTCATCATTGGGGTGGCCGTAGGAGCTGGTGTGGCCTTCCTCGTCCTT
ATGGCAACCATCGTGGCGTTCTGCTGTGCCCCGTTCCAGAGAAGTACGGGAGGGAGATCCGGG
ATCTCAGGGAGGGGGACAGAGAAAAAGGCCAGGCTTAGGCTGCCCCGGAGAGCAAGTAAGCAG
GAGTGCAATGAACAGGGGTCCTAACAGTGCTGTGAGCTCCTGGGGCAGGGAGTGGGTCTGATG
CATCGGTGTATGTGAGCCTGGGCAACATGGCGCCTGGCAGAGTGGGCGCTAGGCTGAGGTGA
CCTGGACTAGACTGAACTTCATCTGCAGGGCAGCCAGCATTTTGGATTGAACACATAGCTCTT
TCAGTCAGGAACTGTACAGAAAGATAGGGGGAAAAGCGGTTTGTGGTTTGATCCTTGCTCTAC
AAGAGCTGTAGTCTAGAGAGACCCCATCTCTACAACAAAATAAAAATAAAGAGCTGCTAGTC
TCACCAGAAAAGCAGGTCACACAGCTGTGGGGGAGTGGGTGGGGAAGCAATAAAGGAAT
TGCTTTGAGAAACTTAA

591/615

FIGURE 586

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA148004
><subunit 1 of 1, 600 aa, 1 stop
><MW: 65308, pI: 8.35, NX(S/T): 5
MKPFQLDLLFVCFLLFSQELGLQKRGCCLVLGMAKDKFRRMNEGQVYSFSQQPQDQVVV
SGQPVTLLCAIPEYDGEFVLWIKDGLALGVGRDLSSYPQYLVVGNHLSGEHHLKILRAELQ
DDAVYECQAIQAAIRSRPARLTVLVPPDDPVILGGPVISLRAGDPLNLTCHADNAKPAAS
IIWLKRKEVINGATYSKTLRLDGKRESIVSTLFI SPGDVENGQSIVCRATNKAIPGGKET
SVTIDIQHPPLVNLVSVEPQPVLEDNVVTFHCSAKANPAVTQYRWAKRGQIIKEASGEVYR
TTVDYTYFSEPVSCVETNALGSTNLSRTVDVYFGPRMTTEPQSLLVDLGSDAIFSCAWTG
NPSLTIVWMKRGSGVLSNEKTLTLKSVRQEDAGKYVCRAVVP RVGAGEREVTLT VNGPP
IISSTQTQHALHGEKGQIKCFIRSTPPPDRIASWKENVLESGTSGRYTVETISTEEGVI
STLTISNIVRADFQTIYNCTAWNSFGSDTEIIRLKEQGSEMKSGAGLEAESVPMAVIIGV
AVGAGVAFLVLMATIVAFCCARSQRSTGGRSGISGRGTEKKARLRLPRRASKQECNEQGS
```

Important features of the protein:**Signal peptide:**

Amino acids 1-17

Transmembrane domain:

Amino acids 534-555

N-glycosylation sites:

Amino acids 167-171;253-257;324-328;498-502

Glycosaminoglycan attachment sites:

Amino acids 523-527;574-578

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 204-208;370-374;588-592

Tyrosine kinase phosphorylation sites:

Amino acids 40-49;300-308;389-397

N-myristoylation sites:Amino acids 45-51;62-68;84-90;103-109;192-198;236-242;
374-380;436-442;478-484;539-545;543-549;
568-574**Amidation site:**

Amino acids 202-206

Leucine zipper pattern:

Amino acids 8-30

592/615

FIGURE 587

CAAAAAAGGAGCATGTCTTCATCCATGAGAGGCCCTCGAAAAATCAATGGTATTTGCATTTCTC
CCAAGAAGGTTGCTTGCCAAAACCTTTTCGGCCATTTTCTGCTTTCAGAGTGAGACAAAGTTCA
AAATGACAGTCTGTGCTCAGCTCATTGAAGGCACTAGATAACCTGCCTGCAGGTACCACTATTCCC
CCACAGAGGGGTTTGTCTTGTCACTTGTGATGACTTGAGGCCAGATAGTTTCCTTGGCTATG
TTAAATAACTCAAGATCAGCTACCGAGTCTGAGATCTCTTCTCTCATGGCATTGGAGCTGGCT
GTGCCTGAGGCAGACCTGGACCGTGGACATGGGGCAATGCCTTGAGCGGAAGGGGAAGCCACT
GAATTTTGGGTGTCACCAGGTAAACAGAGCCCTCAGCATCTGAATAGAACTGAACAGGAACA
GAAGAGATTACACTACATCTGAGATGGAGACCTTTTCCTCTGCTGCTGCTCAGCCTGGGCCTGG
TTCTTGCAGAAGCATCAGAAAGCACAAATGAAGATAATTAAAGAAGAATTTACAGACGAAGAGA
TGCAATATGACATGGCAAAAAGTGGCCAAGAAAAACAGACCATTGAGATATTAATGAACCCGA
TCCTGTTAGTTAAAAAATACCAGCCTCAGCATGTCCAAGGATGATATGTCTTCCACATTACTGA
CATTGAGAAAGTTTACATTATAATGACCCCAAGGGAAACAGTTCGGGTAATGACAAAGAGTGTT
GCAATGACATGACAGTCTGGAGAAAAGTTTCAGAAGCAAACGGATCGTGCAAGTGGAGCAATA
ACTTCATCCGCAGCTCCACAGAAGTGATGCGCAGGGTCCACAGGGCCCCCAGCTGCAAGTTTGTA
CAGAAATCCTGGCATAAGCTGCTGTGAGAGCCTAGAACTGGAAAATACAGTGTGCCAGTTCCT
ACAGGCAAACAATTCCCCAGGTGCCAATAACCATAGTGTTACCTCATTAGAGAAGATATTGACA
GTGCTGACAGGTCATTCTCTGATGAGCTGGTTAGTTTGTGGCTCTAAGTTGTAAATCCCACAG
AGCTTTAGGACTAGGGTCTTACTAAAGAAGGACCTCTTCTTGTTTCATTCTTGTTTAAACCTTT
CCTTAATATCTACTCTTTAGCACTATAGTGAACCTCTGATTATTTATTCTAACTGGAGGAGTG
AAAAATCCAAAATTGTGGATAATTCAATTAAAAGTTATGACTGATACCG

593/615

FIGURE 588

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA149893
><subunit 1 of 1, 199 aa, 1 stop
><MW: 22427, pI: 6.46, NX(S/T): 3
METFPLLLLSLGLVLAEESESTMKIIKEEFTDEEMQYDMAKSGQEKQTIEILMNPILLVK
NTSLSMSKDDMSSTLLTFRSLHYNDPKGNSSGNDKECCNDMTVWRKVSEANGSCKWSNNF
IRSSTEVMRRVHRAPSCKFVQNPGISCCESLELENTVCQFTTGKQFPRCQYHSVTSLEKI
LTVLTGHSLMSWLVCCKSL

Important features of the protein:**Signal peptide:**

Amino acids 1-16

N-glycosylation sites:

Amino acids 61-65;89-93;111-115

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 105-109

N-myristoylation sites:

Amino acids 12-18;88-94;144-150

Microbodies C-terminal targeting signal:

Amino acids 197-201

594/615

FIGURE 589

CAGTCCTGCCGGGACGGTGAGCGCATTACAGCACCTGGACAGCACCGCGGTTGCGCTGCCTCC
AGGGCGGGCCCCGGGCTGCTCCTGCTCCGCAGAGCTACGCCCTCCCCCGGGTGCCCCGGACCC
TGCACTTGCCGCGCTTTCTCTCGCGCTGCTCTGGACCTTGCTAGCCGGCTCTGCACCTCCCAG
AAGCCGTGGGCGCGCCGCTCAGCTGCTCCATCGCCTCACTTTCCAGGCTCGCGCCCGAAGCA
GAGCCATGAGAACCCCAGGGTGCTGGCGAGCCGCTAGCGCCATGGGGCCCCGGCGAGGCGCTG
CTGGCGGGTCTCCTGGTGATGGTACTGGCGGTGGCGCTGCTATCCAACGCACTGGTGCTGCTT
TGTTGCGCTACAGCGCTGAGCTCCGCACCTCGAGCCTCAGGCGTCCTCCTGGTGAATCTGTCT
CTGGGCCACCTGCTGCTGGCGGCGCTGGACATGCCCTTCACGCTGCTCGGTGTGATGCGCGGG
CGGACACCGTCGGCGCCCCGGCGCATGCCAAGTCATTGGCTTCCTGGACACCTTCCTGGCGTCC
AACGCGGCGCTGAGCGTGCGGGCGCTGAGCGCAGACCAGTGGCTGGCAGTGGGCTTCCCCTG
CGCTACGCCGGACGCTGCGACCGCGCTATGCCGGCCTGCTGCTGGGCTGTGCCTGGGGACAG
TCGCTGGCCTTCTCAGGCGCTGCACTTGGCTGCTCGTGGCTTGGCTACAGCAGCGCCTTCGCG
TCCTGTTGCTGCGCCTGCCGCCGAGCCTGAGCGTCCGCGCTTCGCAGCCTTCACCGCCACG
CTCCATGCCGTGGGCTTCGTGCTGCCGCTGGCGGTGCTCTGCCTCACCTCGCTCCAGGTGCAC
CGGGTGGCACGCAGACACTGCCAGCGCATGGACACCGTCACCATGAAGGCGCTCGCGCTGCTC
GCCGACCTGCACCCAGTGTGCGGCAGCGCTGCCTCATCCAGCAGAAGCGGCGCCGCCACCGC
GCCACCAGGAAGATTGGCATTGCTATTGCGACCTTCCTCATCTGCTTTGCCCCGTATGTCATG
ACCAGGCTGGCGGAGCTCGTGCCCTTCGTACCGTGAACGCCAGTGGGGCATCCTCAGCAAG
TGCCTGACCTACAGCAAGGCGGTGGCCGACCGTTACGTACTCTCTGCTCCGCCGGCCGTTTC
CGCCAAGTCCTGGCCGGCATGGTGCACCGGCTGCTGAAGAGAACCCCGCGCCAGCATCCACC
CATGACAGCTCTCTGGATGTGGCCGGCATGGTGCACCACTGCTGAAGAGAACCCCGCGCCCA
GCGTCCACCCACAACGGCTCTGTGGACACAGAGAATGATTCCTGCCTGCAGCAGACACACTGA
GGGCTGGCAGGGCTCATCGCCCCACCTTCTAAGAAGCCCTGTGGAAAGGGCACTGGCCCTG
CCACAGAGATGCCACTGGGGACCCCCAGACACCAGTGGCTTGACTTTGAGCTAAGGCTGAG

595/615

FIGURE 590

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA149930
><subunit 1 of 1, 363 aa, 1 stop
><MW: 39332, pI: 10.42, NX(S/T): 3
MGPGEALLAGLLVMVLAVALLSNALVLLCCAYSAELRTRASGVLLVNL SLGHLLLAALDM
PFTLLGVMRGRTPSAPGACQVIGFLDTFLASNAALSVAALSADQWLAVGFPLRYAGRLRP
RYAGLLLGCAWGQSLAFSGAALGCSWLGYSSAFASCSLRLPPEPERPRFAAFTATLHAVG
FVLPLAVLCLTSLQVHRVARRHCQRM DTVTMKALALLADLHPSVRQRC LIQQKRRRHRAT
RKIGIAIATFLICFAPYVMTRLAELVPFVTVNAQWGILSKCLTYSKAVADPFTYSLLRRP
FRQVLAGMVHRL LKRTPRPASTHDSSLDVAGMVHQLLKRTPRPASTHNGSVDTENDSCLQ
QTH
```

Important features of the protein:**Signal peptide:**

Amino acids 1-24

Transmembrane domains:

Amino acids 46-60;85-103;130-150;175-192;246-264

N-glycosylation sites:

Amino acids 47-51;348-352;355-359

Tyrosine kinase phosphorylation site:

Amino acids 286-295

N-myristoylation sites:Amino acids 66-72;124-130;128-134;132-138;139-145;244-250;
349-355**G-protein coupled receptor proteins:**

Amino acids 72-112

7 transmembrane receptor (rhodopsin family):

Amino acids 22-294

596/615

FIGURE 591

AACATGGCTGCGGCGCCTGGGCTGCTCGTCTGGCTGCTCGTCCGGCTGCCCTGGCGGGTG
CCGGGCCAGCTGGACCCCAGCACTGGCCGGCGGTTCTCGGAGCACAACTCTGCGCGGACGAC
GAATGCAGCATGATGTACCGCGGTGAGGCTCTTGAAGATTTACAGGCCCGGATTGTCGTTTT
GTGAATTTTAAAAAAGGTGATCCTGTATATGTTTACTATAAACTGGCAAGAGGATGGCCTGAA
GTTTGGGCTGGAAGTGTGGACGCACTTTTGGATATTTCCAAAAGATTTAATCCAGGTAGTT
CATGAATATACCAAAGAAGAGCTACAAGTTCCAACAGATGAGACGGATTTTGTGTTTGTGAT
GGAGGAAGAGATGATTTTCATAATTATAATGTAGAAGAACTTTTAGGGTTTTTGGAAGTGTAC
AATTCTGCAGCTACAGATTCTGAGAAAGCTGTAGAAAAAACTTTACAGGATATGAAAAAAAC
CCTGAATTATCTAAGGAAAGGGAACCTGAACCTGAACCAGTAGAAGCCAACCTCAGAGGAAAGT
GATAGTGTATTCTCAGAAAACACTGAGGATCTTCAGGAACAGTTTACAACCTCAGAAGCACCAC
TCCCATGCAAACAGCCAAGCAAATCATGCTCAGGGAGAGCAGGCTTCATTTGAATCTTTTGAA
GAAATGCTGCAAGATAAACTAAAAGTGCCAGAAAGTGAAAAACAACAAACCAGCAATAGTTCT
CAGGTCTCAAATGAACAGGATAAGATTGATGCCTATAAACTTTTGAAAAAAGAAATGACTCTA
GACTTGAAAACCAAATTTGGCTCAACAGCTGATGCACTTGTATCTGATGATGAGACAACCAGA
CTCGTTACTTCATTAGAAGATGATTTTGATGAGGAATTGGATACTGAGTATTATGCAGTTGGA
AAGGAAGATGAGGAGAACCAAGAAGACTTTGATGAGTTGCCATTACTTACCTTTACAGATGGG
GAAGATATGAAAACCTCCAGCAAAGTCTGGCGTTGAGAAATATCCAACAGATAAAGAGCAGAAT
TCAAATGAAGAGGACAAGGTTCACTAAGTGTGCCCCCTGGCATCAAAAATGATGATAAAAAT
ATACTAACACCTGGGGGGACACTATCTTCTCTATTGTACAGGAGGTGAAGAAACAAGAGAT
ACGATGGATTTAGAGAGCTCTAGTTCAGAGGAAGAAAAAGAAGATGATGATGATGCATTAGTC
CCAGATAGCAAACAGGGGAAACCACAGTCAGCAACAGATTATAGTGACCCTGACAATGTAGAT
GATGGTCTTTTTATTGTAGACATTCCCTAAAACAAATAATGACAAAGAAGTAAACGCAGAACAT
CACATTAAAGGAAAAGGGAGGGGAGTTCAGGAATCCAAGAGGGGCTGGTACAAGATGAGACA
GAATTAGAGGATGAAAATCAAGAAGGCTTTAAAACAGAGCCCATAAAACCTATGACCTCTGAGG
TTTCATTGGAAAGAAAGTGTACTGTGCATTATCCATTACAGTAAAGGATTTTCATTGGCTTCAA
AATCCAAAAGTTTATTTTAAAAGGTTTGTGTTAGAACTAAGCTGCCTTGGCAGTGTGCATTT
TTGAGCCAAACAATTCAAAAATGTCATTTCTTCCCTAAATAAAAATCACCTTTTAAGCTAGAG
CGTCCCTACAACCTTTGAAATGTGCAATAAAGAATACCTGTGTTTTAGCTAATGTAGCATATGT
AATTGCAAAATGATTTAGAATGTCATGAAAAATATGAACATTTCCCTGTGGAAATGCTTTAAGA
ACATGTATTTCCATTATCCTATTTTTAGTGTACACCAGCTGAATACGGAGCAATGGTGTATTAT
AAGCGTTTTTTTAACTATCTGGTCACAAAGACTGTTACGCTAAAAATGTTTACTAAAAGATC
ACTAACTATCTCCCTCTTGCTGAAGTTCTTTGTAGTAATAGCTCATAAAAATTTGTTTATT
AATATTTAAAAA

597/615

FIGURE 592

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA150157
><subunit 1 of 1, 499 aa, 1 stop
><MW: 56471, pI: 4.31, NX(S/T): 2
MAAAPGLLVWLLVLRPLPWRVPGQLDPSTGRRFSEHKLCADDECSMMYRGEALEDFTGPDC
RFVNFKKGDPVYVYKLRGWPEVWAGSVGRTFGYFPKDLIQVVHEYTKHEELQVPTDETD
FVCFDGGRRDDFHNYNVEELLGFLELYNSAATDSEKAVEKTLQDMEKNPELSKEREPEPEP
VEANSEESDSVFSENTEDLQEQFTTQKHHSHANSQANHAQGEQASFESFEEMLQDKLKVP
ESENKTSNSSQVSNEQDKIDAYKLLKKEMTLDLKTKEGSTADALVSDDDETTRLVTSLED
DFDEELDTEYYAVGKEDENQEDFDELPLLTFTDGEDMKTPAKSGVEKYPTDKEQNSNEE
DKVQLTVPPGIKNDDKNILTTWGDITFSIVTGGEETRDMDLESSSSEEEKEDDDDALVP
DSKQKGKQSATDYSDDPNVDDGLFIVDIPKTNNNDKEVNAEHHIKGKGRGVQESKRGLVQD
ETELEDENQEGFKTEPIKL

Important features of the protein:**Signal peptide:**

Amino acids 1-22

N-glycosylation sites:

Amino acids 245-249;249-253

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 30-34

Tyrosine kinase phosphorylation site:

Amino acids 66-72

N-myristoylation sites:

Amino acids 392-398;469-475

Amidation site:

Amino acids 28-32

Aminoacyl-transfer RNA synthetases class-II signature 1:

Amino acids 47-70

598/615

FIGURE 593

GGGCCAGTAGAGTGTGTCTGGGTCAGCTGAGTGACTACATCAAAGCTCCCAGCCTTGAAAAAC
ACATGCTGTTCCCAGGCCTCAAGATATTGAAACATTAATTAGATAATTTAAAGTAGCGTTTTTC
TTCTACAATGTCTGAAGAAGTGACCTACGCGACACTCACATTTTCAGGATTCTGCTGGAGCAAG
GAATAACCGAGATGGAAATAACCTAAGAAAAAGAGGGCATCCAGCTCCATCTCCATTTGGCG
TCATGCTGCTCTGGGTCTGGTAACTCTTTGCCTGATGTTGCTGATTGGGCTGGTGACGTTGGG
GATGATGTTTTTGCAGATATCTAATGACATTAACCTCAGATTCAGAGAAATTGAGTCAACTTCA
GAAAACCATCCAACAGCAGCAGGATAACTTATCCCAGCAACTGGGCAACTCCAACAACCTTGTC
CATGGAGGAGGAATTTCTCAAGTCACAGATCTCCAGTCTACTGAAGAGGCAGGAACAAATGGC
CATCAAACCTGTGCCAAGAGCTAATCATTCTACTTCAGACCACAGATGTAATCCATGTCTTAA
GATGTGGCAATGGTACCAAAATAGTTGCTACTATTTTACAACAAATGAGGAGAAAACCTGGGC
TAACAGTAGAAAGGACTGCATAGACAAGAACTCCACCCTAGTGAAGATAGACAGTTTGGAAGA
AAAGGATTTTCTTATGTACAGCCATTACTCATGTTTTTCGTTCTTTTGGCTGGGATTATCATG
GGACTCCTCTGGCAGAAGTTGGTTCTGGGAAGATGGCTCTGTTCCCTCTCCATCCTTGACGT
CTCTAACTATTGAGGGTAAACACAAGCTTTCCATGGAATCCTGGGAAAATTAATAATGATTGT
GAGAATTATAAATACAGACATAAAAAGAGGAGTACAACATACTGAGAAAAGAGCTCCAGTAAC
AAATATTGAAAGGAGATTTAGTACTAAAGAACTTGACCAGATCAATGGATCCAAAGGATGTGC
TTATTTTCAAAAAGGAAATATTTATATTTCTCGCTGTAGTGCTGAAATTTTTTGGATTTGCGA
GAAGACAGCTGCCCCAGTGAAGACTGAGGATTTGGATTAGTATGCTTCTTCCAAATTCTCCAA
GAAGTAAGAGACTTGTGAGTAAGCTCATATGAGGAAAGAGGAAACTACGGTACCAGAGCAAGG
CGAATTCTGCA

599/615

FIGURE 594

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA150163
><subunit 1 of 1, 232 aa, 1 stop
><MW: 26754, pI: 5.80; NX(S/T): 3
MSEEVTYATLTFQDSAGARNNRDGNLRLRGHPAPSPIWRHAALGLVTLCLMLLIGLVTL
GMMFLQISNDINS DSEKLSQLQKTIQQQQDNLSQQLGNSNNLSMEEEFLLKSQISSLLKRQ
EQMAIKLCQELIIHTSDHRCNPPCKMWQWYQNSCYFFTNEEKTWANSRKDCIDKNSTLV
KIDSLEEKDFLMSQPLLMFSFFWLGLSWDSSGRSWFWEDGSVPSPSLYVSNY
```

Important features of the protein:**Transmembrane domain:**

Amino acids 42-62

N-glycosylation sites:

Amino acids 91-95;101-105;176-180

N-myristoylation sites:

Amino acids 17-23;97-103

600/615

FIGURE 595

CGGACGCGTGGGGAAGAGGAGGAGGAGGAAGAAGACGTGGACAAGGACCCCCATCCTACCCAG
AACACCTGCCTGCGCTGCCGCCACTTCTCTTTAAGGGAGAGGAAAAGAGAGCCTAGGAGAACC
ATGGGGGGCTGCGAAGTCCGGGAATTTCTTTTGCAATTTGGTTTCTTCTTGCCATATGCTGACA
GCGTGGCCAGGCGACTGCAGTCACGTCTCCAACAACCAAGTTGTGTTGCTTGATACAACAAC
GTACTGGGAGAGCTAGGATGGAAAACATATCCATTAAATGGGTGGGATGCCATCACTGAAATG
GATGAACATAATAGGCCCCATTCACACATAACCAGGTATGTAATGTAATGGAACCAACCAAAAC
AACTGGCTTCGTACAAACTGGATCTCCCGTGATGCAGCTCAGAAAATTTATGTGGAAATGAAA
TTCACACTAAGGGATTGTAACAGCATCCCATGGGTCTTGGGGACTTGCAAAGAAACATTTAAT
CTGTTTTATATGGAATCAGATGAGTCCCACGGAATTAAATTCAAGCCAAACCAGTATACAAAG
ATCGACACAATTGCTGCTGATGAGAGTTTTACCCAGATGGATTGGGTGATCGCATCCTCAAA
CTCAACACTGAAATTCGTGAGGTGGGGCCTATAGAAAGGAAAGGATTTTATCTGGCTTTTCAA
GACATTGGGGCGTGCAATTGCCCTGGTTTCAGTCCGTGTTTTCTACAAGAAATGCCCTTCACT
GTTTCGTAACCTGGCCATGTTCCCTGATACCATCCAAGGGTTGATTCCTCCTCTTTGGTTGAA
GTACGGGGTTCTTGTGTGAAGAGTGCTGAAGAGCGTGACACTCCTAAACTGTATTGTGGAGCT
GATGGAGATTGGCTGGTTCCTCTTGAAGGTGCATCTGCAGTACAGGATATGAAGAAATTGAG
GGTTCTTGCCATGGAGCCTCAAAGGCCGCTGCTTCTTAGTTGGCCATCTTGGCCCCACCCCGA
AACAGTAACCTTTGAAGAATAAAAGAAAAAGCAAAAGAGTAGCATTACTAAAATATTAAACGG
TTACATTTACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

601/615

FIGURE 596

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA153579
><subunit 1 of 1, 285 aa, 1 stop
><MW: 32368, pI: 5.32, NX(S/T): 0
MGGCEVREFLLQFGFFLPMLTAWPGDCSHVSNNQVVLLDTTTLVGLGELGWKTYPLNGWDAI
TEMDEHNRPIHTYQVCNVMEPNQNNWLRTNWLISRDAQKIYVEMKFTLRDCNSIPWVLGT
CKETFNLFYMESDESHGIKFKPNQYTKIDTIAADESFTQMDLGDRILKLNTEIREVGPIE
RKGFYLAFAQDIGACIALVSVRVFYKKCPFTVRNLAMFPDTIPRVDSSSLVEVRGSCVKSA
EERDTPKLYCGADGDWLVPLGRCICSTGYEEIEGSCHGASKGRCF

Important features of the protein:**Signal peptide:**

Amino acids 1-22

N-myristoylation sites:

Amino acids 192-198;274-280;278-284

Receptor tyrosine kinase class V signature 1:

Amino acids 192-209

Ephrin receptor ligand binding domain:

Amino acids 34-207

602/615

FIGURE 597

ACACTGGCCAAACAAAAACGAAAGCACTCCGTGCTGGAAGTAGGAGGAGAGTCAGGACTCCCA
GGACAGAGAGTGCACAAACTACCCAGCACAGCCCCCTCCGCCCCCTCTGGAGGCTGAAGAGGG
ATTCCAGCCCCCTGCCACCCACAGACACGGGCTGACTGGGGTGTCTGCCCCCTTGGGGGGGG
CAGCACAGGGCCTCAGGCCTGGGTGCCACCTGGCACCTAGAAGATGCCTGTGCCCTGGTTCTT
GCTGTCTTTGGCACTGGGCGGAAGCCCAGTGGTCTTTCTCTGGAGAGGCTTGTGGGGCCTCA
GGACGCTACCCACTGCTCTCGGGGCTCTCCTGCCGCTCTGGGACAGTGACATACTCTGCCT
GCCTGGGGACATCGTGCTGCTCCGGGCCCCGTGCTGGCGCCTACGCACCTGCAGACAGAGCT
GGTGTGAGGTGCCAGAAGGAGACCGACTGTGACCTCTGTCTGCGTGTGGCTGTCCACTTGGC
CGTGCATGGGCACTGGGAAGAGCCTGAAGATGAGGAAAAGTTTGGAGGAGCAGCTGACTCAGG
GGTGGAGGAGCCTAGGAATGCCTCTCTCCAGGCCCAAGTCGTGCTCTCCTTCCAGGCCTACCC
TACTGCCCCGTGCGTCTGTGGAGGTGCAAGTGCCTGCTGCCCTTGTGCAGTTTGGTCAGTC
TGTGGGCTCTGTGGTATATGACTGCTTCGAGGCTGCCCTAGGGAGTGAGGTACGAATCTGGTC
CTATACTCAGCCCAGGTACGAGAAGGAACCAACCACACACAGCAGCTGCCTGCCCTGCCCTG
GCTCAACGTGTGAGCAGATGGTGACAACGTGCATCTGGTTCTGAATGTCTCTGAGGAGCAGCA
CTTCGGCCTCTCCCTGTACTGGAATCAGGTCCAGGGCCCCCAAACCCCGGTGGCACAATA
CCTGACTGGACCGCAGATCATTACCTTGAACCACACAGACCTGGTTCCCTGCCTCTGTATTCA
GGTGTGGCCTCTGGAACCTGACTCCGTTAGGACGAACATCTGCCCTTCAGGGAGGACCCCCG
CGCACACCAGAACCTCTGGCAAGCCGCCGACTGCGACTGCTGACCCTGCAGAGCTGGCTGCT
GGACGCACCGTGTCTGCTGCCCGCAGAAGCGGCACTGTGCTGGCGGGCTCCGGGTGGGGACCC
CTGCCAGCCACTGGTCCCACCGCTTTCTGGGAGAACGTCACTGTGGACAAGGTTCTCGAGTT
CCCATTGCTGAAAGGCCACCCTAACCTCTGTGTTTCAAGTGAACAGCTCGGAGAAGCTGCAGCT
GCAGGAGTGCTTGTGGGCTGACTCCCTGGGGCCTCTCAAAGACGATGTGCTACTGTTGGAGAC
ACGAGGCCCCCAGGACAACAGATCCCTCTGTGCCTTGGAAACCCAGTGGCTGTACTTCACTACC
CAGCAAAGCCTCCACGAGGGCAGCTCGCCTTGGAGAGTACTTACTACAAGACCTGCAGTCAGG
CCAGTGTCTGCAGCTATGGGACGATGACTTGGGAGCGCTATGGGCCTGCCCCATGGACAAATA
CATCCACAAGCGCTGGGCCCTCGTGTGGCTGGCCTGCCTACTCTTTGCCGCTGCGCTTTCCCT
CATCCTCCTTCTCAAAAAGGATCACGCGAAAGGGTGGCTGAGGCTCTTGAAACAGGACGTCCG
CTCGGGGGCGGCCGCCAGGGGCCGCGCGGCTCTGCTCCTTACTCAGCCGATGACTCGGGTTT
CGAGCGCCTGGTGGGCGCCCTGGCGTCGGCCCTGTGCCAGCTGCCGCTGCGCGTGGCCGTAGA
CCTGTGGAGCCGTCTGAACTGAGCGCGCAGGGGCCCCGTGGCTTGGTTTACGCGCAGCGGCG
CCAGACCCCTGCAGGAGGGCGGCGTGGTGGTCTTGCTCTTCTCTCCCGGTGCGGTGGCGCTGTG
CAGCGAGTGGCTACAGGATGGGGTGTCCGGGCCCGGGGCGCACGGCCCCGACGACGCTTCCG
CGCCTCGCTCAGCTGCGTGCTGCCCGACTTCTTGAGGGCCGGGCGCCCCGCGAGCTACGTGGG
GGCCTGCTTCGACAGGCTGCTCCACCCGACGCGCTACCCGCCCTTTTCCGCACCGTGCCCGT
CTTCACACTGCCCTCCCAACTGCCAGACTTCTGGGGGCCCTGCAGCAGCCTCGCGCCCCGCG
TTCCGGGCGGCTCCAAGAGAGAGCGGAGCAAGTGTCCCGGGCCCTTCAGCCAGCCCTGGATAG
CTACTTCCATCCCCGGGGACTCCCGCGCCGGGACGCGGGGTGGGACCAGGGGCGGGACCTGG
GGCGGGGGACGGGACTTAAATAAAGGCAGACGCTGTTTTTCTAAAAAA

603/615

FIGURE 598

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA164625
><subunit 1 of 1, 705 aa, 1 stop
/><MW: 76970, pI: 6.00, NX(S/T): 9
MPVPWFLLSLALGRSPVVLRLVGPQDATHCSPGLSCRLWSDILCLPGDIVPAPGP
VLAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRN
ASLQAQVVLVSFOAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWYSY
QPRYEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQPPKPRWH
KNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLT
LQSWLLDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCV
QVNSSEKLQEQECLWADSLGPLKDDVLLLETRGPQDNRSLEPSGCTSLPSKASTRA
ARLGEYLLQDLQSGQCLQWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSLILL
LKGDHAKGWLRLLLKQDVRSGAAARGRAALLYSADDSGFERLVGALASALCQLPLRVAV
DLWSRRELSAQGPVAFWFAHQRRQTLQEGGVVLLFSPGAVALCSEWLQDGVSGPGAHGP
HDAFRASLSCVLPDFLQGRAPGSYVGACFDRLHPDAVPALFRTVPVFTLPSQLPDFLG
ALQQPRAPRSGRLLQERAEQVSRALQPALDSYFHPPGTAPGRGVGPGAGPGAGDGT
```

Important features of the protein:**Signal peptide:**

Amino acids 1-20

Transmembrane domain:

Amino acids 453-473

N-glycosylation sites:Amino acids 118-122;186-190;198-202;211-215;238-242;
248-252;334-338;357-360;391-395;**Glycosaminoglycan attachment site:**

Amino acids 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 552-556

N-myristoylation sites:Amino acids 107-113;152-158;319-325;438-444;516-522;612-618;
692-698;696-702;700-706

604/615

FIGURE 599

GGTCCTTAATGGCAGCAGCCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTGC
TGTCCGGCTGGTCCCGGGCTGGGCGAGCCGACCCTCACTCTCTTTGCTATGACATCACCGTCA
TCCCTAAGTTTCAACCTGGACACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGACTT
TTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCAGTCCCCTGGGGAAGAACTAA
ATGTCACAACGGCCTGGAAAGCACAGAACCCAGTACTGAGAGAGGTGGTGGACATACTTACAG
AGCAACTGCGTGACATTGAGCTGGAGAATTACACACCCAAGGAACCCCTCACCTGCAGGCAA
GGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGTTTCGATG
GGCAGATCTTCCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCCTGGAGCCA
GAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCTTCCATTACTTCTCAA
TGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACCCCTGGAGCCAA
GTGCAGGAGCACCACTCGCCATGTCCTCAGGCACAACCCAACCTCAGGGCCACAGCCACCACCC
TCATCCTTTGCTGCCTCCTCATCATCCTCCCCTGCTTCATCCTCCCTGGCATCTGAGGAGAGT
CCTTTAGAGTGACAGGTTAAAGCTGATACCAAAGGCTCCTGTGAGCACGGTCTTGATCAAAC
TCGCCCTTCTGTCTGGCCAGCTGCCCACGACCTACGGTGTATGTCCAGTGGCCTCCAGCAGAT
CATGATGACATCATGGACCCAATAGCTCATTCAGTGCCTTGATTCCTTTTGCCAACAATTTTA
CCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACCTGATGGAATTCCTGCA
CTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTTCTTTTTGTTTGGAAAA
TCAAGTACTTCTTTGAATGATGATCTCTTTCTTGCAAATGATATTGTCAGTAAAATAATCAG
TTAGACTTCAGACCTCTGGGATTCTTTCCGTGTCCTGAAAGAGAATTTTAAATTATTTAAT
AAGAAAAAATTTATATTAATGATTGTTTCCTTTAGTAATTTATTGTTCTGTACTGATATTTAA
ATAAAGAGTTCTATTTCCCAAAAAAAAAAAAAAAAAAAAA

605/615

FIGURE 600

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTF
YDCGNKTVTPVSPGLGKKLVTTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQARMS
CEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFSMGD
CIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

Important features:**Signal peptide:**

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

606/615

FIGURE 601

GCAGTCAGAGACTTCCCCCTGCCCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCTT
GCTTCCTGAACTAGCTCACAGTAGCCCCGGCGGCCAGGGCAATCCGACCACATTTCACTCTCA
CCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATGATG
GGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCCCGGC
GCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCCTGCTGACTTTGT
GCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTTCAGTACTACCAGCTCT
CCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAAGATTAGGAAATACGTCCCAAGAGT
TGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAAAC
TCTGTCTGTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAGAACAATGGA
AATGGCATGGAGACAATTGCTACCAGTCTATAAAGACAGCAAAAGTTGGGAGGACTGTAAAT
ATTTCTGCCTTAGTGAAAACCTTACCATGCTGAAGATAAACAAACAAGAAGACCTGGAATTTG
CCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTTTGCGCCCTGACA
GTGGCAAGGCCCTGGCTGTGGATGGATGGAACCCCTTTCACTTCTGAACTGTTCCATATTATAA
TAGATGTCACCAGCCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGGGATGATCTTCTCAA
AGGACTGCAAAGAATTGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAATGGTGAAGCCAGAGA
GCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACTTGATTTCGCCCTCTGCAACTACAAAT
AGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAGACATTGGGAAATGGAACATAA
TCAGGAAAGACTATCTCTCTGACTAGTACAAAATGGGTTCTCGTGTTCCTGTTTCAGGATCAC
CAGCATTTCTGAGCTTGGGTTTATGCACGTATTTAACAGTCACAAGAAGTCTTATTTACATGC
CACCAACCAACCTCAGAAACCCATAATGTCATCTGCCTTCTTGGCTTAGAGATAACTTTTAGC
TCTCTTTCTTCTCAATGTCTAATATCACCTCCCTGTTTTTCATGTCTTCCTTACACTTGGTGGA
ATAAGAACTTTTTGAAGTAGAGGAAATACATTGAGGTAACATCCTTTTCTCTGACAGTCAAG
TAGTCCATCAGAAATTGGCAGTCACTTCCCAGATTGTACCAGCAAATACACAAGGAATTCTTT
TTGTTTGTTCAGTTCATACTAGTCCCTTCCCAATCCATCAGTAAAGACCCCATCTGCCTTGT
CCATGCCGTTTCCCAACAGGGATGTCATTGATATGAGAATCTCAAATCTCAATGCCTTATAA
GCATTCCCTTCTGTGTCCATTAAGACTCTGATAATTGTCTCCCCTCCATAGGAATTTCTCCCA
GGAAAGAAATATATCCCCATCTCCGTTTCATATCAGAACTACCGTCCCCGATATTCCCTTCAG
AGAGATTAAAGACCAGAAAAAAGTGAGCCTCTTCATCTGCACCTGTAATAGTTTCAGTTCCTA
TTTTCTTCCATTGACCCATATTTATACCTTTCAGGTACTGAAGATTTAATAATAATAAATGTA
AATACTGTGAAAAA

607/615

FIGURE 602

MQAKYSSTRDMLDDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCLVLLI
GLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRELY
NKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAASQSY
SEFFYSYWTGLLRPD SGKAWLWMDGTPFTSELFHIIIDVTSPRSRDCVAILNGMIFSKDCKEL
KRCVCERRAGMVKPESLHVPPETLGED

608/615

FIGURE 603

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTCC
CAGCAATATGCATCTTGACAGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCCCT
GTCTGGATGGGCGGCCAGCGATGACCCCATTGAGAAGGTCATTGAAGGGATCAACCGAGGGCT
GAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGAATCACGCATGC
CGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGCAAGGA
GTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGATCAACCA
TGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACGCTGCTGG
ACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCACCAGGCTGG
GAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGGAAAGGAAGT
GGAGAAGCTTGGCCAAGGTGCCCAACCATGCTGCTGGCCAGGCCGGGAAGGAGCTGCAGAATGC
TCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGCAACCATCAAAG
CGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGGGGCCTCAGTCAA
CACGCCTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCATGCCCTTAAACTGG
CATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTCACATCAGCTGACATGACCTGGAGGGG
TTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGGTTGTAAGGGATTGTGAATAAA
CTTGATACACCA

609/615

FIGURE 604

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675

><subunit 1 of 1, 247 aa, 1 stop

><MW: 25335, pI: 7.00, NX(S/T): 0

MHLARLVGSCSLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAGR
EVEKVFNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAGQA
GKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQNAHN
GVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPPFINLPALWRSVANIMP

Important features of the protein:**Signal peptide:**

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

610/615

FIGURE 605

GCGACGCGGGCGGGGCGGCGAGAGGAAACGCGGCGCCGGGCGGGCCCGGCCCTGGAGATGG
TCCCCGGCGCCGCGGGCTGGTGTGTCTCGTGCTCTGGCTCCCCGCGTGCGTCGCGGCCACG
GCTTCCGTATCCATGATTATTTGTACTTTCAAGTGCTGAGTCCTGGGGACATTCGATACATCT
TCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTACACAAGGTATGAGCAGATTACAC
TTGTCCCCGCTGAACCTCCAGAGGCCTGCGGGGAAGTCAGCAACGGTTTCTTCATCCAGGACC
AGATTGCTCTGGTGGAGAGGGGGGGCTGCTCCTTCCTCTCCAAGACTCGGGTGGTCCAGGAGC
ACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTACGTGGAGA
TGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCCTGCTCGGCCGAGACG
GCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTTCCATCCCAG
TCAATGTCACCAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTCTGGTAGAAGA
GTTTGTCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCCAGGAATTTTGC
TACTTGGAATTTGGAGATAGCATCTGGGGACAAGTGAGCCAGGTAGAGGAAAAGGGTTTGGG
CGTTGCTAGGCTGAAAGGGAAGCCACACCACTGGCCTTCCCTTCCCCAGGGCCCCCAAGGGTG
TCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTAGAACCCGAAACAAA
AGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACACTCACCTGGCTCCAGCC
TCCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGGAGTGGTTTAAAGAGCT
GGTGTGTTGGGGACTCAATAAACCTCACTGACTTTTTAGCAATAAAGCTTCTCATCAGGGTG
CAAAAAAAAAAAAAAAAAAAAAAAAAA

611/615

FIGURE 606

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532

><subunit 1 of 1, 188 aa, 1 stop

><MW: 21042, pI: 5.36, NX(S/T): 2

MVPGAAGWCCLVLWLPACVAAHGFRIDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQI
HLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDNAVNDNSFYV
EMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW**Signal peptide:**

amino acids 1-20

612/615

FIGURE 607

GCATTTGCCACTGGTTGCAGATCAGGCGGACGAGGAGCCGGGAAGGCAGAGCC**ATG**TGGCTGC
CCCCTGCTCTGCTCCTTCTCAGCCTCTCAGGCTGTTTCTCCATCCAAGGCCAGAGTCTGTGA
GAGCCCCAGAGCAGGGGTCCCTGACGGTTCAATGCCACTATAAGCAAGGATGGGAGACCTACA
TTAAGTGGTGGTGCCGAGGGGTGCGCTGGGATACATGCAAGATCCTCATTGAAACCAGAGGGT
CGGAGCAAGGAGAGAAGAGTGACCGTGTGTCCATCAAGGACAATCAGAAAAGACCGCACGTTCA
CTGTGACCATGGAGGGGCTCAGGCGAGATGACGCAGATGTTTACTGGTGTGGGATTGAAAAGAA
GAGGACCTGACCTTGGGACTCAAGTGAAAAGTGATCGTTGACCCAGAGGGAGCGGCTTCCACAA
CAGCAAGCTCACCTACCAACAGCAATATGGCAGTGTTTCATCGGCTCCCAACAAGAGGAACCACT
ACATGCTCCTGGTATTTGTGAAGGTGCCCATCTTGCTCATCTTGGTCACTGCCATCCTCTGGT
TGAAGGGGTCTCAGAGGGTCCCTGAGGAGCCAGGGGAACAGCCTATCTACATGAACTTCTCCG
AACCTCTGACTAAAGACATGGCCACT**TAG**AGAGATGGATCTGCAGAGCCTTCCTGCCCTGGCC
ACGTTTCCAGAAGAGACTCGGGCTGTGGAAGGAACATCTACGAGTCCTCGGGATGCAGTGACT
GAGATAGGGGCCCTGGGCCTCCGCCCTGGCCTTGGAGCTGGTGGGCACCTCCCTGTTCTGCAC
AGCTCAGGGACTTAGCCAGGTCTCTCTGAGCCACCATCACCTCCTGGGGTGCCAGCACCTG
TTCTCTTGGTCAGGAGCTGTAGAGATGGAGCTCAAGCACTGGACGACTCTGTCCCCACTGCTG
GAATAACTCGGGCACAGAGCATGGGACCAAAGTACAGAAAGAGGTTGGGGGAGACCCCCCAG
CCCTAGACTTCCATCATTCGGGAGACCAACTCAACACCGTCTTTGCCTGAGAACCTGATATATCC
GTGTTTTTAAATTTTTTTTTTTCTAGCAAAGTTGGGTTTTAATGACTTATGTTTCATAGGAAAC
CTCTCTGATCCACACACAAGGAGGGTGATTCTGGGATGAGTTCCTGGTTCTAGGGCATGAGG
GGCTGGATGGACCCTGTCCCCAGGGAGGACATGGCTCTGAGTCCACAGGGCTGAGGAGGCAAT
GGGAACCTCCCTGGCCCGGCCCGGTGCTTGTCTCCCCCTCCACCTCTTCCTCCTCCTAGCT
CCCCAAGCTCCCTGCCTATTCCCCCACCTCCGAGGGGCTGCAGCTTGGGAGCCTCCTCAGCAT
GACAGCTTGGGTCTCCTCCCCAAAAGAGCCTGTCAGGCCTCAAGAACCACCTCCAGGTGGGGA
GGGCAGTAACGAAAACCATCGCAGGAAATGGCACCCCTCCCTTTTCGGTGATGTTGAAATCATG
TTACTAATGAAAACCTGTCCTAGGGAAAGTGGTCTGTCTCCTCACAGGCTTCACCCACGGCGAT
GAGGCCCTTGAATGTGGTCACTTTGTGCTGTATGGTTGAGGGACCCTCACACCAAAGGGACCT
TCCCATGTGAGATGTGCTCCCGCCCCCACCTGCCCACAAGCAAACACACCACACATGTTCCGGC
ATGTTGCCCTTTGAACACCCATGAGGACGCCTCCAACCTGCTCTTGGTTCTAATAGGGAGTAC
TGACTGTCAGCAGTGGATAAAGGAGAGGGGACCCTCTGGTCCCTAGCATGGCACCCAGAGCCT
CCCCTCTTCTTGTCCTTCAGCCAAAGAGAACTTTCTCTGACTTTGAACTGAATTTAGGTCTC
TGGCCAATGATGGGCCTGAAAATTCCATAATGGCCAGAGAGGAGAGTTTCGAGCCCGGCTAAGA
TCCCCTGAGTCATTCTGTGAGGGACCAAGACCCACAGTCCACCAGCCCCAGGGCCCTACCTCC
TCCGCGGGAGGGAAAGCCAAAGCATGGTGCTTCACCAGCTGGACTCAGGGGCGAGGGGACATG
GGCGCTTGTCAACGTGATGTCATTCTTTCCACCGTTTCTTCCTGTTGATATTCAATGAATC
CGTCAATCTCTCTGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

613/615

FIGURE 608

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA105849
><subunit 1 of 1, 201 aa, 1 stop
><MW: 22689, pI: 7.41, NX(S/T): 1
MWLPPALLLLLSLSCFSIQGPESVRAPEQGSITVQCHYKQGWETYIKWWCRGVRWDTCKI
LIETRGSEQGEKSDRVSISKDNQKDRFTFTVMEGLRRDDADVWCGIERRGPDLTQVKVI
VDPEGAASTTASSPTNSNMAVFIGSHKRNHYMLLVFVKVPILLILVTAILWLKGSQRVPE
EPGEQPIYMNFFSEPLTKDMAT
```

Important features of the protein:**Signal peptide:**

Amino acids 1-17

Transmembrane domain:

Amino acids 151-170

N-glycosylation site:

Amino acids 190-194

Tyrosine kinase phosphorylation site:

Amino acids 95-103

N-myristoylation sites:

Amino acids 66-72;125-131

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 5-16

614/615

FIGURE 609

GATGGCGCAGCCACAGCTTCTGTGAGATTTCGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGGG
GACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCAAA
ACAAGTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTT
CCAGGCCCTTACCTGCTGGGCACCTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACG
ACCTGTGCCACCAACTCGCACTCAGACTCTGAACCTCAGACCTGAAATCTTCTCTTCACGGGAG
GCTTGGCAGTTTTTTCTTACTCCTGTGGTCTCCAGATTTTCAGGCCTAAGATGAAAGCCTCTAGT
CTTGCCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAG
ACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCT
GAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACT
GAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCCTCCTGCGCCATTTGCTAAGACTC
TATCTGGACAGGGTATTTAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGC
AGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCATGCCACATGACA
TGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG
GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATGGAG
GAGACAGAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTCGAGGTCAAGAGCTCCAGTCT
TCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACTGTACTAGTCTTGTGCT
GGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCATGATTGTCTTTATGCATCCCC
AATCTTAATTGAGACCATACTTGTATAAGATTTTTGTAATATCTTTCTGCTATTGGATATATT
TATTAGTTAATATATTTATTTATTTTTTTGCTATTTAATGTATTTATTTTTTTACTTGGACATG
AACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAGAGCAGGTGATGTATTTTTAT
ACAGTAAAAAATAAACCTTGTAATTTCTAGAAGAGTGGCTAGGGGGGTTATTCATTTGTAT
TCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGATATTTGAAATTGAACCAATGAC
TACTTAGGATGGGTTGTGGAATAAGTTTTGATGTGGAATTGCACATCTACCTTACAATTACTG
ACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTATCTTCCAGCCAGGAATCCTACACGG
CCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATACCAAAAAAAAAAAAAAAAAAAAA

615/615

FIGURE 610

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
><subunit 1 of 1, 261 aa, 1 stop
><MW: 29667, pI: 8.76, NX(S/T): 0
MRQFPKTSFDISPEMSFSIYSLQVPAVPG LTCWALTAEPGWGQNGATT CATNSHSDSEL
RPEIFSSREAWQFFLLWSPDFRPKM KASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVI
ATNLQEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVF
KNYQTPDHYTLRKISSLANSLTIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQ
AAVVKALGELDILLQWMEETE
```

Important features of the protein:**Signal peptide:**

Amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 192-196;225-229

N-myristoylation sites:

Amino acids 42-48;46-52;136-142

(19) World Intellectual Property Organization
International Bureau(43) International Publication Date
20 September 2001 (20.09.2001)

PCT

(10) International Publication Number
WO 01/068848 A3

- (51) International Patent Classification⁷: **C12N 15/12**,
15/62, C07K 14/47, 14/705, 16/18, G01N 33/53, C12Q
1/68
- (21) International Application Number: PCT/US01/06520
- (22) International Filing Date: 28 February 2001 (28.02.2001)
- (25) Filing Language: English
- (26) Publication Language: English
- (30) Priority Data:
- | | | |
|----------------|-----------------------------|----|
| PCT/US00/05601 | 1 March 2000 (01.03.2000) | US |
| PCT/US00/05841 | 2 March 2000 (02.03.2000) | US |
| 60/187,202 | 3 March 2000 (03.03.2000) | US |
| 60/186,968 | 6 March 2000 (06.03.2000) | US |
| 60/189,328 | 14 March 2000 (14.03.2000) | US |
| 60/189,320 | 14 March 2000 (14.03.2000) | US |
| PCT/US00/06884 | 15 March 2000 (15.03.2000) | US |
| 60/191,048 | 21 March 2000 (21.03.2000) | US |
| 60/190,828 | 21 March 2000 (21.03.2000) | US |
| 60/191,314 | 21 March 2000 (21.03.2000) | US |
| 60/191,007 | 21 March 2000 (21.03.2000) | US |
| 60/192,655 | 28 March 2000 (28.03.2000) | US |
| 60/193,032 | 29 March 2000 (29.03.2000) | US |
| 60/193,053 | 29 March 2000 (29.03.2000) | US |
| PCT/US00/08439 | 30 March 2000 (30.03.2000) | US |
| 60/194,647 | 4 April 2000 (04.04.2000) | US |
| 60/194,449 | 4 April 2000 (04.04.2000) | US |
| 60/196,820 | 11 April 2000 (11.04.2000) | US |
| 60/195,975 | 11 April 2000 (11.04.2000) | US |
| 60/196,000 | 11 April 2000 (11.04.2000) | US |
| 60/196,187 | 11 April 2000 (11.04.2000) | US |
| 60/196,690 | 11 April 2000 (11.04.2000) | US |
| 60/198,121 | 18 April 2000 (18.04.2000) | US |
| 60/198,585 | 18 April 2000 (18.04.2000) | US |
| 60/199,654 | 25 April 2000 (25.04.2000) | US |
| 60/199,397 | 25 April 2000 (25.04.2000) | US |
| 60/199,550 | 25 April 2000 (25.04.2000) | US |
| 60/201,516 | 3 May 2000 (03.05.2000) | US |
| PCT/US00/13705 | 17 May 2000 (17.05.2000) | US |
| PCT/US00/14042 | 22 May 2000 (22.05.2000) | US |
| PCT/US00/14941 | 30 May 2000 (30.05.2000) | US |
| PCT/US00/15264 | 2 June 2000 (02.06.2000) | US |
| 60/209,832 | 5 June 2000 (05.06.2000) | US |
| PCT/US00/20710 | 28 July 2000 (28.07.2000) | US |
| 09/644,848 | 22 August 2000 (22.08.2000) | US |
| PCT/US00/23328 | 24 August 2000 (24.08.2000) | US |
- (60/000,000 15 September 2000 (15.09.2000) US
PCT/US00/30952 8 November 2000 (08.11.2000) US
PCT/US00/32678 1 December 2000 (01.12.2000) US
PCT/US00/34956 20 December 2000 (20.12.2000) US
- (71) Applicant (for all designated States except US): **GENENTECH, INC.** [US/US]; 1 DNA Way, South San Francisco, CA 94080-4990 (US).
- (72) Inventors; and
- (75) Inventors/Applicants (for US only): **BAKER, Kevin, P.** [GB/US]; 14006 Indian Run Drive, Darnestown, MD 20878 (US). **CHEN, Jian** [US/US]; 121 York Drive, Princeton, NJ 08540 (US). **DESNOYERS, Luc** [CA/US]; 2050 Stockton Street, San Francisco, CA 94133 (US). **GODDARD, Audrey** [CA/US]; 110 Congo Street, San Francisco, CA 94131 (US). **GODOWSKI, Paul, J.** [US/US]; 2627 Easton Drive, Burlingame, CA 94010 (US). **GURNEY, Austin, L.** [US/US]; 1 Debbie Lane, Belmont, CA 94002 (US). **PAN, James** [CA/US]; 2705 Coronet Boulevard, Belmont, CA 94002 (US). **SMITH, Victoria** [AU/US]; 19 Dwight Road, Burlingame, CA 94010 (US). **WATANABE, Colin, K.** [US/US]; 128 Corliss Drive, Moraga, CA 94556 (US). **WOOD, William, I.** [US/US]; 35 Southdown Court, Hillsborough, CA 94010 (US). **ZHANG, Zemin** [CN/US]; 876 Taurus Drive, Foster City, CA 94404 (US).
- (74) Agents: **BARNES, Elizabeth, M.** et al.; c/o Genentech, Inc., MS49, 1 DNA Way, South San Francisco, CA 94080-4990 (US).
- (81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.
- (84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

[Continued on next page]

(54) Title: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

(57) Abstract: The present invention is directed to novel polypeptides and to nucleic acid molecules encoding those polypeptides. Also provided herein are vectors and host cells comprising those nucleic acid sequences, chimeric polypeptide molecules comprising the polypeptides of the present invention fused to heterologous polypeptide sequences, antibodies which bind to the polypeptides of the present invention and to methods for producing the polypeptides of the present invention.

WO 01/068848 A3



Published:

— with international search report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(88) Date of publication of the international search report:
29 August 2002

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 01/06520

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/12 C12N15/62 C07K14/47 C07K14/705 C07K16/18
G01N33/53 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K C12Q G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, BIOSIS, SEQUENCE SEARCH

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 99 63088 A (BAKER KEVIN ;CHEN JIAN (US); GENENTECH INC (US); YUAN JEAN (US); G) 9 December 1999 (1999-12-09) page 1 -page 2; claims 1-26; figures 3,4; examples 1-3,5,139-147 page 281 -page 284 page 305 -page 314 page 345 -page 373 ---	1-24
X	WO 99 54461 A (SCHMITT ARMIN ;SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN BERND) 28 October 1999 (1999-10-28) page 1 -page 7; claims 1-38; figures 1-5; examples 1-4 see SEQ ID NO: 53 (pp.215 and 216), SEQ ID NO: 300 (pp. 350 and 351) page 163 --- -/--	1-24

☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

* Special categories of cited documents :

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

- "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- "&" document member of the same patent family

Date of the actual completion of the international search

28 February 2002

Date of mailing of the international search report

06.06.2002

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
NL - 2280 HV Rijswijk
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,
Fax: (+31-70) 340-3016

Authorized officer

Oderwald, H

INTERNATIONAL SEARCH REPORT

Inter. Application No

PCT/US 01/06520

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X, L	WO 00 73454 A (GENENTECH INC) 7 December 2000 (2000-12-07) page 1 -page 2; claims 1-118; figures 3,4; examples 1-3,5,139-172 page 43 -page 44 page 283 -page 288 page 304 -page 316 page 338 page 371 -page 398 ---	1-24
P,X	WO 00 58473 A (CURAGEN CORP ;LEACH MARTIN (US); SHIMKETS RICHARD A (US)) 5 October 2000 (2000-10-05) see SEQ ID NOs: 3231 and 3232 (pp. 2436 and 2437) page 1 -page 4; claims 1-32 ---	1-24
E	WO 01 57190 A (CAO YICHENG ;CHEN RUI HONG (US); GOODRICH RYLE (US); HYSEQ INC (US) 9 August 2001 (2001-08-09) page 1 -page 97; claims 1-28; examples 1-9 -& DATABASE EM GSN [Online] EBI, Hinxton, UK; AC/ID AAK52618, "SEQ ID NO: 2147" XP002191775 abstract -& DATABASE EM GSP [Online] EBI, Hinxton, UK; AC/ID AAM78501, "SEQ ID NO: 1163" XP002191776 abstract -----	1-24

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 01/06520

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

Although claims 20 and 21 are directed to a method of treatment of the human/animal body (in so far as in vivo methods are concerned), the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-24 (all partially)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: claims 1-24 partially

An isolated nucleic acid SEQ ID NO: 1 which encodes amino acid sequence SEQ ID NO: 2. A vector, a host cell, a process for producing a polypeptide, an isolated polypeptide encoded by said nucleic acid. A chimeric molecule, an antibody, methods for stimulating the release of TNF-alpha, for stimulating the proliferation or differentiation, for detecting the presence of tumor, an oligonucleotide probe.

Inventions 2-305: claims 1-24 partially

same as invention 1 but comprising the polynucleotide and amino acid sequence in the order given in claims 1 and 2 (invention 2 is limited to SEQ ID NO: 3 and 4 and invention 305 is limited to SEQ ID NO: 609 and 610).

INTERNATIONAL SEARCH REPORT

Information on patent family members

Intern. Application No

PCT/US 01/06520

Patent document cited in search report		Publication date		Patent family member(s)	Publication date
WO 9963088	A	09-12-1999	AU	4328699 A	20-12-1999
			CA	2328895 A1	09-12-1999
			WO	9963088 A2	09-12-1999
			AU	2212299 A	26-07-1999
			WO	9935170 A2	15-07-1999

WO 9954461	A	28-10-1999	DE	19817948 A1	21-10-1999
			WO	9954461 A2	28-10-1999
			EP	1071775 A2	31-01-2001

WO 0073454	A	07-12-2000	AU	1748200 A	19-06-2000
			AU	1932000 A	03-07-2000
			AU	2192800 A	12-07-2000
			AU	2215300 A	28-12-2000
			AU	2495200 A	28-09-2000
			AU	2600800 A	28-09-2000
			AU	2879400 A	31-07-2001
			AU	3246100 A	28-12-2000
			AU	3381600 A	28-09-2000
			AU	3514400 A	28-09-2000
			AU	3774300 A	18-12-2000
			AU	4328699 A	20-12-1999
			AU	5441200 A	18-12-2000
			AU	5460100 A	18-12-2000
			AU	5591100 A	18-12-2000
			EP	1173563 A1	23-01-2002
			EP	1159419 A1	05-12-2001
			EP	1185648 A2	13-03-2002
			EP	1135485 A2	26-09-2001
			EP	1141285 A2	10-10-2001
			EP	1141289 A2	10-10-2001
			WO	0053753 A2	14-09-2000
			WO	0053755 A2	14-09-2000
			WO	0153486 A1	26-07-2001
			WO	0075327 A1	14-12-2000
			WO	0053757 A2	14-09-2000
			WO	0053758 A2	14-09-2000
			WO	0073454 A1	07-12-2000
			WO	0073445 A2	07-12-2000
			WO	0073348 A2	07-12-2000
			WO	0073452 A2	07-12-2000
			WO	0032221 A2	08-06-2000
			WO	0036102 A2	22-06-2000
			WO	0037640 A2	29-06-2000
			WO	0075316 A1	14-12-2000
			US	2002058309 A1	16-05-2002
			AU	2883600 A	28-09-2000
			AU	2883700 A	09-01-2001
			WO	0053756 A2	14-09-2000
			WO	0078961 A1	28-12-2000
			AU	2883900 A	30-01-2001
			WO	0104311 A1	18-01-2001
			AU	1749800 A	04-10-2000
			AU	1749900 A	12-07-2000
			AU	2390700 A	05-02-2001
			AU	2399300 A	28-09-2000
			AU	3107000 A	19-06-2000
			AU	4011300 A	05-02-2001

INTERNATIONAL SEARCH REPORT
Information on patent family members

International Application No
PCT/US 01/06520

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 0058473	A	05-10-2000	AU 3774500 A 16-10-2000
		EP 1165784 A2 02-01-2002	
		WO 0058473 A2 05-10-2000	
WO 0157190	A	09-08-2001	AU 2591801 A 31-07-2001
		AU 3128801 A 14-08-2001	
		AU 3297101 A 07-08-2001	
		AU 3300301 A 07-08-2001	
		AU 3329301 A 14-08-2001	
		AU 3484701 A 14-08-2001	
		AU 3484801 A 14-08-2001	
		AU 3486501 A 14-08-2001	
		AU 3494401 A 14-08-2001	
		AU 3665801 A 14-08-2001	
		AU 3666001 A 14-08-2001	
		AU 3666301 A 14-08-2001	
		AU 3672101 A 14-08-2001	
		AU 4314201 A 14-08-2001	
		WO 0153326 A1 26-07-2001	
		WO 0155334 A2 02-08-2001	
		WO 0155335 A2 02-08-2001	
		WO 0157255 A1 09-08-2001	
		WO 0157260 A1 09-08-2001	
		WO 0157175 A2 09-08-2001	
		WO 0157261 A1 09-08-2001	
		WO 0157262 A1 09-08-2001	
		WO 0157187 A2 09-08-2001	
		WO 0157265 A1 09-08-2001	
		WO 0157188 A2 09-08-2001	
		WO 0157266 A1 09-08-2001	
		WO 0157267 A1 09-08-2001	
		WO 0157190 A2 09-08-2001	